



A DOCPHOENIX

**APPL PARTS**

IMIS	NPL
Internal Misc. Paper	Non-Patent Literature
LET.	OATH
Misc. Incoming Letter	Oath or Declaration
371P	PET.
PCT Papers in a 371 Application	Petition
A...	RETMAL
Amendment Including Elections	Mail Returned by USPS
ABST	SEQLIST
Abstract	Sequence Listing
ADS	SPEC
Application Data Sheet	Specification
AF/D	SPEC NO
Affidavit or Exhibit Received	Specification Not in English
APPENDIX	TRNA
Appendix	Transmittal New Application
ARTIFACT	
Artifact	
BIB	CTMS
Bib Data Sheet	Misc. Office Action
CLM	1449
Claim	Signed 1449
COMPUTER	892
Computer Program Listing	
CRFL	ABN
All CRF Papers for Backfile	Abandonment
DIST	APDEC
Terminal Disclaimer Filed	Board of Appeals Decision
DRW	APEA
Drawings	Examiner Answer
FOR	CTAV
Foreign Reference	Count Advisory Action
FRPR	CTEQ
Foreign Priority Papers	Count Ex parte Quayle
IDS	CTFR
IDS Including 1449	Count Final Rejection

NPL	CTNF
Non-Patent Literature	Count Non-Final
OATH	CTRS
Oath or Declaration	Count Restriction
PET.	EXIN
Petition	Examiner Interview
RETMAL	M903
Mail Returned by USPS	DO/EO Acceptance
SEQLIST	M905
Sequence Listing	DO/EO Missing Requirement
SPEC	NFDR
Specification	Formal Drawing Required
SPEC NO	NOA
Specification Not in English	Notice of Allowance
TRNA	PETDEC
Transmittal New Application	Petition Decision

**OUTGOING**

CTMS	
Misc. Office Action	
1449	
Signed 1449	
892	
ABN	
Abandonment	
APDEC	
Board of Appeals Decision	
APEA	
Examiner Answer	
CTAV	
Count Advisory Action	
CTEQ	
Count Ex parte Quayle	
CTFR	
Count Final Rejection	

**INCOMING**

AP.B	
Appeal Brief	
C.AD	
Change of Address	
N/AP	
Notice of Appeal	
PA..	
Change in Power of Attorney	
REM	
Applicant Remarks in Amendment	
XT/	
Extension of Time filed separate	

**File Wrapper**

FWCLM	
File Wrapper Claim	
IIFW	
File Wrapper Issue Information	
SRFW	
File Wrapper Search Info	

<b>Internal</b>	ECBOX
	Evidence Copy Box Identification
SRNT	WCLM
Examiner Search Notes	Claim Worksheet
CLMPTO	WFEE
PTO Prepared Complete Claim Set	Fee Worksheet

ફાન્ડ કરી શકતું હોય એ કેવી રીતે કરી શકતું હોય

Seq num	Seq id	Contig Source	Primer 3 pos	Primer Basis	Selection Database Hit	ncbi gi	aat Score	Blast Prob	% id	% cvrg	Description	
17831	ENU01625	ANI61C30:45	67-86	NAP	483-504	g2462677	141	48	0.0004	27	(Z99568) hypothetical protein.	
17832	ENU01626	..	80,4101		69-89	490-512	NAP	g2909624	152	1.00E-36	44	[Schizosaccharomyces pombe] (AL021942) hypothetical protein Rv0565c [Mycobacterium tuberculosis]
17833	ENU01627	ANI61C7014:	54-75	481-500	NAP	3929..4417	g1353008	148	35	0.3	hypothetical 53.5 KD protein in GCD4-POS18 intergenic region ; hypothetical protein YJL123c - yeast (Saccharomyces cerevisiae) ; (Z49398) ORF YJL123c [Saccharomyces cerevisiae]	
17834	ENU01628	ANI61S4363:	37-65	462-483	NAP	554..66	g1352891	422	153	5.00E-37	44	40 putative glycosyltransferase HOCl precursor ; probable membrane protein YJR075w - yeast (Saccharomyces cerevisiae) ; (Z49575) ORF YJR075w [Saccharomyces cerevisiae] ; (L47993) ORF YJR075w [Saccharomyces cerevisiae] ; (U62942) Hoclip [Saccharomyces cerevisiae] (AL021748) hypothetical
17835	ENU01629	ANI61C2320:	22-47	444-468	NAP	1370..1858	g2842511	966	177	5.00E-44	50	[Schizosaccharomyces pombe] (AF072850) cytochrome p450 CYP4C19 [Lytechinus anamensis] (AL023287) probable helicase [Schizosaccharomyces pombe] (AF039713) Similar to phosphoglycerate mutase; coded for by C. elegans cDNA yk357d11.5; coded for by C. elegans cDNA yk38gc10.5; coded for by C. elegans cDNA yk384f12.5; coded for by C. elegans cDNA cml0f9; coded for by C. elegans cDNA cml1g...
17836	ENU01630	ANI61C347:2	39-60	468-487	NAP	134..2624	g3452329	194	93	1.00E-18	39	[Schizosaccharomyces pombe] (AF072850) cytochrome p450 CYP4C19 [Lytechinus anamensis] (AL023287) probable helicase [Schizosaccharomyces pombe] (AF039713) Similar to phosphoglycerate mutase; coded for by C. elegans cDNA yk357d11.5; coded for by C. elegans cDNA yk38gc10.5; coded for by C. elegans cDNA yk384f12.5; coded for by C. elegans cDNA cml0f9; coded for by C. elegans cDNA cml1g...
17837	ENU01631	ANI61C556:5	23-56	453-473	NAP	422..4929	g3116120	136	79	2.00E-14	27	[Schizosaccharomyces pombe] (AF039713) Similar to phosphoglycerate mutase; coded for by C. elegans cDNA yk357d11.5; coded for by C. elegans cDNA yk38gc10.5; coded for by C. elegans cDNA yk384f12.5; coded for by C. elegans cDNA cml0f9; coded for by C. elegans cDNA cml1g...
17838	ENU01632	ANI61C3163:	41-72	457-492	NAP	1048..555	g2773203	598	215	1.00E-55	61	[Schizosaccharomyces pombe] (AF039713) Similar to phosphoglycerate mutase; coded for by C. elegans cDNA yk357d11.5; coded for by C. elegans cDNA yk38gc10.5; coded for by C. elegans cDNA yk384f12.5; coded for by C. elegans cDNA cml0f9; coded for by C. elegans cDNA cml1g...
17839	ENU01633	ANI61C3353:	66-86	492-518	NAP	162..656	g2851420	253	79	2.00E-14	33	"hypothetical 88.1 KD protein in GLTS-SELC intergenic region ; (AE000443) orf, hypothetical protein [Escherichia coli]" (Z98330) ribosomal protein [Schizosaccharomyces pombe]
17840	ENU01634	ANI61C1118	52-71	478-506	NAP	5:8243..7747	g2330823	319	95	2.00E-24	65	

Seq num	Seq id	Contig	Source	Primer 3 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat	Blast Score	Blast Prob	% id	% cvrg	Description
17841	ENU01635	...		65-84	497-521	NAP	g2132957	75	3.00E-13	30	31			
17842	ENU01636	ANI61C4567:	48-74	486-505	NAP		g3135996	589	120	8.00E-27	41	32		probable membrane protein YOR378w - yeast ( <i>Saccharomyces cerevisiae</i> ); (Z75286) ORF YOR378w
17843	ENU01637	ANI61S483:3	27-50	466-485	NAP	4..534	g2137490	465	185	2.00E-46	54	27		[ <i>Saccharomyces cerevisiae</i> ] (AL023589) spliceosome-associated protein [Schizosaccharomyces pombe]; lymphocyte specific helicase - mouse; (U25691) lymphocyte specific helicase [Mus musculus]
17844	ENU01638	ANI61C2329:	27-47	457-488	NAP	4237..4740	g2330786	969	152	2.00E-36	47	40		(Z98601) diphospho-ovalonate decarboxylase [Schizosaccharomyces pombe] (AL031853) conserved ATP-GTP binding protein [Schizosaccharomyces pombe]
17845	ENU01639	ANI61C5098:	56-75	498-517	NAP	1101..598	g3738207	339	147	5.00E-35	43	50		(Z92774) fadD3 [Mycobacterium tuberculosis]
17846	ENU01640	ANI61C2362:	28-48	470-490	NAP	791..296	g1877292	206	52	9.00E-12	30	32		(Y17393) prefoldin subunit 2 [Mus musculus]
17847	ENU01641	ANI61C7547:	44-72	473-507	NAP	1875..2380	g3212116	127	63	0.000000	30	91		(L47106) kinesin [Neurospora crassa]
17848	ENU01642	ANI61C6627:	54-71	499-518	NAP	155..661	g1947184	579	122	4.00E-41	81	14		(AF015825) unknown [Bacillus subtilis]; (Z99110) yjIB [Bacillus subtilis]
17849	ENU01643	ANI61C1152:	23-54	466-489	NAP	509..1	g2612899	147	52	5.00E-10	35	95		(AL023794) putative proline oxidase precursor [Schizosaccharomyces pombe]
17850	ENU01644	ANI61C7562:	23-46	462-490	NAP	360..869	g3192023	187	101	5.00E-21	36	33		fruit protein PKIWI501 ; hypothetical protein - kiwi fruit; (L27810) pKIWI501 [ <i>Actinidia deliciosa</i> ] (D64003) hypothetical protein [Synechocystis sp.]
17851	ENU01645	ANI61C2007:	22-49	474-493	NAP	90..603	g1170600	140	36	0.14	30	91		"omega-6 fatty acid desaturase, endoplasmic reticulum (delta-12 desaturase); (L26296) delta-12 desaturase [ <i>Arabidopsis thaliana</i> ] " (ABO8078) oligo-1,4 - 1,4-glucantransferase / amyo-1,6-glucosidase [ <i>Saccharomyces cerevisiae</i> ] "
17852	ENU01646	ANI61C4822:	66-93	506-537	NAP	45..558	g1001214	443	156	1.00E-37	45	33		
17853	ENU01647	ANI61S344:1	33-54	475-505	NAP	2..526	g1169598	954	370	e-102	98	44		
17854	ENU01648	ANI61C5920:	62-81	505-536	NAP	821..305	g3986291	544	152	9.00E-41	57	9		

Seq num	Seq id	Contig Source	Primer 3 pos	Primer Basis	Selection Database Hit	aat ncbi gi	Score 922	Prob 202	% id 3.00E-62	% cvrg 83	% Description 27	
17855	ENU01649	ANI61C9533:	64-83	NAP	g4185903						(AJ132432) fimbriin [Gibberella pulicaria]	
17856	ENU01650	ANI61C4266:	42-67	NAP	g118774	1172	177	5.00E-44	60	21	DNA ligase (polydeoxyribonucleotide synthase (ATP)) ; DNA ligase (ATP) (EC 6.5.1.) - fission yeast (Schizosaccharomyces pombe) ; (X05107) DNA ligase	
17857	ENU01651	ANI61C8612:	72-90	528-550	NAP	g2131348	383	56	1.00E-16	39	26	[Schizosaccharomyces pombe] hypothetical protein YDL156w - yeast (Saccharomyces cerevisiae) ; (X97751) D1536 [Saccharomyces cerevisiae] ; (Z74204) ORF YDL156w [Saccharomyces cerevisiae]
17858	ENU01652	ANI61C6664:	68-87	531-550	NAP	g4538926	357	124	5.00E-28	43	23	(AL049483) putative phosphatidylserine decarboxylase [Arabidopsis thaliana]
17859	ENU01653	ANI61C7770:	41-65	505-526	NAP	g2494301	1373	271	3.00E-72	78	39	eukaryotic translation initiation factor 2 gamma subunit (EIF-2-gamma) ; (U37354) initiation factor eIF-2 gamma subunit [Schizosaccharomyces pombe] (AL031523) hypothetical protein [Schizosaccharomyces pombe]
17860	ENU01654	ANI61C4206:	49-68	508-534	NAP	g3560221	328	143	8.00E-34	43	50	glutathione peroxidase homolog YBR244W ; probable glutathione peroxidase (EC 1.11.1.9) - yeast (Saccharomyces cerevisiae) ; (Z36113) ORF YBR244w [Saccharomyces cerevisiae]
17861	ENU01655	ANI61C3455:	22-55	490-511	NAP	g585222	485	182	2.00E-45	60	90	general amino acid permease AGP2 ; probable amino acid transport protein YBR132c - yeast (Saccharomyces cerevisiae) ; (X75891) YBR1007
			1377..1908								[Saccharomyces cerevisiae] ; ORF YBR132c [Saccharomyces cerevisiae] ; YBR1007 gene [Saccharomyces cerevisiae]	
17862	ENU01656	ANI61C3754:	56-75	525-545	NAP	g586542	855	149	1.00E-35	41	29	
			5352..5883									

Seq num	Seq id	Contig Source	Primer 3 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
17863	ENU01657	ANI61C7497:	22-41	492-512	NAP	g729611	807	189	9.00E-48				GOG5vVRG4VAN2 ; vanadate resistance protein VAN2 - yeast (Saccharomyces cerevisiae); (L33915)
			932..400										vanadate resistant protein [Saccharomyces cerevisiae]; (U15599) Van2p [Saccharomyces cerevisiae]; (Z72747) ORF YGL225w [Saccharomyces cerevisiae]; VRG4 gene [Saccharomyces cerevisiae] (AF036546) protein kinase CK2 beta
17864	ENU01658	ANI61C9506:	61-82	531-551	NAP	g3093417	512	173	6.00E-43	49	58		subunit [Candida albicans]
		865..743				g731928	393	163	7.00E-40	46	73		hypothetical 27.4 KD protein in HYR1 3'region ; hypothetical protein YIR042c - yeast (Saccharomyces cerevisiae); (Z46902) unknown [Saccharomyces cerevisiae];
17865	ENU01659	ANI61C9637:	25-46	498-517	NAP	5288..5822							lactam utilization protein LAMB ; lactam utilization protein lambB - [Emericella nidulans] (AL031545) putative coatmer delta subunit [Schizosaccharomyces pombe] putative transporter C11D3.18C; (Z68166) unknown [Schizosaccharomyces pombe] (Y15277) cytochrome P450 monooxygenase [Gibberella fujikuroi] (AF080119) similar to Schizosaccharomyces pombe isp4 protein (GB:D14061) [Arabidopsis thaliana] (AF052586) beta-ketoacyl reductase [Pseudomonas aeruginosa] RTA1 protein ; RTA1 protein - yeast (Saccharomyces cerevisiae); (Z72998) ORF YGR213c [Saccharomyces cerevisiae]; (X84736) RTA1 [Saccharomyces cerevisiae]
17866	ENU01660	ANI61C8632:	50-78	525-544	NAP	1385..855	g583381	1296	257	4.00E-84	94	68	
17867	ENU01661	ANI61C1444:	66-85	542-561	NAP	1040..1577	g3581908	589	122	5.00E-49	70	67	
17868	ENU01662	ANI61C2252:	22-52	490-517	NAP	70..606	g1351714	103	47	0.00008	22	32	
17869	ENU01663	ANI61C2212:	29-51	506-525	NAP	2027..2565	g3549879	768	124	5.00E-28	49	30	
17870	ENU01664	ANI61C1102	45-64	522-543	NAP	7..562..22	g3600039	183	95	4.00E-19	30	23	
17871	ENU01665	ANI61C9234:	52-71	531-550	NAP		g2970667	215	56	8.00E-15	41	46	
		1247..707											[Pseudomonas aeruginosa]
17872	ENU01666	ANI61C322:4	53-73	538-559	NAP	374..4922	g1710802	199	75	3.00E-13	33	56	
													RTA1 protein ; RTA1 protein - yeast (Saccharomyces cerevisiae); (Z72998) ORF YGR213c [Saccharomyces cerevisiae]; (X84736) RTA1 [Saccharomyces cerevisiae]

Seq num	Seq id	Contig Source	Primer 3 pos	Primer 3 pos Basis	Selection Database Hit	ncbi gi	aat Score	Blast Prob Score	% id	% cvrg	Description		
17873	ENU01667	ANI61C8425:	22-46	NAP	g498-530	g466190	551	213	5.00E-55	54	80	ribosomal large subunit pseudouridine synthase B (pseudouridylate synthase) (uracil hydrolase); hypothetical protein X13 - <i>Bacillus subtilis</i> ; (L09228) ORF X13 [Bacillus subtilis]; (Z99116) similar to hypothetical proteins [Bacillus subtilis] (X82490) unnamed protein product	
17874	ENU01668	ANI61C461:8	54-74	NAP	539-563	58..1409	g2274947	177	79	2.00E-14	28	61	[ <i>Fusarium oxysporum</i> ] (AL023590) Glutathione S-transferase [Schizosaccharomyces pombe]
17875	ENU01669	ANI61C2346:	57-87	NAP	550-569	2599..2045	g3136036	189	68	1.00E-14	33	58	histidine biosynthesis bifunctional amidotransferase / cyclase; amidotransferase HIS7 (EC 2.4.2.-) / cyclase HIS7 - yeast ( <i>Saccharomyces cerevisiae</i> ); (Z36117) ORF YBR248c [Saccharomyces cerevisiae] hypothetical 57.2 KD protein in MET8-HPC2 intergenic region ; hypothetical protein YBR214w - yeast ( <i>Saccharomyces cerevisiae</i> ); (Z36083) ORF YBR214w [Saccharomyces cerevisiae]
17876	ENU01670	ANI61C6107:	62-94	NAP	555-576	5339..4783	g585255	588	231	2.00E-60	70	29	amidotransferase HIS7 (EC 2.4.2.-) / cyclase HIS7 - yeast ( <i>Saccharomyces cerevisiae</i> ); (Z36117) ORF YBR248c [Saccharomyces cerevisiae] hypothetical 57.2 KD protein in MET8-HPC2 intergenic region ; hypothetical protein YBR214w - yeast ( <i>Saccharomyces cerevisiae</i> ); (Z36083) ORF YBR214w [Saccharomyces cerevisiae]
17877	ENU01671	ANI61C3450:	72-96	NAP	677..120	g586334	307	77	8.00E-14	37	35	myo-inositol transporter 1 ; (X98622) [Schizosaccharomyces pombe] (Y11113) endoglucanase IV [ <i>Hypocrea jecorina</i> ] probable membrane protein YPL224c - yeast ( <i>Saccharomyces cerevisiae</i> ); (Z73580) ORF YPL224c [Saccharomyces cerevisiae] probable oxidoreductase homolog YJR096W; aldehyde reductase ( <i>Saccharomyces cerevisiae</i> ); (Z49596) ORF YJR096w [Saccharomyces cerevisiae] (U88308) C32E8.5 gene product	
17878	ENU01672	ANI61C1133	68-87	NAP	8..560..3	g2500938	380	127	7.00E-31	46	32	[ <i>Caenorhabditis elegans</i> ] (AF053318) CCR4-associated factor 1 [Homo sapiens]	
17879	ENU01673	ANI61C7642:	62-81	NAP	157..716	g2315274	220	87	7.00E-17	38	52	probable membrane protein YPL224c - yeast ( <i>Saccharomyces cerevisiae</i> ); (Z73580) ORF YPL224c [Saccharomyces cerevisiae] probable oxidoreductase homolog YJR096W; aldehyde reductase ( <i>Saccharomyces cerevisiae</i> ); (Z49596) ORF YJR096w [Saccharomyces cerevisiae] (U88308) C32E8.5 gene product	
17880	ENU01674	ANI61C3041:	22-46	NAP	202..762	g2133005	317	71	8.00E-19	38	36	[ <i>Caenorhabditis elegans</i> ] (AF053318) CCR4-associated factor 1 [Homo sapiens]	
17881	ENU01675	ANI61C8628:	41-60	NAP	2821..2259	g1176340	313	94	9.00E-21	36	57		

Seq num	Seq id	Contig Source	Primer 3 pos	Primer Basis	Selection	Blast aat	Blast Score	Prob	% id	% cvtg	Description	
17884	ENU01678	ANI61C1228:	45-64	NAP	g1706503	2105	135	3.00E-31	41	12	DNA polymerase alpha (DNA polymerase I) ; DNA-directed DNA polymerase (EC 2.7.7.) - yeast	
17885	ENU01679	ANI61C9640:	55-78	558-579	NAP	g1657510	1307	201	3.00E-51	52	37	(Saccharomyces cerevisiae) ; (Z71378) ORF YNL102w [Saccharomyces cerevisiae] (U73857) betaine-aldehyde dehydrogenase [Escherichia coli]
17886	ENU01680	ANI61C7173:	48-68	559-578	NAP	g2507155	179	59	0.000000	34	19	verprolin ; verprolin - yeast (Saccharomyces cerevisiae); (U19028) Vrp1p [Saccharomyces cerevisiae]; MDP2 gene [Saccharomyces cerevisiae]
17887	ENU01681	ANI61C7819:	72-91	586-605	NAP	g134976	359	45	0.0004			glucose transporter (sugar carrier) ; glucose transport protein STP1 - Arabidopsis thaliana ; (X55350) glucose transporter [Arabidopsis thaliana]
17888	ENU01682	ANI61C652:5	52-71	562-586	NAP	g1731385	334	96	2.00E-19	37	33	probable monooxygenase MTCY31.20 ; (Z73.01) hypothetical protein Rv0892 [Mycobacterium tuberculosis]
17889	ENU01683	ANI61C553:8:	22-41	537-558	NAP	g125886	475	77	1.00E-23	38	47	lactate 2-monooxygenase (lactate oxidase) ; lactate 2-monooxygenase (EC 1.13.12.4) - Mycobacterium smegmatis ; (I05402) L-lactate 2-monooxygenase [Mycobacterium smegmatis]
17890	ENU01684	ANI61C1189:	36-63	554-574	NAP	g401205	288	86	2.00E-16	41	97	tropomyosin ; tropomyosin - yeast (Schizosaccharomyces pombe) ; (L04126) tropomyosin [Schizosaccharomyces pombe] tropomyosin [Schizosaccharomyces pombe]
17891	ENU01685	ANI61C8980:	22-48	542-561	NAP	g730338	1174	262	2.00E-69	67	30	lysophospholipase precursor (phospholipase B) ; lysophospholipase (EC 3.1.1.5) - Penicillium notatum (fragment) ; (X60348) lysophospholipase [Penicillium chrysogenum]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database	Hit ncbi gi	aat Score	Blast Score	Prob	% id	% cvrg	Description
17892	ENU01686	ANI61C5264:	60..79	577..599	NAP	g1666269	328	149	2.00E-35	41	74	(Z8201)	cytochrome P450 [A garicus bisporus]
17893	ENU01687	ANI61C1059	25..55	543..566	NAP	g125399	724	214	3.00E-55				serine/threonine-protein kinase KIN28 (EC 2.7.1.-) - yeast (Saccharomyces cerevisiae); (X04423) protein kinase [Saccharomyces cerevisiae]; (X95644) ORF 2330 [Saccharomyces cerevisiae]; (Z7456) ORF YDL108w [Saccharomyces cerevisiae]; protein kinase [Saccharomyces cerevisiae]
17894	ENU01688	ANI61C2075:	22..46	539..563	NAP	g1170905	777	157	6.00E-38	61	50		24 KD metalloproteinase precursor (deuterolysin); metalloproteinase (EC 3.4.-) 23K - Aspergillus flavus; (L37524) metalloproteinase [Aspergillus flavus] dimethylglycine dehydrogenase precursor (ME2GLYDH); dimethylglycine dehydrogenase - rat; (X55995) dimethylglycine dehydrogenase [Rattus norvegicus] (Z98533) rho gdp dissociation inhibitor. [Schizosaccharomyces pombe]
17895	ENU01689	ANI61C2888:	24..44	537..567	NAP	g2498527	234	97	9.00E-20	36	21		
			6274..5689										"OVCA_1=candidate tumor suppressor [human, fetal brain, Peptide, 443 aa]"
17896	ENU01690	ANI61C8417;	58..78	585..606	NAP	g2330853	351	119	2.00E-26	45	74		
17897	ENU01691	ANI61C8659:	70..98	602..619	NAP	g3080529	223	101	6.00E-21	37	64		
17898	ENU01692	ANI61C8489:	23..42	551..573	NAP	g1723237	148	62	2.00E-12	31	12		
			699..107										
17899	ENU01693	ANI61C754:7	26..46	553..576	NAP	g1438796	1015	245	1.00E-64	61	43		
			86..194										

Seq num	Seq id	Contig Source	Primer 3 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
17900	ENU01694	ANI61C6597:	68-87	600-619	NAP	g132744	474	146	3.00E-38				"60S ribosomal protein L17 ; ribosomal protein L23 e, cytosolic - yeast (Saccharomyces cerevisiae); (X01694)
			8113..8706										ribosomal protein L17 [Saccharomyces cerevisiae]; (X79489) L23 B x-137
													[Saccharomyces cerevisiae]; (Z35848) ORF YBL087c [Saccharomyces cerevisiae]; (U18916) Rpl117bp: Ribosomal protein, large subunit [Saccharomyces cerevisiae]; (U15653) ribosomal protein L17B
17901	ENU01695	ANI61C6603:	36-55	571-590	NAP	g3426129	717	152	2.00E-36	47	13	"(AL031307) leptomycin B resistance protein, ABC transporter [Schizosaccharomyces pombe]" hypothetical 118.4 KD protein in WRS1-PKH2 intergenic region ; hypothetical protein YOL098c - yeast (Saccharomyces cerevisiae); (Z48149) similarity with D. melanogaster insulinase [Saccharomyces cerevisiae]; (Z74840) ORF YOL098c [Saccharomyces cerevisiae]"	
17903	ENU01697	ANI61C2471:	55-74	589-610	NAP	g3885329	560	210	7.00E-54	47	46	(AC005623) alien-like protein [Arabidopsis thaliana] (AB011003) UDP-N-	
17904	ENU01698	ANI61C7526:	23-42	557-579	NAP	g3413964	458	161	5.00E-39	55	36	[Candida albicans] probable 1-acetyl-SN-glycerol-3-phosphate acetyltransferase (1-AcGPA T)	
17905	ENU01699	ANI61C8576:	23-44	560-579	NAP	g464422	491	176	1.00E-43			(lysophosphatidic acid acyltransferase) (LPAAT) ; probable sn2:acylglyceride fatty acyltransferase (EC 2.3.1.-) - yeast (Saccharomyces cerevisiae); (L13282) acyltransferase [Saccharomyces cerevisiae]; (Z74100) ORF YDL052c [Saccharomyces cerevisiae]	

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat	Blast Score	Blast Prob	% id	% cvrg	Description
17906	ENU01700	ANI61C1038	22-55	55-578	NAP	g583972	461	161	5.00E-39	48	58	58	SCO2 protein precursor ; SCO1 protein homolog SCO2 - yeast (Saccharomyces cerevisiae) ; (X76078) YBR0308
17907	ENU01701	ANI61C9637:	72-91	604-629	NAP	g118109	560	214	3.00E-55				[Saccharomyces cerevisiae] ; ORF YBR0308
17908	ENU01702	ANI61C8628:	22-44	563-582	NAP	g2088561	165	84	9.00E-16	31	60	(PPIASE) (rotamase) (cyclophilin) (cyclosporin A-binding protein) (CPH) ; peptidyl-prolyl isomerase (EC 5.2.1.8) A - fission yeast (Schizosaccharomyces pombe) ; (X53223) cyclophilin (AA 1-162) [Schizosaccharomyces pombe] ; (D83992) peptidyl-prolyl cis-trans isomerase [Schizosaccharomyces pombe]	
17909	ENU01703	ANI61C5399:	71-92	603-632	NAP	g2808725	48	0.0004					(U95053) glutamate-cysteine ligase regulatory subunit [Mus musculus] (AL021428) hypothetical protein Rv0068 [Mycobacterium tuberculosis]
17910	ENU01704	ANI61C4146:	22-48	561-583	NAP	g1944416	617	134	5.00E-31	40	21		(D87078) similar to D.melanogaster pumilio protein (S22026); similar to human KIAA0099 protein(D43951) [Homo sapiens]
17911	ENU01705	ANI61C8125:	22-53	560-584	NAP	g117800	730	211	4.00E-54	60	73		cyanamide hydratase (urea hydrolyase) ; cyanamide hydratase (EC 4.2.1.69) - fungus (Myrothecium verrucaria) ; (M59078) cyanamide hydratase [Myrothecium verrucaria] (AL0222070) mago-nashi homolog [Schizosaccharomyces pombe]
17912	ENU01706	ANI61C9584:	22-53	553-586	NAP	g2950474	340	96	2.00E-19	57	97		[Schizosaccharomyces pombe] (AL033389) putative allantate permease [Schizosaccharomyces pombe]
17913	ENU01707	ANI61C5212:	72-97	611-638	NAP	g3850093	294	86	2.00E-16	33	36		60S ribosomal protein L15; (Y15321) putative ribosomal protein L15 [Aspergillus niger] (U24698) norsolorinic acid reductase [Aspergillus parasiticus]
17915	ENU01709	ANI61C1135	29-49	576-598	NAP	g1200177	916	85	3.00E-32	42	47		
		2:991..1603											

Seq num	Seq id	Contig Source	Primer 3 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	Score	Score	Blast Prob	% id	% cvrg	Description
17916	ENU01710	ANI61C1038	22-54	571-591	NAP	g1730665	121	61	0.000000	24	90	TIM23-ARE2 intergenic region ; probable membrane protein YNR018w ; -yeast ( <i>Saccharomyces cerevisiae</i> ) ; (Z71633) ORF YNR018w	
17917	ENU01711	ANI61C8430:	55-73	609-628	NAP	g2507240	213	88	6.00E-17	39	31	[ <i>Saccharomyces cerevisiae</i> ] aspartic proteinase 3 precursor (YAPSIN 1) ; aspergillopepsin I (EC 3.4.23.18) YAP3 precursor - yeast ( <i>Saccharomyces cerevisiae</i> ) ; (U53877) Yap3p; aspartic proteinase [Saccharomyces cerevisiae] ; (X89514) Aspartyl protease [ <i>Saccharomyces cerevisiae</i> ] ; (Z73292) ORF YLR120c [ <i>Saccharomyces cerevisiae</i> ]	
17918	ENU01712	ANI61C4637:	56-76	611-630	NAP	g2276352	429	173	1.00E-42	47	49	(Z97992) conserved hypothetical protein [ <i>Schizosaccharomyces pombe</i> ] succinate dehydrogenase (ubiquinone) iron-sulfur protein precursor (IP) ; (AF042062) succinate dehydrogenase iron-sulphur protein [ <i>Mycosphaerella graminicola</i> ] putative transporter C11D3.18C ; (Z68166) unknown	
17919	ENU01713	ANI61C9863:	22-44	571-596	NAP	g3334166	904	276	8.00E-74	81	57	[ <i>Schizosaccharomyces pombe</i> ] putative transporter C11D3.18C ; (Z68166) unknown	
17920	ENU01714	ANI61C9609:	26-47	582-602	NAP	g1351714	695	115	3.00E-26	36	40	[ <i>Schizosaccharomyces pombe</i> ] putative transporter C11D3.18C ; (Z68166) unknown	
17921	ENU01715	ANI61C9609:	26-47	582-602	NAP	g1351714	695	115	3.00E-26	36	40	[ <i>Schizosaccharomyces pombe</i> ] putative transporter C11D3.18C ; (Z68166) unknown	
17922	ENU01716	ANI61C6570:	24-52	582-601	NAP	g2388943	659	204	5.00E-52	53	52	"(Z98978) SPAC27E2.03c; putative gtp-binding protein, len:392a, a, similar eg. to YBR025C, YBN5_Yeast, P38219, hypothetica1_44.2_kd protein, (394aa), fasta scores, opt:664, E():0, (63.7% identity in 391 aa overlap), also sim... "	
17923	ENU01717	ANI61C9806:	25-44	584-606	NAP	g3810864	422	66	2.00E-18	36	53	(AL032681) alcohol dehydrogenase [ <i>Schizosaccharomyces pombe</i> ]	

Seq num	Seq id	Contig Source	Primer 3 pos	Primer Basis	Selection	aat	Blast Score	Blast Prob	% id	% cvrg	Description	
			5 pos	NAP	Database Hit	ncbi gi	Score	Prob				
17924	ENU01718	ANI61C3200:	47-66	597-630	g2498268	143	61	0.000000	36	36	copper transport protein CTR3 (copper transporter 3); probable membrane protein YLR411w - yeast	
		3021..2396									(Saccharomyces cerevisiae); (U20162)	
											Ctr3p [Saccharomyces cerevisiae]; (U81482) copper transporter 3	
											[Saccharomyces cerevisiae]	
17925	ENU01719	ANI61C5549:	60-81	622-644	NAP	g1723536	633	110	4.00E-39	42	25	probable eukaryotic translation initiation factor 3 beta subunit (EIF-3 beta); (Z70691) eukaryotic translation initiation factor 3 beta subunit (AL022117) putative o-
		191..818									methyltransferase	
											[Schizosaccharomyces pombe] (Z99162) farnesyltransferase beta subunit [Schizosaccharomyces pombe]	
17927	ENU01721	ANI61C4472:	58-79	611-642	NAP	g2408017	229	78	7.00E-22	41	39	(AL031545) hypothetical tyrosidine receptor domain containing protein [Schizosaccharomyces pombe]
		796..170									signal recognition particle 54 K protein homolog; signal recognition particle 54K protein homolog-Aspergillus niger; (L38317) sppA gene product [Aspergillus niger]; sppA gene product [Aspergillus niger]	
											(AF030296) ubiquitin conjugating enzyme UBC1 [Glomerella cingulata]	
17931	ENU01725	ANI61C3265:	67-88	639-658	NAP	g2352898	780	116	1.00E-49	52	50	(AF012091) cystein rich protein [Metarhizium anisopliae]
		1748..1480									"endo-1,4-beta-xylanase 2 precursor (xylanase 2) (1,4-beta-D-xylan xylanohydrolase 2); endo-1,4-beta-xylanase (EC 3.2.1.8) 2 precursor - Emericella nidulans; (Z49893)	
17932	ENU01726	ANI61C1074	46-65	617-639	NAP	g1722902	1116	250	5.00E-98	96	88	xylanase [Emericella nidulans]" hypothetical protein YOL151w - yeast
		6:1250..615									(Saccharomyces cerevisiae); (Z48239) orf2 [Saccharomyces cerevisiae]; (Z74893) ORF YOL151w	
											[Saccharomyces cerevisiae]	
17933	ENU01727	ANI61C7309:	63-82	626-657	NAP	g2132023	300	93	3.00E-20	33	55	
		1500..864										

Seq num	Seq id	Contig Source	Primer 3 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
17934	ENU01728	ANI61C3091:	44-64	617-638	NAP	g131622	281	65	4.00E-20				"phosphoribosylglycinamide formyltransferase (GART) (GAR transformylase)" (5'- phosphoribosylglycinamide transformylase); ADE8 protein - yeast (Saccharomyces cerevisiae); (M16585) ADE8 gene product [Saccharomyces cerevisiae]; (U32274) Ade8p: glycaminamide ribotide transformylase, EC number 2.1.2.2; YDR408C; CAI: 0.12 [Saccharomyces cerevisiae]; ADE8 gene [Saccharomyces cerevisiae]; ADE8 gene [Saccharomyces cerevisiae] "
17935	ENU01729	ANI61C468:2	30-49	605-624	NAP	g1351673	423	141	4.00E-33	42	57		hypothetical 37.7 KD protein C1F7.12 in chromosome I ; hypothetical protein SPAC1F7.12 - fission yeast (Schizosaccharomyces pombe); (Z67998) unknown
17936	ENU01730	ANI61C7926:	39-58	609-633	NAP	g23388903	558	210	7.00E-54	57	37		[Schizosaccharomyces pombe] (Z98974) putative cytochrome p450 [Schizosaccharomyces pombe]
17937	ENU01731	ANI61C1107	32-51	607-629	NAP	g2132219	249	72	7.00E-22	40	100		hypothetical protein YPL170w - yeast (Saccharomyces cerevisiae); (Z73526) ORF YPL170w [Saccharomyces cerevisiae] ; (X96770) P2515 protein [Saccharomyces cerevisiae]
17938	ENU01732	ANI61C6672:	56-76	629-653	NAP	g1730734	144	68	8.00E-11	24	17		hypothetical 128.1 KD protein in OMP2-MSC5 intergenic region; probable membrane protein YNL054w - yeast (Saccharomyces cerevisiae); (U12141) Ynl2467p [Saccharomyces cerevisiae] ; (Z71330) ORF YNL054w [Saccharomyces cerevisiae]
17939	ENU01733	ANI61S4240:	23-54	594-621	NAP	g2244937	997	334	3.00E-99	95	40		(Z97339) hypothetical protein [Arabidopsis thaliana]
17940	ENU01734	ANI61C354:1	35-54	619-638	NAP	g3850084	483	133	9.00E-31	41	61		(AL033389) alcohol dehydrogenase [Schizosaccharomyces pombe]

Seq num	Seq id	Contig Source	Primer 3 pos	Primer 3 pos Basis	Selection Database Hit	aat	Blast Score	Blast Prob	% id	% cvrg	Description	
17941	ENU01735	ANI61C1069	49-68	NAP	g2132301	219	62	0.000000	30	84	hypothetical protein YPR143w - yeast (Saccharomyces cerevisiae); (U40829) Note that there is an overlapping ORF on the other strand (27648-27085)	
17942	ENU01736	ANI61C1646:	72-91	641-676	NAP	g3581866	298	137	6.00E-32	40	76	(AL031541) putative dehydrogenase [Streptomyces coelicolor]
17943	ENU01737	ANI61C1050	23-55	611-633	NAP	g1083640	186	85	6.00E-16	26	39	cytochrome P450III - rat; (X79991) cytochrome P450II [Rattus norvegicus]; (D38381) P450 6beta-2 [Rattus norvegicus]; cytochrome P450 hypothetical 27.4 KD protein C30D10.14 in chromosome II ; (Z97992) conserved hypothetical protein [Schizosaccharomyces pombe] (Saccharomyces cerevisiae); (Z67750) putative protein [Saccharomyces cerevisiae]; (Z74214) ORF YDL166c [Saccharomyces cerevisiae]
17944	ENU01738	ANI61C1116	55-77	646-666	NAP	g3219917	212	64	4.00E-18	28	84	putative p450 monooxygenase [Emericella nidulans]
			0:1150..1803			g2131352	336	101	5.00E-21	48	87	probable sterigmatocystin biosynthesis P450 monooxygenase STCS (cytochrome P450 59); (U34740) putative p450 monooxygenase (cytochrome P450 59); (U34740) putative p450 monooxygenase
17945	ENU01739	ANI61C8325:	22-45	612-638	NAP	g2493387	2647	458	e-128	98	43	Deoxyhypusine synthase; (U22400) deoxyhypusine synthase [Neurospora crassa]
17946	ENU01740	ANI61C7771:	30-50	629-646	NAP	g1352268	911	325	1.00E-88	77	60	hypothetical 52.3 KD protein C56F8.06C in chromosome I precursor ; (Z69728) unknown
17947	ENU01741	ANI61C8376:	39..700	657-676	NAP	g1723438	219	74	8.00E-13	43	19	[Schizosaccharomyces pombe] (Z95395) hypothetical protein [Schizosaccharomyces pombe] (AL031825) putative membrane transport protein
17948	ENU01742	ANI61C744:7	32-54	632-651	NAP	g2462674	356	122	2.00E-27	32	57	[Schizosaccharomyces pombe] (Ydr257cp [Saccharomyces cerevisiae]); (U51030)
17949	ENU01743	ANI61C9987:	23-43	624-643	NAP	g3702646	276	104	6.00E-22	34	36	[Schizosaccharomyces pombe] (AL031825) putative membrane transport protein
17950	ENU01744	ANI61C2574:	22-54	620-642	NAP	g2131405	462	150	7.00E-36	51	51	[Schizosaccharomyces pombe] hypothetical protein YDR257c - yeast (Saccharomyces cerevisiae); (U51030)
17951	ENU01745	ANI61C3010:	49-69	651-670	NAP							
			256..920									

Seq num	Seq id	Contig Source	Primer 3 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
17952	ENU01746	ANI61C9890:	49-68	652-673	NAP	g549768	133	55	0.00000	5			hypothetical protein 61.1 KD protein in YPT52-DBP7 intergenic region ; hypothetical protein YKR016w - yeast (Saccharomyces cerevisiae) ; (Z28241) ORF YKR016w [Saccharomyces cerevisiae]
17953	ENU01747	ANI61C4162:	23-46	627-647	NAP	g3913152	919	336	1.00E-91	70	66		"alpha-L-arabinofuranosidase precursor (arabinoxylan arabinofuranohydrolyase) ; (Z78010) (1,4)-beta-D-arabinoxylan arabinofuranohydrolyase [Aspergillus tubingensis]"
17954	ENU01748	ANI61C8530:	43-63	647-668	NAP	g2492755	704	113	5.00E-50	54	72		sorbitol utilization protein SOU2 ; (AF02134) Sou2p [Candida albicans] (Z98533) putative ma-directed mta polymerase [Schizosaccharomyces pombe]
17955	ENU01749	ANI61C7365:	37-56	629-664	NAP	g2330856	841	75	5.00E-17	32	18		(U33007) hypothetical protein YDR440w - yeast (Saccharomyces cerevisiae) ; (U33007) Ydr440wp; CAI: 0.13 [Saccharomyces cerevisiae]
17956	ENU01750	ANI61C3463:	67-86	674-699	NAP	g2131494	346	91	8.00E-18	35	38		citrate transport protein - yeast (Saccharomyces cerevisiae); (X76053) YBR2039-ORF [Saccharomyces cerevisiae]; (Z36160) ORF YBR291c [Saccharomyces cerevisiae]; ORF YBR2039 [Saccharomyces cerevisiae] (Z99292) hypothetical protein [Schizosaccharomyces pombe] (L47321) glycoprotein 150 [Murine herpesvirus 68]; (Y09060) serine threonine rich glycoprotein [murine herpesvirus 68]; (U97553) glycoprotein 150 [murine herpesvirus 68]
17957	ENU01751	ANI61C8563:	22-44	632-656	NAP	g626251	280	47	1.00E-11				M-phase inducer phosphatase ; protein-tyrosine-phosphatase (EC 3.1.3.48) nimT - Emericella nidulans ; (X64601) NIMT/CDC25 [Emericella nidulans] (AL023776) hypothetical protein [Schizosaccharomyces pombe]
17958	ENU01752	ANI61C319:4	24-51	637-659	NAP	g2414577	431	88	1.00E-34	40	69		
17959	ENU01753	ANI61C331:1	40-59	660-679	NAP	g1333636	197	43	0.003				
17960	ENU01754	ANI61C737:1	25-48	648-667	NAP	g266564	1297	343	e-124	96	41		
17961	ENU01755	ANI61C8708:	32-59	656-675	NAP	g3184056	76	46	0.0002				

Seq num	Seq id	Contig	Source	Primer 3 pos	Primer 3 pos	Selection Basis	Database	Hit	ncbi	gi	aat	Blast Score	Blast Prob	% id	% cvrg	Description							
17962	ENU01756	ANI61C6889	47-66	g2132389	233	1.00E-60	57	73	"phosphate transport protein, mitochondrial - yeast (Saccharomyces cerevisiae) ; (X92441) YOR50-12 [Saccharomyces cerevisiae] ; (Z75130) ORF YOR222w [Saccharomyces cerevisiae]"														
17963	ENU01757	ANI61C70:24	22-45	645-667	NAP	g2496730	369	169	2.00E-41	40	55	hypothetical protein Y4OU precursor ; (AE000089) Y4OU [Rhizobium sp. NGR234]											
17964	ENU01758	ANI61C7798:	28-47	655-675	NAP	g2132397	344	134	5.00E-31	44	42	PO55 protein - yeast (Saccharomyces cerevisiae) ; (Z73544) ORF YPL188w [Saccharomyces cerevisiae]											
17965	ENU01759	ANI61C8193:	22-48	642-673	NAP	g1351368	360	100	2.00E-35	RNA polymerase II holoenzyme cyclin-like subunit ; cyclin homolog UME3 - yeast (Saccharomyces cerevisiae) ; (U20635) Ssn8p [Saccharomyces cerevisiae] ; (U20221) RNA polymerase II holoenzyme cyclin-like subunit [Saccharomyces cerevisiae] ; (U16248) cyclin [Saccharomyces cerevisiae] ; (Z71301) ORF YNL025c [Saccharomyces cerevisiae] ; RNA polymerase II regulatory protein [Saccharomyces cerevisiae]													
17966	ENU01760	ANI61C5471:	22-41	657-676	NAP	g1703215	283	129	2.00E-29	29	36	general alpha-glucoside permease ; alpha-glucoside transport protein - yeast (Saccharomyces cerevisiae) ; (Z73074) ORF YGR289c [Saccharomyces cerevisiae]											
17967	ENU01761	ANI61C9593:	22-49	655-677	NAP	g731806	707	270	5.00E-72	56	20	"probable calcium-transporting ATPase 7 ; probable membrane protein YIL048w - yeast (Saccharomyces cerevisiae) ; (Z38060) orf, len: 1151, CAI: 0.17, similar to S30768 S30768 probable ATPase - yeast (Saccharomyces cerevisiae)"											

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat	Blast Score	Blast Prob	% id	% cvrg	Description
17968	ENU01762	ANI61C1070	60..79	696..715	NAP	g1730823	610	136	2.00E-31	38	36	probable membrane protein YNL219c - probable mannosyltransferase ALG9 ; probable membrane protein YNL219c - yeast [Saccharomyces cerevisiae] ; (Z71495) ORF YNL219c	
17969	ENU01763	ANI61C7105: 22..44	652..680	NAP		g586542	859	95	1.00E-41	46	36	[Saccharomyces cerevisiae] ; [Saccharomyces cerevisiae]; YBR132c [Saccharomyces cerevisiae] ; YBR1007 gene [Saccharomyces cerevisiae]	
17970	ENU01764	ANI61C3637: 28..63	669..688	NAP		g2088525	352	83	4.00E-18	37	64	(U70619) heroin esterase [Rhodococcus sp.]	
17971	ENU01765	ANI61C1020: 53..76	695..714	NAP	706..3	g125935	137	65	5.00E-10	32	19	lactose permease ; lactose permease - yeast (Kluyveromyces marxianus var. lactis) ; (X06997) lactose permease (AA 1..587) [Kluyveromyces lacticis] (AL035226) major facilitator superfamily protein	
17972	ENU01766	ANI61C4189: 35..54	674..697	NAP	2709..2005	g4160574	519	63	2.00E-18	33	40	[Schizosaccharomyces pombe] (AL023589) membrane transporter [Schizosaccharomyces pombe] hypothetical 26.1 KD protein in POP4-SHM1 intergenic region ; hypothetical protein YBR261c - yeast (Saccharomyces cerevisiae) ; (X70529) ORF YBR1729 [Saccharomyces cerevisiae] ; (Z36130) ORF YBR261c [Saccharomyces cerevisiae]	
17973	ENU01767	ANI61C8086: 56..76	701..720	NAP	2503..1797	g3135989	619	183	1.00E-45	39	40	hypothetical 26.1 KD protein in POP4-SHM1 intergenic region ; hypothetical protein YBR261c - yeast (Saccharomyces cerevisiae) ; (X70529) ORF YBR1729 [Saccharomyces cerevisiae] ; (Z36130) ORF YBR261c [Saccharomyces cerevisiae]	
17974	ENU01768	ANI61C7151: 24..45	670..689	NAP	490..1197	g586379	359	120	6.00E-36	40	98	unknown ; (AF046024) UB43 [Homo sapiens] ; (AB012190) Nedd8-activating enzyme hUBA3 [Homo sapiens] (AL035396) SRG1-like protein [Arabidopsis thaliana] (AF06492) SONA [Emericella nidulans]	
17975	ENU01769	ANI61C8423: 39..59	686..705	NAP	208..916	g4507765	660	204	5.00E-52	46	53		
17976	ENU01770	ANI61C2775: 71..91	715..737	NAP		g4454019	45	0.00007					
17977	ENU01771	ANI61C9647: 36..55	681..704	NAP	1724..1014	g3202044	1440	496	c-140	98	65		

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Primer Basis	Selection	Blast gi	aat Score	Blast Prob	% id	% cvrg	Description	
						Database Hit	ncbi gi	889	301	3.00E-81	60	53	
17978	ENU01772	ANI61C7619:	70-89	711-738	NAP							"saccharopine dehydrogenase [NADP+, L-glutamate forming]; saccharopine dehydrogenase (NADP+, L-glutamate-forming) (EC 1.5.1.10)- yeast (Saccharomyces cerevisiae); (X77363) saccharopine dehydrogenase (NADP+, L-glutamate forming)	
			1340..630									[Saccharomyces cerevisiae]; (Z71665) ORF YNR050c [Saccharomyces cerevisiae]"	
17979	ENU01773	ANI61C1147	57-79	706-726	NAP	1..36..747	g2624697	823	266	5.00E-76	76	53	Pectin Lyase A
17980	ENU01774	ANI61C8541:	54-76	704-723	NAP	3665..2954	g1709941	298	106	2.00E-22	27	35	proline-specific permease ; proline transport protein - yeast (Saccharomyces cerevisiae); (X95720) O6345 [Saccharomyces cerevisiae]; (Z75256) ORF YOR348c
17981	ENU01775	ANI61C6911:	35-56	687-707	NAP	1061..347	g3130055	90	41	0.000000	28	64	[Saccharomyces cerevisiae] (AL023518) hypothetical protein
17982	ENU01776	ANI61C578:8	22-41	678-697	NAP	1..798	g1175461	212	75	5.00E-13			[Schizosaccharomyces pombe] "hypothetical 23.7 KD protein C13G6.14 in chromosome I"; hypothetical protein SPAC13G6.14 - fission yeast (Schizosaccharomyces pombe), hypothetical protein SPAC24B11.03 - fission yeast (Schizosaccharomyces pombe); (Z54308) hypothetical protein [Schizosaccharomyces pombe]; [Schizosaccharomyces pombe]; (Z67757) unknown
17983	ENU01777	ANI61C1120	22-41	680-699	NAP	8..2075..1355	g2500078	676	151	2.00E-55	68	94	[Schizosaccharomyces pombe] "RAS-2 protein ; (D16137) NC-ras-2 protein [Neurospora crassa]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Primer Basis	Selection	aat	Blast Score	Blast Prob	% id	% cvrg	Description
17984	ENU01778	ANI61C1029	22-51	680-699	NAP	g1730800	334	120	1.00E-37	37	85	hypothetical 28.8 KD protein in PSD1-SKO1 intergenic region ; hypothetical protein YNL168c - yeast
17985	ENU01779	ANI61C1253:	68-87	728-748	NAP	g1545805	653	102	9.00E-27	66	44	(Z71444) ORF YNL168c [Saccharomyces cerevisiae] (D64052) cytochrome P450 like _TBP [Nicotiana tabacum] (AL031534) Major facilitator superfamily protein
17986	ENU01780	ANI61C4046:	58-83	706-741	NAP	g3560142	680	132	3.00E-30	34	38	[Schizosaccharomyces pombe] xanthine dehydrogenase (purine hydroxylase I) ; xanthine dehydrogenase (EC 1.1.1.204) - Emericella nidulans ; (X82827) xanthine dehydrogenase [Emericella nidulans]
17987	ENU01781	ANI61C6939:	61-80	729-748	NAP	g2493965	729	218	5.00E-70	64	15	hypothetical 143.7 KD protein C11D3.15 in chromosome I ; (Z68166) unknown [Schizosaccharomyces pombe] (Z99118) similar to opine catabolism [Bacillus subtilis] (AE000680) glutamyl-tRNA (Gln) amidotransferase subunit A [Aquifex aeolicus] (AP000003) 388aa long hypothetical amino acid amidohydrolase [Pyrococcus horikoshii] (AJ001909) transcriptional activator [Aspergillus niger] O-methylsterigmatocystin oxidoreductase (OMST oxidoreductase) (cytochrome P450 64) ; (U81806) OMST-oxidoreductase [Aspergillus flavus] ; (U81807) OMST-oxidoreductase [Aspergillus flavus]
17988	ENU01782	ANI61C6754:	25-45	693-712	NAP	g1351711	3300	181	9.00E-72	59	18	hypothetical 143.7 KD protein C11D3.15 in chromosome I ; (Z68166) unknown [Schizosaccharomyces pombe] (Z99118) similar to opine catabolism [Bacillus subtilis] (AE000680) glutamyl-tRNA (Gln) amidotransferase subunit A [Aquifex aeolicus] (AP000003) 388aa long hypothetical amino acid amidohydrolase [Pyrococcus horikoshii] (AJ001909) transcriptional activator [Aspergillus niger] O-methylsterigmatocystin oxidoreductase (OMST oxidoreductase) (cytochrome P450 64) ; (U81806) OMST-oxidoreductase [Aspergillus flavus] ; (U81807) OMST-oxidoreductase [Aspergillus flavus]
17989	ENU01783	ANI61C177:2	43-62	713-732	NAP	g2635242	234	93	2.00E-18	31	61	hypothetical 143.7 KD protein C11D3.15 in chromosome I ; (Z68166) unknown [Schizosaccharomyces pombe] (Z99118) similar to opine catabolism [Bacillus subtilis] (AE000680) glutamyl-tRNA (Gln) amidotransferase subunit A [Aquifex aeolicus] (AP000003) 388aa long hypothetical amino acid amidohydrolase [Pyrococcus horikoshii] (AJ001909) transcriptional activator [Aspergillus niger] O-methylsterigmatocystin oxidoreductase (OMST oxidoreductase) (cytochrome P450 64) ; (U81806) OMST-oxidoreductase [Aspergillus flavus] ; (U81807) OMST-oxidoreductase [Aspergillus flavus]
17990	ENU01784	ANI61C6621:	25-44	696-715	NAP	g2982954	658	139	1.00E-32	42	44	hypothetical 143.7 KD protein C11D3.15 in chromosome I ; (Z68166) unknown [Schizosaccharomyces pombe] (Z99118) similar to opine catabolism [Bacillus subtilis] (AE000680) glutamyl-tRNA (Gln) amidotransferase subunit A [Aquifex aeolicus] (AP000003) 388aa long hypothetical amino acid amidohydrolase [Pyrococcus horikoshii] (AJ001909) transcriptional activator [Aspergillus niger] O-methylsterigmatocystin oxidoreductase (OMST oxidoreductase) (cytochrome P450 64) ; (U81806) OMST-oxidoreductase [Aspergillus flavus] ; (U81807) OMST-oxidoreductase [Aspergillus flavus]
17991	ENU01785	ANI61C1038	24-43	689-714	NAP	g3257130	388	109	2.00E-23	35	57	hypothetical 143.7 KD protein C11D3.15 in chromosome I ; (Z68166) unknown [Schizosaccharomyces pombe] (Z99118) similar to opine catabolism [Bacillus subtilis] (AE000680) glutamyl-tRNA (Gln) amidotransferase subunit A [Aquifex aeolicus] (AP000003) 388aa long hypothetical amino acid amidohydrolase [Pyrococcus horikoshii] (AJ001909) transcriptional activator [Aspergillus niger] O-methylsterigmatocystin oxidoreductase (OMST oxidoreductase) (cytochrome P450 64) ; (U81806) OMST-oxidoreductase [Aspergillus flavus] ; (U81807) OMST-oxidoreductase [Aspergillus flavus]
17992	ENU01786	ANI61C380:1	26-49	698-717	NAP	g2808634	545	150	1.00E-35	46	20	hypothetical 143.7 KD protein C11D3.15 in chromosome I ; (Z68166) unknown [Schizosaccharomyces pombe] (Z99118) similar to opine catabolism [Bacillus subtilis] (AE000680) glutamyl-tRNA (Gln) amidotransferase subunit A [Aquifex aeolicus] (AP000003) 388aa long hypothetical amino acid amidohydrolase [Pyrococcus horikoshii] (AJ001909) transcriptional activator [Aspergillus niger] O-methylsterigmatocystin oxidoreductase (OMST oxidoreductase) (cytochrome P450 64) ; (U81806) OMST-oxidoreductase [Aspergillus flavus] ; (U81807) OMST-oxidoreductase [Aspergillus flavus]
17993	ENU01787	ANI61C124:7	27-47	700-719	NAP	g3914244	70	2.00E-15				hypothetical 143.7 KD protein C11D3.15 in chromosome I ; (Z68166) unknown [Schizosaccharomyces pombe] (Z99118) similar to opine catabolism [Bacillus subtilis] (AE000680) glutamyl-tRNA (Gln) amidotransferase subunit A [Aquifex aeolicus] (AP000003) 388aa long hypothetical amino acid amidohydrolase [Pyrococcus horikoshii] (AJ001909) transcriptional activator [Aspergillus niger] O-methylsterigmatocystin oxidoreductase (OMST oxidoreductase) (cytochrome P450 64) ; (U81806) OMST-oxidoreductase [Aspergillus flavus] ; (U81807) OMST-oxidoreductase [Aspergillus flavus]
			..741									

Seq num	Seq id	Contig Source	Primer 3 pos	Primer 3 pos Basis	Selection Database Hit	aat	Blast Score	Blast Prob	% id	% cvrg	Description	
17994	ENU01788	ANI61C3719:	67-90	NAP	g1352938	479	188	4.00E-47	43	61	hypothetical protein 39.7 KD protein in HOM6-PMT4 intergenic region ; hypothetical protein YJR142w - yeast (Saccharomyces cerevisiae) ; (Z49642) ORF YJR142w [Saccharomyces cerevisiae]	
17995	ENU01789	ANI61C846:2	22-49	700-719	NAP	g1351369	850	275	3.00E-73	60	41	meiotic mRNA stability protein kinase UME5 ; (U20222) Srb10p [Saccharomyces cerevisiae] ; RNA polymerase II regulatory protein [Saccharomyces cerevisiae]
17996	ENU01790	ANI61C8292:	22-57	699-720	NAP	g118066	495	186	1.00E-46	41	45	cyclohexanone monooxygenase ; (M19029) cyclohexanone monooxygenase [Acinetobacter sp.] putative CDP-diacylglycerol--serine O-phosphatidyltransferase (phosphatidylserine synthase) ; (Z86109) unknown [Saccharomyces pastorianus]
17997	ENU01791	ANI61C2524:	60-80	738-759	NAP	g2493572	414	175	2.00E-43	41	45	hypothetical 150.9 KD protein C6G9_04 in chromosome I ; (Z81317) hypothetical protein [Schizosaccharomyces pombe] (Z98595) putative snf2 family helicase [Schizosaccharomyces pombe] choline transport protein ; choline transport protein - yeast (Saccharomyces cerevisiae) ; (J05603) choline transport protein [Saccharomyces cerevisiae] ; (Z72599) ORF YGL077c [Saccharomyces cerevisiae]
17998	ENU01792	ANI61C1071	32-51	713-737	NAP	g2842695	79	58	0.000000	23	17	[Schizosaccharomyces pombe] (Z98595) putative snf2 family helicase [Schizosaccharomyces pombe] choline transport protein ; choline transport protein - yeast (Saccharomyces cerevisiae) ; (J05603) choline transport protein [Saccharomyces cerevisiae] ; (Z72599) ORF YGL077c [Saccharomyces cerevisiae]
17999	ENU01793	ANI61C3292:	63-83	749-769	NAP	g2330659	222	59	2.00E-14	29	16	hypothetical protein
18000	ENU01794	ANI61S1000:	52-71	738-759	NAP	g117619	76	3.00E-13	30	37	choline transport protein [Saccharomyces cerevisiae] ; (Z72599) ORF YGL077c [Saccharomyces cerevisiae]	

Seq num	Seq id	Contig Source	Primer 3 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat	Blast Score	Blast Prob	% id	% covrg	Description
18001	ENU01795	ANI61C5352:	57-83	748-768	NAP	g3123159	493	202	1.00E-51	45	60	60	hypothetical protein 40_4_KD TRP-ASP repeats containing protein C14B1.4 in chromosome III ; (Z37139) similar to guanine nucleotide binding protein; cDNA EST EMBL:T00917 comes from this gene; cDNA EST CEMSE07F comes from this gene; cDNA EST EMBL:T00918 comes from this gene; cDNA EST EMBL:D70900 comes from this gene; cD...
18002	ENU01796	ANI61C6476:	68-89	750-781	NAP	g2804298	680	92	6.00E-31	37	39	(AB010439) steroid monooxygenase [Rhodococcus rhodochrous] (AC000133) ORF [Emericella nidulans]	
18003	ENU01797	ANI61C1116	61-80	749-775	NAP	g1870210	1452	481	e-135	98	53	(AL031174) beta-transducin [Schizosaccharomyces pombe] putative seryl-tRNA synthetase YHR011W (serine--tRNA ligase) (SERRS) ; serine--tRNA ligase homolog - yeast (Saccharomyces cerevisiae) ; (U10400) Yhr011wp [Saccharomyces cerevisiae]	
18006	ENU01800	ANI50C2350	23-58	720-744	NAP	g3560242	251	2.00E-67	55	75	"(AL031532) yeast gtr2 homolog, novel small GTPase subfamily protein [Schizosaccharomyces pombe]" putative flavin-containing monoamine oxidase MTV014_14 ; (AL021646) hypothetical protein Rv3170 [Mycobacterium tuberculosis] (AF097728) pyruvate carboxylase [Aspergillus terreus]		
18007	ENU01801	ANI61C1420:	22-47	724-743	NAP	g3913051	244	76	3.00E-13	30	55	RAS-related protein RAB-11B ; GTP-binding protein Rab11b - mouse ; (L26528) Rab11b [Mus musculus] ("D86544) hydroxyquinol-1,2-dioxygenase [Raistonia picketti]"	
18008	ENU01802	ANI61C6541:	22-44	723-744	NAP	g3806120	3163	392	e-108	89	19		
18009	ENU01803	ANI61C1003	22-56	726-750	NAP	g1172815	699	251	6.00E-74	78	91		
18010	ENU01804	ANI50C6358	47-73	756-775	NAP	g1437475	151	3.00E-42	40	80			
		_1..803..33											

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	.ncbi gi	Score	Score Prob	% id	% cvrg	Description
18011	ENU01805	ANI61C8273:	72-91	771-803	NAP	g1346665	128	53	0.000002 35	35	33	"N-terminal acetyltransferase 2 (amino-terminal, alpha-amino, acetyltransferase 2); protein N-acetyltransferase (EC 2.3.1.-) NAT2 - yeast [Saccharomyces cerevisiae]; (X85807) ORF G6630 [Saccharomyces cerevisiae]; (Z72932) ORF YGR147c [Saccharomyces cerevisiae]"
18012	ENU01806	ANI61C3339:	54-73	756-786	NAP	g2132957	768	271	5.00E-72 53	49	49	probable membrane protein YOR378w - yeast [Saccharomyces cerevisiae]; (Z75286) ORF YOR378w [Saccharomyces cerevisiae] (Y17243) cytochrome P450 [Gibberella fujikuroi]
18013	ENU01807	ANI61C3910:	51-70	765-784	NAP	g4127832	220	106	2.00E-22 32	46	46	(AL021839) myb family DNA binding protein [Schizosaccharomyces pombe]
18014	ENU01808	ANI61C1094	43-62	743-778	NAP	g2894269	225	68	8.00E-11 44	29	29	phosphoribosylaminoimidazole carboxylase (AIR carboxylase) (AIRC); (UT0673)
18015	ENU01809	ANI61C9734:	54-73	758-790	NAP	g2500019	1081	123	5.00E-29 48	39	39	phosphoribosylaminoimidazole carboxylase [Filobasidiella neoformans]
18016	ENU01810	ANI61C9817:	35-54	748-773	NAP	g1352887	525	157	7.00E-43 51	70	70	hypothetical protein in HAM1-PEM2 intergenic region; hypothetical protein YJR070c - yeast (Saccharomyces cerevisiae); (Z49570) ORF YJR070c [Saccharomyces cerevisiae]; (L47993) ORF YJR070c [Saccharomyces cerevisiae]
18017	ENU01811	ANI61C8177:	35-54	755-774	NAP	g4507053	223	85	5.00E-16 34	45	45	unknown ; (D87432) Similar to Schistosoma mansoni amino acid permease (L23068). [Homo sapiens] (D17548) protein-tyrosine phosphatase [Saccharomyces cerevisiae]; (X98493) ACC oxidase [Nicotiana tabacum]
18018	ENU01812	ANI61C7083:	38-58	762-781	NAP	g459243	155	86	3.00E-16 33	29	29	(X63998) aminopeptidase yscII [Saccharomyces cerevisiae]
18019	ENU01813	ANI61C1049	37-57	758-780	NAP	g2826769	83	2.00E-15				(AL023796) cyclin C homologue [Schizosaccharomyces pombe]
18020	ENU01814	ANI61C1857:	39-58	765-783	NAP	g3368	2245	207	8.00E-53 41	28	28	(X63998) aminopeptidase yscII [Saccharomyces cerevisiae]
18021	ENU01815	ANI61C5906:	27-46	753-772	NAP	g3192038	395	129	3.00E-29 32	74	74	(AL023796) cyclin C homologue [Schizosaccharomyces pombe]
			1318..531									

Seq num	Seq id	Contig Source	Primer 3 pos	Primer 3 pos Basis	Selection Database Hit	aat ncbi gi	Score	Score Prob	% id	% cvrg	Description
18022	ENU01816	ANI61C9151:	22-53	NAP	g2500768	963	190	5.00E-66	61	66	Septin homolog [Schizosaccharomyces pombe]
18023	ENU01817	ANI61C9777:	58-78	NAP	g2665711	82	1.00E-19				(AF035413) AgaG [Agrobacterium tumefaciens]
18024	ENU01818	ANI61C9875:	52-71	NAP	g1705594	1074	327	6.00E-89	67	47	peroxisome assembly protein CAR1 (peroxin-2) ; car1 protein - Podospora anserina ; (X87329) peroxisome assembly factor [Podospora anserina]
18025	ENU01819	ANI61C6977:	22-46	NAP	g1077411	721	240	8.00E-67	56	20	hypothetical protein YLR189c - yeast (Saccharomyces cerevisiae) ; (U17246) Ylr189cp [Saccharomyces cerevisiae] (AJ009657) Mu3 subunit of clathrin-associated protein complex AP-3 [Drosophila melanogaster]
18026	ENU01820	ANI61C1134:	22-43	NAP	g3341417	62	2.00E-20				"asparaginyl-tRNA synthetase, mitochondrial precursor (asparagine-tRNA ligase) (ASNRS) ; hypothetical protein YCR024c - yeast (Saccharomyces cerevisiae) ; (X59720) YCR024c, len492 [Saccharomyces cerevisiae]"
18027	ENU01821	ANI61C1485:	25-44	NAP	g135160	639	165	3.00E-40	40	51	"asparaginyl-tRNA synthetase, mitochondrial import receptor subunit TOM40 (MOM38 protein) (translocase of outer membrane 40 KD subunit) ; mitochondrial import receptor MOM38 - Neurospora crassa ; (X56883) outer membrane protein [Neurospora crassa] ; outer membrane protein MOM38 [Neurospora crassa]
18028	ENU01822	ANI61C5728:	24-46	NAP	g3925768	675	115	9.00E-34	46	70	(AL034352) putative GTP-binding protein [Schizosaccharomyces pombe] (AF095899) PDI related protein A [Aspergillus niger]
18029	ENU01823	ANI61C8692:	56-75	NAP	g3873259	1526	257	5.00E-68	58	56	mitochondrial import receptor subunit TOM40 (MOM38 protein) (translocase of outer membrane 40 KD subunit) ; mitochondrial import receptor MOM38 - Neurospora crassa ; (X56883) outer membrane protein [Neurospora crassa] ; outer membrane protein MOM38 [Neurospora crassa]
18030	ENU01824	ANI61C7436:	58-77	NAP	g127218	924	257	5.00E-68	57	66	actin interacting protein 2 ; AIP2 protein - yeast (Saccharomyces cerevisiae) ; (U35667) Aip2p [Saccharomyces cerevisiae] ; (Z67750) putative protein [Saccharomyces cerevisiae] ; (Z74226) ORF YDL178w [Saccharomyces cerevisiae]
18031	ENU01825	ANI61C3438:	22-45	NAP	g1168396	833	298	2.00E-80	58	50	
			1120..309								

Seq num	Seq id	Contig Source	5' pos	Primer 3' pos	Primer Basis	Selection Database	Hit	.ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18032	ENU01826	ANI61C1214:	24..52	780..799	NAP	g130806	249	56	0.000000	35	22	3		pre-mRNA processing RNA helicase PRPs ; pre-mRNA processing protein PRPs - yeast (Saccharomyces cerevisiae) ; (M33191) PRPs [Saccharomyces cerevisiae] ; (Z36106) ORF YBR237w [Saccharomyces cerevisiae]
18033	ENU01827	ANI61C5721:	22..51	769..799	NAP	g2498971	369	56	4.00E-28	36	54			putative sterigmatocystin biosynthesis monooxygenase STCW ; (U34740)
18034	ENU01828	ANI61C5721:	22..51	769..799	NAP	g2498971	369	56	4.00E-28	36	54			putative FAD-containing monooxygenase [Emericella nidulans] putative sterigmatocystin biosynthesis monooxygenase STCW ; (U34740) putative FAD-containing monooxygenase [Emericella nidulans] (AC006223) hypothetical protein [Arabidopsis thaliana]
18035	ENU01829	ANI61C9612:	22..53	767..799	NAP	g4263703	221	101	2.00E-23	33	53			putative DNA-directed RNA polymerase III 130 KD polypeptide (RNA polymerase III subunit 2) ; (Z69727) putative DNA-directed RNA polymerase III 130 kd subunit [Schizosaccharomyces pombe] (AL034382) putative spindle pole body component, putative gamma-tubulin interacting protein, yeast SCP98 homolog [Schizosaccharomyces pombe]"
18037	ENU01831	ANI61C7971:	22..51	783..813	NAP	g3947884	625	146	2.00E-34	48	70			(AF05286) guanine deaminase GDA [Homo sapiens]
18039	ENU01833	ANI61C5959:	51..70	827..849	NAP	g115699	1548	226	2.00E-90	58	57			"catalase (PXP-9) ; catalase (EC 1.11.1.6), peroxisomal - yeast (Candida tropicalis) ; (X13978) catalase (AA 1 - 485) [Candida tropicalis] ; (X06660) catalase (AA 1 - 485) [Candida tropicalis] ; peroxisomal catalase [Candida tropicalis]" (Z99261) putative aminotransferase [Schizosaccharomyces pombe]
18040	ENU01834	ANI61C9843:	55..74	837..856	NAP	g2414656	694	234	7.00E-61	47	54			

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18041	ENU01835	ANI61C1438:	24-45	807-826	NAP	g2127591	137	57	0.000000	29	81	N-acetyl/phosphinothricin-tripeptide-deacetylase - Streptomyces viridochromogenes ; (X65195) N-acetylphosphinothricin-tripeptide-deacetylase [Streptomyces viridochromogenes]	
18042	ENU01836	ANI61C1600:	24-43	811-831	NAP	g2293194	289	89	2.00E-32	(AF008220) yteR [Bacillus subtilis]; (Z99119) similar to hypothetical proteins [Bacillus subtilis]			
18043	ENU01837	ANI61C6951:	26-45	816-835	NAP	g4050050	648	159	8.00E-72	54	82	(AL031180) putative 2-hydroxyacid dehydrogenase [Schizosaccharomyces pombe]	
18044	ENU01838	ANI61C9508:	32-55	817-842	NAP	g3395556	676	66	2.00E-32	51	59	sporulation protein SPS19 (sporulation-specific protein SPX19); sporulation protein SPS19 - yeast (Saccharomyces cerevisiae); (X78898) NI1362	
18045	ENU01839	ANI61C7122:	57-77	845-867	NAP	g730864	506	152	3.00E-38	53	71	[Saccharomyces cerevisiae]; (Z71479) ORF YNL202w [Saccharomyces cerevisiae]	
18046	ENU01840	ANI61C1011	68-87	860-879	NAP	g2494910	1455	255	3.00E-67	47	33	hypothetical 91.7 KD TRP-ASP repeats containing protein in NUP116-FAR3 intergenic region ; probable membrane protein YMR049c - yeast (Saccharomyces cerevisiae); (Z49703) unknown [Saccharomyces cerevisiae] (Z75526) Weak similarity to Staphylococcus autolysin gene (TR-G765072); cDNA EST EMBL:M89336 comes from this gene; cDNA EST yk505d12.3 comes from this gene [Caenorhabditis elegans] (AC004850) vacuolar assembly protein VPS41 homolog (S53) [Homo sapiens] mutS (E. coli) homolog 3 ; (U61981) hMSH3 [Homo sapiens] (U09352) 67 kDa Myosin-crossreactive streptococcal antigen [Streptococcus pyogenum]	
18047	ENU01841	ANI61C122:1	47-69	840-859	NAP	g3874039	295	90	2.00E-17	42	27		
18048	ENU01842	ANI61C8569:	40-65	834-853	NAP	g4309891	317	124	7.00E-28	37	33		
18049	ENU01843	ANI61C2388:	49-69	843-863	NAP	g4505249	1372	278	4.00E-74	48	25		
18050	ENU01844	ANI61C3304:	22-45	814-836	NAP	g517205	305	149	3.00E-35	33	47		
			3423..2567										

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18051	ENU01845	ANI61C924:4	70-92	867-890	NAP	g3810847	341	161	8.00E-39	39	37	(AL032684) zinc finger protein	
18052	ENU01846	ANI61C8857:	29-48	824-854	NAP	g2492894	1809	331	5.00E-90	56	13	[Schizosaccharomyces pombe] adenylylate cyclase (ATP pyrophosphate-lyase) (adenylyl cyclase); adenylylate cyclase (EC 4.6.1.1) - Podospora anserina ; (L43413) adenylyl cyclase [Podospora anserina]	
18053	ENU01847	ANI61C4219:	44-68	850-869	NAP	g2132252	703	74	1.00E-12	28	40	[Saccharomyces cerevisiae]; (Z73619) hypothetical protein YPL263c - yeast ORF YPL263c [Saccharomyces cerevisiae]	
18054	ENU01848	ANI61C5719:	49-79	856-878	NAP	g1717749	522	153	1.00E-45	41	32	"potassium transport protein ; (Z69369) SPAC3F10.02c; potassium transport gene, len: 841, co nflct with PIR:S50225 potassium transport protein homolog at position 4549 causes frameshift near N-terminus [Schizosaccharomyces pombe]" hypothetical 37.2 KD protein C12C2.09C in chromosome II ; (Z54140) conserved hypothetical protein [Schizosaccharomyces pombe] (AL022298) UDP-galactose transporter homologue [Schizosaccharomyces pombe]	
18055	ENU01849	ANI61C6777:	50-69	854-881	NAP	g1175428	583	229	3.00E-59	41	89	[AL023592] zinc finger protein [Schizosaccharomyces pombe] alcohol dehydrogenase III ; alcohol dehydrogenase (EC 1.1.1.1) III - Emericella nidulans ; (X02764) alcohol dehydrogenase 3 [Emericella nidulans] (U94348) acetyl-coenzyme A synthetase [Pyrobaculum aerophilum] (U38783) orf of unknown function; Method: conceptual translation supplied by author	
18056	ENU01850	ANI61C8505:	59-79	870-891	NAP	g3080508	510	168	4.00E-41	45	68	[Schizosaccharomyces pombe] (AL023592) zinc finger protein C12C2.09C in chromosome II ; (Z54140) conserved hypothetical protein [Schizosaccharomyces pombe] (AL022298) UDP-galactose transporter homologue [Schizosaccharomyces pombe]	
18057	ENU01851	ANI61C8544:	72-93	880-904	NAP	g3136060	281	145	5.00E-34	34	59	[Schizosaccharomyces pombe] alcohol dehydrogenase III ; alcohol dehydrogenase (EC 1.1.1.1) III - Emericella nidulans ; (X02764) alcohol dehydrogenase 3 [Emericella nidulans] (U94348) acetyl-coenzyme A synthetase [Pyrobaculum aerophilum] (U38783) orf of unknown function; Method: conceptual translation supplied by author	
18058	ENU01852	ANI61C7094:	42-61	863-882	NAP	g113382	323	50	0.00002	36	58	[Schizosaccharomyces pombe] (Z69254) alpha-galactosidase [Hypocrea jecorina] (AL033389) alcohol dehydrogenase [Schizosaccharomyces pombe]	
18059	ENU01853	ANI61C5249:	26-45	848-867	NAP	g4100125	317	89	3.00E-34	40	37	[Schizosaccharomyces pombe] (Z69254) alpha-galactosidase [Hypocrea jecorina] (AL033389) alcohol dehydrogenase [Schizosaccharomyces pombe]	
18060	ENU01854	ANI61C1107	33-57	856-875	NAP	g1145409	110	76	3.00E-13	26	42	[Schizosaccharomyces pombe] (Z69254) alpha-galactosidase [Hypocrea jecorina] (AL033389) alcohol dehydrogenase [Schizosaccharomyces pombe]	
18061	ENU01855	ANI61C1082	43-62	857-885	NAP	g1580818	1121	439	e-122	67	39	[Schizosaccharomyces pombe] (Z69254) alpha-galactosidase [Hypocrea jecorina] (AL033389) alcohol dehydrogenase [Schizosaccharomyces pombe]	
18062	ENU01856	ANI61C1077	42-62	865-884	NAP	g3850084	543	86	2.00E-35	44	72	[Schizosaccharomyces pombe]	
			5:2172..1288										

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Primer 846-868	Selection Basis	Database Hit	ncbi gi	Score	Blast Score	Blast Prob	% id	% cvrg	Description
18063	ENU01857	ANI61C5563:	25-45			NAP	g3873847	153	89	3.00E-17	35	29	(Z82256) cDNA EST EMBL:D67325	
			970..85											comes from this gene; cDNA EST EMBL:C13315 comes from this gene; cDNA EST EMBL:D37596 comes from this gene; cDNA EST EMBL:D69512 comes from this gene; cDNA EST EMBL:C11315 comes from this gene; cDN...
18064	ENU01858	ANI61C9914:	59-78	883-902	NAP		g1723213	499	146	2.00E-34	40	54	hypothetical 51.5 KD protein C3H8.02 in chromosome 1 ; (Z69086) unknown	
			1844..2729											[Schizosaccharomyces pombe] (AL022600) hypothetical protein
18065	ENU01859	ANI61C4664:	24-43	854-874	NAP		g3080538	623	182	2.00E-45	48	61	[Schizosaccharomyces pombe]	
			653..1545										ubiquitin-conjugating enzyme E2-21 KD (ubiquitin-protein ligase) (ubiquitin carrier protein) (peroxin-4) ; (AF061604) ubiquitin-conjugating enzyme homolog peroxin 4 [Pichia angusta]	
18067	ENU01861	ANI61C7946:	52-74	888-907	NAP		g2414602	434	85	8.00E-16	37	56	(Z99295) pre-mrna splicing factor	
			2004..1107										[Schizosaccharomyces pombe] (X98931) heat shock protein 70 [Emericella nidulans]	
18068	ENU01862	ANI61C1054	34-56	873-892	NAP		g2764949	1252	334	3.00E-96	97	43	myo-inositol transporter 1 ; (X98622) myo-inositol transporter	
			8:1613..720										[Schizosaccharomyces pombe] (L48797) toxin pump [Cochliobolus carbonum] (AF010145) hexose transporter	
18069	ENU01863	ANI61C5778:	39-58	871-901	NAP		g2500938	988	238	4.00E-62	41	52	[Aspergillus parasiticus]	
			1808..2712										hypothetical 40.7 KD protein in OPDE 3 region (ORF2) ; hypothetical protein 2 - Pseudomonas aeruginosa ; (Z14064) ORF2 [Pseudomonas aeruginosa]	
18070	ENU01864	ANI61C2559:	67-86	905-930	NAP		g1063421	99	4.00E-20				hypothetical 37.7 KD protein C1F7.12 in chromosome 1 ; hypothetical protein SPAC1F7.12 - fission yeast	
			227..1131										(Schizosaccharomyces pombe) ; (Z67998) unknown	
18071	ENU01865	ANI61C257:1	22-53	861-886	NAP		g2306977	1117	124	1.00E-41	56	42	[Schizosaccharomyces pombe]	
			317..410										hypothetical 40.7 KD protein in OPDE 3 region (ORF2) ; hypothetical protein 2 - Pseudomonas aeruginosa ; (Z14064)	
18072	ENU01866	ANI61C5632:	22-47	868-887	NAP		g732227	502	80	4.00E-32	42	79	hypothetical 37.7 KD protein C1F7.12 in chromosome 1 ; hypothetical protein SPAC1F7.12 - fission yeast	
			31..938										(Schizosaccharomyces pombe) ; (Z67998) unknown	
18073	ENU01867	ANI61C1078	54-73	900-919	NAP		g1351673	521	174	7.00E-43	42	66	[Schizosaccharomyces pombe]	
			4:1116..209											

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Prob	% id	% cvrg	Description
18074	ENU01868	ANI61C1004	67-86	921-940	NAP	g2842513	139	49	4.00E-14	25	90	(AL021748) superoxide dismutase	
18075	ENU01869	ANI61C562:8	71-91	925-944	NAP	g134297	482	155	4.00E-47	40	70	[Schizosaccharomyces pombe] SCJ1 protein ; SCJ1 protein - yeast (Saccharomyces cerevisiae) ; (X58679) SCJ1 [Saccharomyces cerevisiae] ; (Z49809) unknown [Saccharomyces cerevisiae] ; heat shock protein [Saccharomyces cerevisiae]	
18076	ENU01870	ANI61C1004	67-86	921-940	NAP	g2842513	139	49	4.00E-14	25	90	(AL021748) superoxide dismutase	
18077	ENU01871	ANI61C924:2	72-91	911-946	NAP	g1706692	1046	206	1.00E-52	52	61	[Schizosaccharomyces pombe] C-24(28) sterol reductase ; probable transport protein ERG4 - yeast (Saccharomyces cerevisiae) ; (Z72534) ORF YGL012w [Saccharomyces cerevisiae]	
18078	ENU01872	ANI61C7696:	39-59	896-915	NAP	g2598593	39	0.034				(Y15369) MtN12 [Medicago truncatula]	
18079	ENU01873	ANI61C1754:	57-78	909-934	NAP	g3368	96	8.00E-26				(X63998) aminopeptidase yscII [Saccharomyces cerevisiae] (U84489) septin B [Emericella nidulans]	
18080	ENU01874	ANI61C6862:	22-46	882-905	NAP	g1791305	610	149	1.00E-57	43	70	sterigmatocystin biosynthesis regulatory protein ; sterigmatocystin synthesis transcriptional regulator aflR -Emericella nidulans ; (L34740) pathway specific transcription factor [Emericella nidulans]	
18081	ENU01875	ANI50C1_17	24-43	889-908	NAP	g1703202	168	4.00E-41	38	68		hypothetical 40.4 KD protein in PES4-HIS2 intergenic region ; (D50617) YFR024C [Saccharomyces cerevisiae] (AC000132) Similar to S. pombe ISP4 (gb D83992), [Arabidopsis thaliana] Polyketide synthase HETM ; hetM protein - Anabaena sp. (PCC 7120) ; (L22883) polyketide synthase [Anabaena sp.]	
18082	ENU01876	ANI61C352:9	23-42	888-907	NAP	g1176004	480	192	4.00E-48	39	82	(AL022304) ttp-ast repeats containing protein [Schizosaccharomyces pombe] (Z98531) hypothetical protein [Schizosaccharomyces pombe]	
18083	ENU01877	ANI61C4038:	71-93	936-957	NAP	g2160185	299	101	8.00E-21	26	42		
18084	ENU01878	ANI61C1100	32-53	897-919	NAP	g585251	77	1.00E-13					
18085	ENU01879	ANI61C8862:	22-54	888-910	NAP	g3006183	381	97	9.00E-38	37	67		
18086	ENU01880	ANI61C1020	34-59	907-926	NAP	g2330840	417	118	1.00E-41	38	90		

Seq num	Seq id	Contig Source	Primer 3 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat	Blast Score	Blast Prob	% id	% cvrg	Description
18087	ENU01881	ANI61C5467:	22-46	902-921	NAP	g2494694	431	158	6.00E-38	34	63	Cutinase gene palindrome-binding protein (PBP) ; palindrome-binding protein - fungus ( <i>Fusarium solani</i> ) ; (U23722) cutinase gene palindrome-binding protein [ <i>Fusarium solani</i> f. sp. pisi]	
18088	ENU01882	ANI61C1058:	59-80	186-219	NAP	g3878134	201	75	8.00E-14	47	84	(Z68218) K01H12.1 [Caenorhabditis elegans]	
18089	ENU01883	ANI61C1068	55-74	221-240	NAP	g732947	37	0.018				[Saccharomyces cerevisiae] (Z30582) SmX4 protein	
18090	ENU01884	ANI61C1103	66-85	313-332	NAP	g1870220	221	88	2.00E-17	42	76	(AC000133) ORF [Emericella midulans]	
18091	ENU01885	ANI61C9818:	52-71	343-362	NAP	g417695	203	57	0.000000	06		DNA-directed RNA polymerase I A12.2 ; DNA-directed RNA polymerase (EC 2.7.7.6) 1 chain A12.2 - yeast ( <i>Saccharomyces cerevisiae</i> ) ; (L00708) RNA polymerase I subunit A12.2	
18092	ENU01886	ANI61C8397:	48-67	372-391	NAP	g416604	205	74	5.00E-13			[Saccharomyces cerevisiae] ; (L35564) RNA polymerase I A12.2 subunit [Saccharomyces cerevisiae] ; (Z49563) ORF YJR063w [ <i>Saccharomyces cerevisiae</i> ] ; (L47993) ORF YJR063w [ <i>Saccharomyces cerevisiae</i> ] ; (L47993) ORF YJR063w [ <i>Saccharomyces cerevisiae</i> ] ; alcohol dehydrogenase (acceptor) ; alcohol dehydrogenase - <i>Pseudomonas oleovorans</i> ; (X65936) alcohol dehydrogenase [ <i>Pseudomonas oleovorans</i> ] (AF036424) mucin-like protein	
18093	ENU01887	ANI61C1044	53-72	381-400	NAP	g3064176	33	0.81				[ <i>Trypanosoma cruzi</i> ] probable isovaleryl-CoA dehydrogenase (IVD) ; C02DS.1 protein - <i>Caenorhabditis elegans</i> ; (L16622) homology with isovaleryl-CoA dehydrogenase protein; putative [ <i>Caenorhabditis elegans</i> ]	
18094	ENU01888	ANI61C458:4	55-73	400-420	NAP	g462428	143	68	2.00E-11	33	39		
		09..2											

Seq num	Seq id	Contig Source	Primer 3 pos	Primer Basis	Selection	Blast aat	Blast Prob	% id	% cvrg	Description	
					Database Hit	ncbi gi	Score	Score			
18095	ENU01889	ANI61C7499:	59-87	NAP	g2127839	180	65	2.00E-10	32	"deoxycytidine triphosphate deaminase homolog - <i>Methanococcus jannaschii</i> ; (U67553) deoxycytidine triphosphate deaminase, putative (dcd) [Methanococcus jannaschii]"	
18096	ENU01890	ANI61C3183:	32-51	NAP	g400513	33	0.0007			NADH-ubiquinone oxidoreductase B22 subunit (complex I-B22) (CI-B22); NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain CI-B22 - bovine; (X64836) NADH-ubiquinone oxidoreductase complex B22 subunit [Bos taurus]	
18097	ENU01891	ANI61C1610:	36-56	395-414	NAP	g1078673	1228	40	0.006	31	gamma-adaptin - smut fungus ( <i>Ustilago maydis</i> ) ; (Z46804) gamma-adaptin [Ustilago maydis] (Z299753) hypothetical protein [Schizosaccharomyces pombe] (AL031603) 60s ribosomal protein [Schizosaccharomyces pombe] probable sterigmatocystin biosynthesis P450 monooxygenase STCF (cytochrome P450 60A2); (U34740) putative p450 monooxygenase [Emeticcella nidulans]
18098	ENU01892	ANI61C4480:	22-44	382-401	NAP	g2465151	111	53	0.00000140	74	[Ustilago maydis] (Z299753) hypothetical protein [Schizosaccharomyces pombe] (AL031603) 60s ribosomal protein [Schizosaccharomyces pombe] probable sterigmatocystin biosynthesis P450 monooxygenase STCF (cytochrome P450 60A2); (U34740) putative p450 monooxygenase [Emeticcella nidulans]
18099	ENU01893	ANI61C6633:	66-83	434-452	NAP	g3646455	432	61	0.00000077	53	[Ustilago maydis] (Z299753) hypothetical protein [Schizosaccharomyces pombe] (AL031603) 60s ribosomal protein [Schizosaccharomyces pombe] probable sterigmatocystin biosynthesis P450 monooxygenase STCF (cytochrome P450 60A2); (U34740) putative p450 monooxygenase [Emeticcella nidulans]
18100	ENU01894	ANI61C2205:	30-49	400-419	NAP	g2493389	179	56	0.00000039	21	[Ustilago maydis] (Z299753) hypothetical protein [Schizosaccharomyces pombe] (AL031603) 60s ribosomal protein [Schizosaccharomyces pombe] probable sterigmatocystin biosynthesis P450 monooxygenase STCF (cytochrome P450 60A2); (U34740) putative p450 monooxygenase [Emeticcella nidulans]
18101	ENU01895	ANI61C6093:	31-49	409-426	NAP	g2132183	760	138	3.00E-32	50	[Ustilago maydis] (Z299753) hypothetical protein [Schizosaccharomyces pombe] (AL031603) 60s ribosomal protein [Schizosaccharomyces pombe] probable sterigmatocystin biosynthesis P450 monooxygenase STCF (cytochrome P450 60A2); (U34740) putative p450 monooxygenase [Emeticcella nidulans]
18102	ENU01896	ANI61C1021	53-72	429-448	NAP	g3024608	488	138	3.00E-44	63	[Ustilago maydis] (Z299753) hypothetical protein [Schizosaccharomyces pombe] (AL031603) 60s ribosomal protein [Schizosaccharomyces pombe] probable sterigmatocystin biosynthesis P450 monooxygenase STCF (cytochrome P450 60A2); (U34740) putative p450 monooxygenase [Emeticcella nidulans]
18103	ENU01897	ANI61C1106	56-75	433-452	NAP	g1730822	804	157	3.00E-38	52	[Ustilago maydis] (Z299753) hypothetical protein [Schizosaccharomyces pombe] (AL031603) 60s ribosomal protein [Schizosaccharomyces pombe] probable sterigmatocystin biosynthesis P450 monooxygenase STCF (cytochrome P450 60A2); (U34740) putative p450 monooxygenase [Emeticcella nidulans]
18104	ENU01898	ANI61C1828:	55-72	434-453	NAP	g3687238	493	176	7.00E-44	57	[Ustilago maydis] (Z299753) hypothetical protein [Schizosaccharomyces pombe] (AL031603) 60s ribosomal protein [Schizosaccharomyces pombe] probable sterigmatocystin biosynthesis P450 monooxygenase STCF (cytochrome P450 60A2); (U34740) putative p450 monooxygenase [Emeticcella nidulans]
18105	ENU01899	ANI61C3632:	30-51	416-435	NAP	g538067	189	97	6.00E-20	36	[Ustilago maydis] (Z299753) hypothetical protein [Schizosaccharomyces pombe] (AL031603) 60s ribosomal protein [Schizosaccharomyces pombe] probable sterigmatocystin biosynthesis P450 monooxygenase STCF (cytochrome P450 60A2); (U34740) putative p450 monooxygenase [Emeticcella nidulans]
			9..456								

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18106	ENU01900	ANI61C1108:	58-77	445-463	NAP	g731968	426	141	2.00E-33	50	45	hypothetical 35.9 KD protein in HXT8-CRT1 intergenic region ; hypothetical protein YJL213w - yeast	
18107	ENU01901	ANI61C4859:	71-90	462-481	NAP	g731347	56	7.00E-17					(Saccharomyces cerevisiae) ; (Z34098) ORF [Saccharomyces cerevisiae] ; (Z49488) ORF YJL213w [Saccharomyces cerevisiae]
18108	ENU01902	ANI61C3691:	40-59	432-451	NAP	g2435542	89	45	0.0004	37	70	[Caenorhabditis elegans] (AF026204) No definition line found	
18109	ENU01903	ANI61C9317:	25-44	419-443	NAP	g1346942	399	125	2.00E-28	50	84	"60S ribosomal protein YL16B ; ribosomal protein L6.e.B, cytosolic - yeast (Saccharomyces cerevisiae) ; (U22382) Rpl16bp; 60S ribosomal protein YL16B [Saccharomyces cerevisiae]"	
18110	ENU01904	ANI61C1116	63-83	472-491	NAP	g127568	292	82	3.00E-15	31	51	"Interferon-induced GTP-binding protein MX ; Mx resistance protein homolog - perch (fragment); (M27252) [Perca fluviatilis] gene with homology to murine Mx genes, partial cds., gene product [Perca fluviatilis]" (AL023518) hypothetical protein	
18111	ENU01905	ANI61C1389:	72-98	481-501	NAP	g3130056	206	80	7.00E-15	37	22	[Schizosaccharomyces pombe] hypothetical 31.6 KD protein C2E12.03C in chromosome 1; (Z69726) unknown	
18112	ENU01906	ANI61C3296:	61-80	479-500	NAP	g1723416	297	104	4.00E-22	39	50	[Schizosaccharomyces pombe] aromatic L-amino acid decarboxylase [Rattus norvegicus] Nitrate reductase 3 (NR) ; (U20450) nitrate reductase [Zea mays] (AF088906) clock-controlled gene-9 protein [Neurospora crassa]	
18113	ENU01907	ANI61C3109:	41-58	470-488	NAP	g975309	802	103	2.00E-31	49	29		
18114	ENU01908	ANI61C3335:	36-55	465-484	NAP	g1352497	1224	112	5.00E-28	42	18		
18115	ENU01909	ANI50C844_	27-46	460-479	NAP	g3746895	63	0.000000	001				

Seq num	Seq id	Contig Source	Primer 3 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat	Blast Score	Blast Prob	% id	% cvrg	Description
18116	ENU01910	ANI61C1026	53..72	494..513	NAP	g465665	310	135	2.00E-31	41	68	"hypothetical CAPI intergenic region ; hypothetical protein YKL009w - yeast (Saccharomyces cerevisiae) ; (S53418) ribosomal protein L10 homolog [Saccharomyces cerevisiae=yeast, Peptid, 236 aa] [Saccharomyces cerevisiae] ; (Z28009) ORF YKL009w [Saccharomyces cerevisiae]"	
18117	ENU01911	ANI61C9065:	58..76	502..521	NAP	g1491795	503	159	2.00E-38	41	18	"[U39812] beta-1,4-mannanase [Caldicellulosiruptor saccharolyticus]"	
18118	ENU01912	ANI61C1043	51..68	498..517	NAP	g4107287	459	50	0.000000	001		(AL035076) putative allantate permease [Schizosaccharomyces pombe]	
18119	ENU01913	ANI61C3562:	55..73	505..524	NAP	g4586977	3318	176	1.00E-43	47	7	(AB018382) Mok13; Mok13 is homologous to Mok1 which is an alpha-glucan synthase [Schizosaccharomyces pombe]	
18120	ENU01914	ANI61C5666:	49..67	512..531	NAP	g3122291	661	161	4.00E-48	70	49	Inorganic pyrophosphatase (PPASE); (A1001000) inorganic pyrophosphate phospho-hydrolase; [Pichia pastoris] hypothetical 16.6 KD protein in ATL5 region (ORF3); (D17366) ORF3 [Staphylococcus aureus]; (L41499) ORF3 [Staphylococcus aureus]	
18121	ENU01915	ANI61C3340:	68..87	541..560	NAP	g1723227	109	39	0.017			"(U21319) similar to alcohol dehydrogenase, highest similarity to B. japonicum FIXR protein (SP:FIXR_BRAJA, P05406)	
18122	ENU01916	ANI61C7507:	50..69	528..547	NAP	g687834	45	39	0.023			[Caenorhabditis elegans] (AC000133) ORF [Emericella nidulans]	
18123	ENU01917	ANI61C1802:	24..44	505..524	NAP	g1870209	332	104	3.00E-22	41	32	"origin recognition complex protein, subunit 2 ; (U38472) essential ORC2-related fission replication factor Orp2 [Schizosaccharomyces pombe]; (AL049474) origin recognition complex protein, subunit 2. [Schizosaccharomyces pombe]"	
18124	ENU01918	ANI61C4995:	54..71	537..556	NAP	g2498711	230	99	2.00E-20	34	31		

Seq num	Seq id	Contig Source	Primer 3 pos	Primer 3 pos	Selection Basis	Database Hit	nebi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18125	ENU01919	ANI61C4995:	54-71	537-556	NAP	g2498711	230	99	2.00E-20	34	31	"origin recognition complex protein, subunit 2 ; (U38472) essential ORC2-related fission replication factor Orp2 [Schizosaccharomyces pombe]; (AL049474) origin recognition complex protein, subunit 2.	
18126	ENU01920	ANI61C8394:	24-43	507-526	NAP	g117804	244	119	1.00E-26			[Schizosaccharomyces pombe]" cytochrome B2 precursor (L-lactate dehydrogenase (cytochrome)) (L-lactate ferricytochrome C oxidoreductase) (L-LCR); L-lactate dehydrogenase (cytochrome) (EC 1.1.2.3) precursor - yeast (Saccharomyces cerevisiae); (X03215) cytochrome b2 precursor [Saccharomyces cerevisiae]; (Z46729) cytochrome b2 precursor [Saccharomyces cerevisiae] (AL022070) hsp grpe homolog [Schizosaccharomyces pombe] 66 kDa stress protein p66 [Physarum polycephalum]	
18127	ENU01921	ANI61C7977:	62-81	545-564	NAP	g2950485	313	137	5.00E-32	45	73	"High affinity methionine permease; methionine transport protein, high affinity - yeast (Saccharomyces cerevisiae); (U40316) high affinity methionine permease [Saccharomyces cerevisiae]; (Z72840) ORF YGR055w [Saccharomyces cerevisiae]" (Y16261) CRO1 protein [Podospora anserina]	
18128	ENU01922	ANI61C7152:	41-58	525-545	NAP	g3123032	275	125	2.00E-28	32	30	"AMP deaminase (myoadenylate deaminase); AMP deaminase (EC 3.5.4.6) - yeast (Saccharomyces cerevisiae); (Z46659) AMD1 gene, len: 810, CAI: 0.19, AMP deaminase [Saccharomyces cerevisiae]" (Z99532) myo-inositol transporter [Schizosaccharomyces pombe]	
18129	ENU01923	ANI61C3573:	37-61	523-542	NAP	g1709181	434	45	0.000000	27	27		
18130	ENU01924	ANI61C8580:	31-52	522-541	NAP	g2808541	871	108	2.00E-23	39	25		
18131	ENU01925	ANI61C8962:	65-84	559-578	NAP	g1351916	1951	272	1.00E-72	68	22	"AMP deaminase (myoadenylate deaminase); AMP deaminase (EC 3.5.4.6) - yeast (Saccharomyces cerevisiae); (Z46659) AMD1 gene, len: 810, CAI: 0.19, AMP deaminase [Saccharomyces cerevisiae]" (Z99532) myo-inositol transporter [Schizosaccharomyces pombe]	
18132	ENU01926	ANI61C1026	38-57	548-567	NAP	g2440196	487	147	6.00E-35	48	64		

Seq num	Seq id	Contig Source	Primer 3 pos	Primer 3 pos	Selection Basis	Database Hit	blast gi	aat	Blast Score	Blast Prob	% id	% cvrg	Description
18133	ENU01927	ANI61C6374:	59-78	570-588	NAP	g140499	649	184	5.00E-46	57	67	"putative 30.7 KD methyltransferase in TSM1-ARE1 intergenic region ; hypothetical protein YCR047c - yeast (Saccharomyces cerevisiae) ; (X59720) YCR047c, [len:275 [Saccharomyces cerevisiae]"	
18134	ENU01928	ANI61C8578:	55-73	585-604	NAP	g2493143	440	121	4.00E-27	71	88	Vacuolar ATP synthase 16 KD proteolipid subunit ; (U02877) vacuolar ATPase subunit c [Candida tropicalis]	
18135	ENU01929	ANI61C3426:	51-70	583-602	NAP	g2398816	312	103	9.00E-22	30	46	(Z99126) putative mannosyl transferase [Schizosaccharomyces pombe]	
18136	ENU01930	ANI61C1156:	37-61	572-591	NAP	g2645229	156	67	9.00E-11	32	40	(U78597) kinesin light chain [Plectonema boryanum]	
18137	ENU01931	ANI61C5927:	63-81	604-623	NAP	g3914384	536	90	5.00E-45	65	86	probable peroxisomal membrane protein PMP20 (allergen ASP F 3) ; (U58050) peroxisomal-like protein [Aspergillus fumigatus]	
18138	ENU01932	ANI61C823:4	68-87	614-633	NAP	g1168817	236	60	1.00E-18	33	16	cell division control protein 7 ; protein kinase cdc7 - fission yeast (Schizosaccharomyces pombe) ; (X78799) cdc7 [Schizosaccharomyces pombe] ; (AL035337) cell division control protein 7 [Schizosaccharomyces pombe]	
18139	ENU01933	ANI61C5908:	71-90	628-647	NAP	g730018	1750	317	4.00E-86	77	26	"S-methyltetrahydropteroylglutamate—homocysteine methyltransferase (methionine synthase, vitamin-B12 independent isozyme) (cobalamin-independent methionine synthase) (delta-P8 protein) ; 5-methyltetrahydropteroylglutamate--homocysteine S-methyltransferase (EC 2.1.1.14) - yeast (Saccharomyces cerevisiae) ; (U118839) Metfp: 5-methyltetrahydropteroyl triglutamate--homocysteine methyltransferase [Saccharomyces cerevisiae] ; (U32508) N5-methyltetrahydrofolate homocysteine methyltransferase [Saccharomyces cerevisiae]"	

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat	Blast Score	Blast Prob	% id	% cvrg	Description
18140	ENU01934	ANI61C3096:	49-67	608-627	NAP	g3929350	3103	259	1.00E-68	65	22		Peroxisomal hydratase-dehydrogenase-epimerase (HDE) (multifunctional beta-oxidation protein) [contains: 2-enoyl-CoA hydratase ; D-3-hydroxyacyl CoA dehydrogenase ] ; multifunctional beta-oxidation protein - Neurospora crassa ; (X80052)
18141	ENU01935	ANI61C6914:	51-71	610-629	NAP	g4501859	550	101	4.00E-44				"acyl-Coenzyme A dehydrogenase, short/branched chain precursor; acyl-CoA dehydrogenase, short/branched chain specific precursor (SBCAD) (2-methyl branched chain acyl-CoA dehydrogenase) (2-MEBCAD); short/branched chain acyl-CoA dehydrogenase (EC 1.3.-.) precursor - human ; (U12778) acyl-CoA dehydrogenase [Homo sapiens]" (AF034089) calcineurin subunit B [Neurospora crassa]
18142	ENU01936	ANI61C1103	49-68	612-631	NAP	g2645886	627	210	5.00E-54	87	92		[Emericella nidulans] quinate permease (quinate transporter); quinate transport protein - Emericella nidulans ; (X13525) quinate permease (AL031262) hypothetical protein [Schizosaccharomyces pombe] cytochrome B ; ubiquinol-cytochrome-c reductase (EC 1.10.2.2) cytochrome b - Emericella nidulans mitochondrion (SGC3) ; (J01389) apocytochrome b [Emericella nidulans] (AB009078) L-2,3-butanediol dehydrogenase [Brevibacterium saccharolyticum] casein kinase II beta chain (CK II) ; (X74274) casein kinase II beta subunit [Schizosaccharomyces pombe]
18147	ENU01941	ANI61C4563:	50-71	631-649	NAP	g729881	641	226	1.00E-58	58	85		

Seq num	Seq id	Contig Source	Primer 3 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18148	ENU01942	ANI61C9471:	64-83	43..685	NAP	g1718099	846	254	5.00E-67	76	54	vacuolar ATP synthase subunit AC39 (V-ATPase AC39 subunit) ; (V-ATPase 41 KD subunit) ; (U36470) vacuolar ATPase 41 kDa subunit [Neurospora crassa]	
18149	ENU01943	ANI61C2909:	45-62	628-651	NAP	756..108	g1723727	481	115	1.00E-31	62	42	hypothetical 41.0 KD protein in YIP1-CBP4 intergenic region ; hypothetical protein YGR173w- yeast (Saccharomyces cerevisiae) ; (Z72958) ORF YGR173w [Saccharomyces cerevisiae] (AJ1223998) PCZA361.15
18150	ENU01944	ANI61C6178:	32-51	625-648	NAP	682..24	g2894179	356	148	4.00E-35	43	65	[Amycolatopsis orientalis] (AB010465) lactonohydrolase [Fusarium oxysporum] (D83988) reductase [Colletotrichum lagenarium]
18151	ENU01945	ANI61C1138	53-72	650-669	NAP	3.2574..1916	g3810873	144	55	0.000000	32	45	hypothetical 33.3 KD protein in PERR-ARGF intergenic region ; (AE000134) putative lyase/synthase [Escherichia coli]
18152	ENU01946	ANI61C8219:	50-69	650-669	NAP	742..81	g1902911	89	4.00E-17	5		vegetable incompatibility protein HET-E-1 ; (L28125) beta transducin-like protein [Podospora anserina] (AE000737) fructose-1,6-bisphosphate aldolase class II [Aequifex aeolicus]"	
18153	ENU01947	ANI61C7493:	67-84	667-686	NAP	4028..3367	g2494090	208	62	1.00E-11	37	55	"(AF029354) exo-beta-1,3-glucanase [Ampelomyces quisqualis]" "ATP phosphoribosyltransferase ; ATP phosphoribosyltransferase (EC 2.4.2.17) - yeast (Candida albicans) ; (X83871) ATP phosphoribosyltransferase [Candida albicans]
18154	ENU01948	ANI61C1055	31-50	635-653	NAP	7.133..538	g3023956	885	189	1.00E-47	42	16	"(AE000737) fructose-1,6-
18155	ENU01949	ANI61C3688:	39-58	643-662	NAP	4356..3691	g2983787	238	86	3.00E-16	39	46	bisphosphate aldolase class II [Aequifex aeolicus]"
18156	ENU01950	ANI61C8586:	39-58	647-666	NAP	1110..441	g3004863	967	262	2.00E-69	57	27	"(AF029354) exo-beta-1,3-glucanase [Ampelomyces quisqualis]" "ATP phosphoribosyltransferase ; ATP phosphoribosyltransferase (EC
18157	ENU01951	ANI61C2388:	56-75	673-692	NAP	4438..5116	g1170278	510	194	5.00E-49	56	62	2.4.2.17) - yeast (Candida albicans) ; (X83871) ATP phosphoribosyltransferase [Candida albicans]
18158	ENU01952	ANI61C5085	69-88	687-706	NAP	605..4326	g825440	927	183	2.00E-82	92	87	(L42299) RAS [Aspergillus fumigatus]

નોંધ કરી શકતું હોય અને આપણી જીવિતની વિધાની પ્રદર્શની

Seq num	Seq id	Contig Source	Primer 3 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvg	Description
18159	ENU01953	ANI61C2966:	50-67	677-697	NAP	g127568	224	112	2.00E-24	37	58	"interferon-induced GTP-binding protein MX ; MX resistance protein homolog - perch (fragment); (M27252)	
			2334..1644										[ <i>Perca fluviatilis</i> ] gene with homology to murine Mx genes, partial cds., gene product [ <i>Perca fluviatilis</i> ] "
18160	ENU01954	ANI61C7836:	51-70	687-705	NAP	g2687850	659	116	4.00E-45	45	34	(Y15839) fatty acid transporter protein [Cochliobolus heterostrophus]	
18161	ENU01955	ANI61C1016	36-55	671-690	NAP	g1526987	423	110	3.00E-45	49	89	(U13050) pectate lyase D [Fusarium solani f. sp. pisi]	
18162	ENU01956	ANI61C2322:	66-85	706-725	NAP	g4481956	290	100	8.00E-28	51	36	(AL035637) putative uracil kinase- cytosine deaminase-bifunctional enzyme [Schizosaccharomyces pombe] (X89453) DRPLA [Rattus norvegicus]	
18163	ENU01957	ANI61C7012:	49-68	689-709	NAP	g9955557	36	0.21					
		843..141											
18164	ENU01958	ANI61C1806:	27-46	671-695	NAP	g280478	446	117	2.00E-39	55	96	NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) 22K chain precursor - Neurospora crassa	
18165	ENU01959	ANI61C6073:	22-45	675-694	NAP	g1351299	260	126	1.00E-28	36	24	putative potassium transport protein C1F5.12; (Z68136) unknown [Schizosaccharomyces pombe]	
18166	ENU01960	ANI61C3790:	68-87	721-741	NAP	g1711561	304	122	3.00E-27	31	41	sugar transporter STL1 ; sugar transport protein STP1 - yeast ( <i>Saccharomyces cerevisiae</i> ) ; (U33057) Stlp; plasma membrane sugar transporter; CAI: 0.19 [ <i>Saccharomyces cerevisiae</i> ]	
18167	ENU01961	ANI61C905:4	60-79	731-750	NAP	g2494905	618	178	4.00E-44	48	49	microtubule-associated protein YTM1 ; hypothetical protein YOR272w - yeast ( <i>Saccharomyces cerevisiae</i> ) ; (X89633) hypothetical protein [ <i>Saccharomyces cerevisiae</i> ] ; (Z75180) ORF YOR272w [ <i>Saccharomyces cerevisiae</i> ] ; (U92821) microtubule-associated protein [ <i>Saccharomyces cerevisiae</i> ]	

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvg	Description	
18168	ENU01962	ANI61C6665:	47..66	723..744	NAP	g1723254	673	130	1.00E-29	55	63	63	probable phosphoribosylformimino-5-aminoimidazole carboxamide ribotide isomerase ; (Z69369) putative phosphoribosylformimino-5-aminoimidazole carboxamide ribotide isomerase [Schizosaccharomyces pombe]	
18169	ENU01963	ANI61C2704:	70..89	754..773	NAP	g115595	225	67	4.00E-16	34	69	69	F-actin capping protein alpha subunit ; actin-capping protein alpha chain - yeast (Saccharomyces cerevisiae) ; (X61398) Capping Protein Alpha Subunit [Saccharomyces cerevisiae] ; (Z22807) ORF YKL007w	
18170	ENU01964	ANI50C1415	22..50	722..741	NAP	g2133335	221	5.00E-57	42	47	47	47	[Saccharomyces cerevisiae] CAP1 [Saccharomyces cerevisiae] transposase - fungus (Cochliobolus carbonum)	
18171	ENU01965	ANI61C7152:	4..1:81..842	72..91	778..797	NAP	g3192028	312	113	1.00E-24	36	85	85	(AL023794) hypothetical protein [Schizosaccharomyces pombe]
18172	ENU01966	ANI61C1188:	1895..2662	41..60	752..771	NAP	g4507791	510	148	8.00E-47	56	96	96	unknown ; (AF075599) ubiquitin conjugating enzyme 12 [Homo sapiens] ; (AB012191) Nedd8-conjugating enzyme hUbc12 [Homo sapiens] (Z97050) ilvD [Mycobacterium tuberculosis]
18173	ENU01967	ANI61C1125	70..89	787..806	NAP	g2213526	342	121	7.00E-27	33	42	42	hypothetical 49.5 kD protein in UBP3-PET122 intergenic region ; hypothetical protein YER152c - yeast (Saccharomyces cerevisiae) ; (U18917) Yer152cp [Saccharomyces cerevisiae] (AF080235) reductase homolog [Streptomyces cyanogenus]	
18175	ENU01969	ANI61C3627:	40..59	767..786	NAP	g4240421	97	3.00E-22						
			1765..977											

Seq num	Seq id	Contig Source	5 pos	Primer 3 pos	Primer Basis	Selection	Database	Hit	nebi gi	Score	Score Prob	% id	% cvrg	Description
18176	ENU01970	ANI61C3268:	71-90	801-821	NAP	g121146	1021	293	1.00E-78	66	47	47	47	geranylgeranyl pyrophosphate synthetase (GGPP synthetase) (dimethylallyltransferase / geranyltransferase / farnesyltransferase ; geranylgeranyl pyrophosphate synthetase - <i>Neurospora crassa</i> ; (U20940) geranylgeranyl pyrophosphate synthetase [[ <i>Neurospora crassa</i> ] "arabinan endo-1,5-alpha-L-arabinosidase A precursor (endo-1,5-alpha-L-arabinanase A) (ABN A); (L23430) endo-1,5-alpha-L-Arabinase [Aspergillus niger]; endo-1,5-alpha-L-arabinase [Aspergillus niger]" transcription initiation protein SPT6; SPT6 protein - yeast ( <i>Saccharomyces cerevisiae</i> ); (M34391) SPT6 protein [Saccharomyces cerevisiae]; (Z72899) ORF YGR116w [ <i>Saccharomyces cerevisiae</i> ] (U58946) transposase [Aspergillus awamori] (D63703) isobutene-forming enzyme and benzoate 4-hydroxylase [Rhodotorula minuta] (AC005824) unknown protein [Arabidopsis thaliana] hypothetical 61.1 KD protein C11D3.05 in chromosome I; (Z68166) unknown [ <i>Schizosaccharomyces pombe</i> ] (X91867) CPC3 protein [ <i>Neurospora crassa</i> ] catalase ; catalase (EC 1.11.1.6) - <i>Haemophilus influenzae</i> (strain Rd KW20); (U32774) catalase (hktE) [ <i>Haemophilus influenzae</i> Rd] (AF070657) glutathione S-transferase subunit 13 homolog [ <i>Homo sapiens</i> ]
18177	ENU01971	ANI61C9212:	65-84	791-816	NAP	g1168269	414	131	5.00E-30	41	76	76	76	geranylgeranyl pyrophosphate synthetase - <i>Neurospora crassa</i> ; (U20940) geranylgeranyl pyrophosphate synthetase [[ <i>Neurospora crassa</i> ] "arabinan endo-1,5-alpha-L-arabinosidase A precursor (endo-1,5-alpha-L-arabinanase A) (ABN A); (L23430) endo-1,5-alpha-L-Arabinase [Aspergillus niger]; endo-1,5-alpha-L-arabinase [Aspergillus niger]" transcription initiation protein SPT6; SPT6 protein - yeast ( <i>Saccharomyces cerevisiae</i> ); (M34391) SPT6 protein [Saccharomyces cerevisiae]; (Z72899) ORF YGR116w [ <i>Saccharomyces cerevisiae</i> ] (U58946) transposase [Aspergillus awamori] (D63703) isobutene-forming enzyme and benzoate 4-hydroxylase [Rhodotorula minuta] (AC005824) unknown protein [Arabidopsis thaliana] hypothetical 61.1 KD protein C11D3.05 in chromosome I; (Z68166) unknown [ <i>Schizosaccharomyces pombe</i> ] (X91867) CPC3 protein [ <i>Neurospora crassa</i> ] catalase ; catalase (EC 1.11.1.6) - <i>Haemophilus influenzae</i> (strain Rd KW20); (U32774) catalase (hktE) [ <i>Haemophilus influenzae</i> Rd] (AF070657) glutathione S-transferase subunit 13 homolog [ <i>Homo sapiens</i> ]]
18178	ENU01972	ANI61C1330:	66-84	800-819	NAP	g134854	907	123	4.00E-41	37	17	17	17	"arabinan endo-1,5-alpha-L-arabinosidase A precursor (endo-1,5-alpha-L-arabinanase A) (ABN A); (L23430) endo-1,5-alpha-L-Arabinase [Aspergillus niger]; endo-1,5-alpha-L-arabinase [Aspergillus niger]" transcription initiation protein SPT6; SPT6 protein - yeast ( <i>Saccharomyces cerevisiae</i> ); (M34391) SPT6 protein [Saccharomyces cerevisiae]; (Z72899) ORF YGR116w [ <i>Saccharomyces cerevisiae</i> ] (U58946) transposase [Aspergillus awamori] (D63703) isobutene-forming enzyme and benzoate 4-hydroxylase [Rhodotorula minuta] (AC005824) unknown protein [Arabidopsis thaliana] hypothetical 61.1 KD protein C11D3.05 in chromosome I; (Z68166) unknown [ <i>Schizosaccharomyces pombe</i> ] (X91867) CPC3 protein [ <i>Neurospora crassa</i> ] catalase ; catalase (EC 1.11.1.6) - <i>Haemophilus influenzae</i> (strain Rd KW20); (U32774) catalase (hktE) [ <i>Haemophilus influenzae</i> Rd] (AF070657) glutathione S-transferase subunit 13 homolog [ <i>Homo sapiens</i> ]]
18179	ENU01973	ANI61C8126:	66-86	804-823	NAP	g1805251	1222	311	4.00E-84	55	47	47	47	"arabinan endo-1,5-alpha-L-arabinosidase A precursor (endo-1,5-alpha-L-arabinanase A) (ABN A); (L23430) endo-1,5-alpha-L-Arabinase [Aspergillus niger]; endo-1,5-alpha-L-arabinase [Aspergillus niger]" transcription initiation protein SPT6; SPT6 protein - yeast ( <i>Saccharomyces cerevisiae</i> ); (M34391) SPT6 protein [Saccharomyces cerevisiae]; (Z72899) ORF YGR116w [ <i>Saccharomyces cerevisiae</i> ] (U58946) transposase [Aspergillus awamori] (D63703) isobutene-forming enzyme and benzoate 4-hydroxylase [Rhodotorula minuta] (AC005824) unknown protein [Arabidopsis thaliana] hypothetical 61.1 KD protein C11D3.05 in chromosome I; (Z68166) unknown [ <i>Schizosaccharomyces pombe</i> ] (X91867) CPC3 protein [ <i>Neurospora crassa</i> ] catalase ; catalase (EC 1.11.1.6) - <i>Haemophilus influenzae</i> (strain Rd KW20); (U32774) catalase (hktE) [ <i>Haemophilus influenzae</i> Rd] (AF070657) glutathione S-transferase subunit 13 homolog [ <i>Homo sapiens</i> ]]
18180	ENU01974	ANI61C9741:	67-85	805-824	NAP	g1020413	119	83	2.00E-15	26	42	42	42	"arabinan endo-1,5-alpha-L-arabinosidase A precursor (endo-1,5-alpha-L-arabinanase A) (ABN A); (L23430) endo-1,5-alpha-L-Arabinase [Aspergillus niger]; endo-1,5-alpha-L-arabinase [Aspergillus niger]" transcription initiation protein SPT6; SPT6 protein - yeast ( <i>Saccharomyces cerevisiae</i> ); (M34391) SPT6 protein [Saccharomyces cerevisiae]; (Z72899) ORF YGR116w [ <i>Saccharomyces cerevisiae</i> ] (U58946) transposase [Aspergillus awamori] (D63703) isobutene-forming enzyme and benzoate 4-hydroxylase [Rhodotorula minuta] (AC005824) unknown protein [Arabidopsis thaliana] hypothetical 61.1 KD protein C11D3.05 in chromosome I; (Z68166) unknown [ <i>Schizosaccharomyces pombe</i> ] (X91867) CPC3 protein [ <i>Neurospora crassa</i> ] catalase ; catalase (EC 1.11.1.6) - <i>Haemophilus influenzae</i> (strain Rd KW20); (U32774) catalase (hktE) [ <i>Haemophilus influenzae</i> Rd] (AF070657) glutathione S-transferase subunit 13 homolog [ <i>Homo sapiens</i> ]]
18181	ENU01975	ANI61C9072:	37-57	780-799	NAP	g3860264	344	68	5.00E-22	39	54	54	54	"arabinan endo-1,5-alpha-L-arabinosidase A precursor (endo-1,5-alpha-L-arabinanase A) (ABN A); (L23430) endo-1,5-alpha-L-Arabinase [Aspergillus niger]; endo-1,5-alpha-L-arabinase [Aspergillus niger]" transcription initiation protein SPT6; SPT6 protein - yeast ( <i>Saccharomyces cerevisiae</i> ); (M34391) SPT6 protein [Saccharomyces cerevisiae]; (Z72899) ORF YGR116w [ <i>Saccharomyces cerevisiae</i> ] (U58946) transposase [Aspergillus awamori] (D63703) isobutene-forming enzyme and benzoate 4-hydroxylase [Rhodotorula minuta] (AC005824) unknown protein [Arabidopsis thaliana] hypothetical 61.1 KD protein C11D3.05 in chromosome I; (Z68166) unknown [ <i>Schizosaccharomyces pombe</i> ] (X91867) CPC3 protein [ <i>Neurospora crassa</i> ] catalase ; catalase (EC 1.11.1.6) - <i>Haemophilus influenzae</i> (strain Rd KW20); (U32774) catalase (hktE) [ <i>Haemophilus influenzae</i> Rd] (AF070657) glutathione S-transferase subunit 13 homolog [ <i>Homo sapiens</i> ]]
18182	ENU01976	ANI61C8695:	63-82	809-830	NAP	g1351702	765	129	2.00E-29	36	40	40	40	"arabinan endo-1,5-alpha-L-arabinosidase A precursor (endo-1,5-alpha-L-arabinanase A) (ABN A); (L23430) endo-1,5-alpha-L-Arabinase [Aspergillus niger]; endo-1,5-alpha-L-arabinase [Aspergillus niger]" transcription initiation protein SPT6; SPT6 protein - yeast ( <i>Saccharomyces cerevisiae</i> ); (M34391) SPT6 protein [Saccharomyces cerevisiae]; (Z72899) ORF YGR116w [ <i>Saccharomyces cerevisiae</i> ] (U58946) transposase [Aspergillus awamori] (D63703) isobutene-forming enzyme and benzoate 4-hydroxylase [Rhodotorula minuta] (AC005824) unknown protein [Arabidopsis thaliana] hypothetical 61.1 KD protein C11D3.05 in chromosome I; (Z68166) unknown [ <i>Schizosaccharomyces pombe</i> ] (X91867) CPC3 protein [ <i>Neurospora crassa</i> ] catalase ; catalase (EC 1.11.1.6) - <i>Haemophilus influenzae</i> (strain Rd KW20); (U32774) catalase (hktE) [ <i>Haemophilus influenzae</i> Rd] (AF070657) glutathione S-transferase subunit 13 homolog [ <i>Homo sapiens</i> ]]
18183	ENU01977	ANI61C1015	66-85	816-835	NAP	g33355628	557	111	1.00E-37	35	15	15	15	"arabinan endo-1,5-alpha-L-arabinosidase A precursor (endo-1,5-alpha-L-arabinanase A) (ABN A); (L23430) endo-1,5-alpha-L-Arabinase [Aspergillus niger]; endo-1,5-alpha-L-arabinase [Aspergillus niger]" transcription initiation protein SPT6; SPT6 protein - yeast ( <i>Saccharomyces cerevisiae</i> ); (M34391) SPT6 protein [Saccharomyces cerevisiae]; (Z72899) ORF YGR116w [ <i>Saccharomyces cerevisiae</i> ] (U58946) transposase [Aspergillus awamori] (D63703) isobutene-forming enzyme and benzoate 4-hydroxylase [Rhodotorula minuta] (AC005824) unknown protein [Arabidopsis thaliana] hypothetical 61.1 KD protein C11D3.05 in chromosome I; (Z68166) unknown [ <i>Schizosaccharomyces pombe</i> ] (X91867) CPC3 protein [ <i>Neurospora crassa</i> ] catalase ; catalase (EC 1.11.1.6) - <i>Haemophilus influenzae</i> (strain Rd KW20); (U32774) catalase (hktE) [ <i>Haemophilus influenzae</i> Rd] (AF070657) glutathione S-transferase subunit 13 homolog [ <i>Homo sapiens</i> ]]
18184	ENU01978	ANI50C1469	36-55	785-808	NAP	g1168784	83	7.00E-30	37	45	45	45	45	"arabinan endo-1,5-alpha-L-arabinosidase A precursor (endo-1,5-alpha-L-arabinanase A) (ABN A); (L23430) endo-1,5-alpha-L-Arabinase [Aspergillus niger]; endo-1,5-alpha-L-arabinase [Aspergillus niger]" transcription initiation protein SPT6; SPT6 protein - yeast ( <i>Saccharomyces cerevisiae</i> ); (M34391) SPT6 protein [Saccharomyces cerevisiae]; (Z72899) ORF YGR116w [ <i>Saccharomyces cerevisiae</i> ] (U58946) transposase [Aspergillus awamori] (D63703) isobutene-forming enzyme and benzoate 4-hydroxylase [Rhodotorula minuta] (AC005824) unknown protein [Arabidopsis thaliana] hypothetical 61.1 KD protein C11D3.05 in chromosome I; (Z68166) unknown [ <i>Schizosaccharomyces pombe</i> ] (X91867) CPC3 protein [ <i>Neurospora crassa</i> ] catalase ; catalase (EC 1.11.1.6) - <i>Haemophilus influenzae</i> (strain Rd KW20); (U32774) catalase (hktE) [ <i>Haemophilus influenzae</i> Rd] (AF070657) glutathione S-transferase subunit 13 homolog [ <i>Homo sapiens</i> ]]
18185	ENU01979	ANI61C3072:	28-47	781-804	NAP	g4454690	54	0.000001						"arabinan endo-1,5-alpha-L-arabinosidase A precursor (endo-1,5-alpha-L-arabinanase A) (ABN A); (L23430) endo-1,5-alpha-L-Arabinase [Aspergillus niger]; endo-1,5-alpha-L-arabinase [Aspergillus niger]" transcription initiation protein SPT6; SPT6 protein - yeast ( <i>Saccharomyces cerevisiae</i> ); (M34391) SPT6 protein [Saccharomyces cerevisiae]; (Z72899) ORF YGR116w [ <i>Saccharomyces cerevisiae</i> ] (U58946) transposase [Aspergillus awamori] (D63703) isobutene-forming enzyme and benzoate 4-hydroxylase [Rhodotorula minuta] (AC005824) unknown protein [Arabidopsis thaliana] hypothetical 61.1 KD protein C11D3.05 in chromosome I; (Z68166) unknown [ <i>Schizosaccharomyces pombe</i> ] (X91867) CPC3 protein [ <i>Neurospora crassa</i> ] catalase ; catalase (EC 1.11.1.6) - <i>Haemophilus influenzae</i> (strain Rd KW20); (U32774) catalase (hktE) [ <i>Haemophilus influenzae</i> Rd] (AF070657) glutathione S-transferase subunit 13 homolog [ <i>Homo sapiens</i> ]]

Seq num	Seq id	Contig Source	Primer 3 pos	Primer 5 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18186	ENU01980	ANI61C1073	70..87	828..847	NAP	g1351671	165	83	3.00E-15				hypothetical 25.4 KD protein C1F7.10 in chromosome I ; hypothetical protein SPAC1F7.10 - fission yeast
4:1983..1164													(Schizosaccharomyces pombe) ; (Z67998) unknown
18187	ENU01981	ANI61C4097:	56..75	814..834	NAP	g586299	630	203	2.00E-51	50	67		[Schizosaccharomyces pombe] hypothetical oxidoreductase in RPB5- CDC28 intergenic region ; probable membrane protein YBR159w - yeast (Saccharomyces cerevisiae) ; (Z36028) ORF YBR159w [Saccharomyces cerevisiae]
234..1054													
18188	ENU01982	ANI61C6237:	71..91	836..855	NAP	g732189	735	157	9.00E-38	37	61		hypothetical 49.1 KD protein in SSB2-SPX18 intergenic region ; hypothetical protein YNL207w - yeast
1362..2188													(Saccharomyces cerevisiae) ; (X78898) N1342 [Saccharomyces cerevisiae] ; (Z71483) ORF YNL207w
18189	ENU01983	ANI61C1754:	22..44	790..809	NAP	g466171	827	215	3.00E-79	89	96		[Saccharomyces cerevisiae] "GTP-binding protein YPT1 ; GTP-binding protein ypt1 - Neurospora crassa ; (S51252) NCYPT1=putative small GTP-binding protein
3010..2181													[Neurospora crassa, Peptide, 203 aa] [Neurospora crassa] ; small GTP-binding protein "[Neurospora crassa]" (AL035210) halotolerance protein
18190	ENU01984	ANI61C9551:	26..45	812..831	NAP	g4160397	782	257	5.00E-68	49	76		[Schizosaccharomyces pombe] putative sterigmatocystin biosynthesis monooxygenase STCW ; (U34740) putative FAD-containing
5918..5071													monooxygenase [Emmericella nidulans] (Z98602) putative siroheme synthase [Schizosaccharomyces pombe]
18191	ENU01985	ANI61C7226:	42..61	839..858	NAP	g2498971	2547	599	e-171	99	58		(AL021815) putative cis-muconate cyclosomerase [Schizosaccharomyces pombe]
967..1825													
18192	ENU01986	ANI61C7492:	49..68	851..880	NAP	g2330809	571	217	7.00E-57	50	96		
456..1329													
18193	ENU01987	ANI61C6496:	42..61	863..887	NAP	g2879855	954	179	2.00E-44	48	45		
695..61													

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Blast at	Blast at	% id	% cvrg	Description
18194	ENU01988	ANI61C1410:	58-77	891-910	NAP	g3024813	280	125	3.00E-28	"vanillyl)-alcohol oxidase (aryl-alcohol oxidase) (4-allylphenol oxidase); Chain A, Structure Of The Octameric Flavoenzyme Vanillyl-Alcohol Oxidase In Complex With Isoeugenol; Chain B, Structure Of The Octameric Flavoenzyme Vanillyl-Alcohol Oxidase In Complex With Isoeugenol; Chain A, Structure Of The Octameric Flavoenzyme Vanillyl-Alcohol Oxidase ; Chain B, Structure Of The Octameric Flavoenzyme Vanillyl-Alcohol Oxidase ; Chain A, Structure Of The Octameric Flavoenzyme Vanillyl-Alcohol Oxidase In Complex With P-Cresol ; Chain B, Structure Of The Octameric Flavoenzyme Vanillyl-Alcohol Oxidase In Complex With P-Cresol ; Chain A, Structure Of The Octameric Flavoenzyme Vanillyl-Alcohol Oxidase In Complex With 2-Nitro-P-Cresol ; Chain A, Structure Of The Octameric Flavoenzyme Vanillyl-Alcohol Oxidase In Complex With 2-Nitro-P-Cresol ; Chain A, Structure Of The Octameric Flavoenzyme Vanillyl-Alcohol Oxidase In Complex With 4-(1-Heptenyl)phenol ; Chain B, Structure Of The Octameric Flavoenzyme Vanillyl-Alcohol Oxidase In Complex With 4-(1-Heptenyl)phenol "
18195	ENU01989	ANI61C9556:	36-57	869-888	NAP	g3451313	242	65	1.00E-15	34
18196	ENU01990	ANI61C298:1	60-79	897-916	NAP	g3024443	464	160	1.00E-38	38
			948..1050					92		pyrroline-5-carboxylate reductase (EC 1.5.1.2)-Zalerion arboricola ; (U33266) pyrroline carboxylate reductase [Zalerion arboricola]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvg	Description
18197	ENU01991	ANI61C8349:	64..83	903..922	NAP	g3738171	507	145	3.00E-40	44	87	"(AL0311856) atp synthase gamma chain, mitochondrial precursor [Schizosaccharomyces pombe]"	
18198	ENU01992	ANI61C8021:	70..89	913..932	NAP	g2498731	206	50	2.00E-18	39	64	probable NADP-dependent oxidoreductase P1 ; zeta-crystallin homolog - Arabidopsis thaliana ; (Z49768) zeta-crystallin homologue [Arabidopsis thaliana]	
18199	ENU01993	ANI61C3602:	22..46	881..900	NAP	g730689	261	75	1.00E-12	32	89	RTM1 protein ; RTM1 protein - yeast (Saccharomyces cerevisiae) ; (U02618) RTM1 gene product [Saccharomyces cerevisiae]	
18200	ENU01994	ANI61C9410:	53..72	912..931	NAP	g3718005	1054	387	e-107	62	52	(AJ006652) alternative NADH-dehydrogenase [Yarrowia lipolytica] lipoamide acyltransferase component precursor of branched-chain alpha-keto acid dehydrogenase complex (E2) (Dihydrolipoamide branched chain transacylase) (BCKAD E2 subunit) ; dihydrolipoamide transacylase	
18201	ENU01995	ANI61C9218:	46..65	915..934	NAP	g1709438	621	242	3.00E-63			precursor - mouse ; (L42996) acyltransferase [Mus musculus] ; branched chain alpha-ketoacid dehydrogenase;subunit=E2 [Mus musculus]	
18202	ENU01996	ANI61C3555:	61..80	937..956	NAP	g1001835	320	145	5.00E-34	33	79	(D64005) nitrilase [Synechocystis sp.]	
18203	ENU01997	ANI61C8559:	50..75	929..948	NAP	g4432914	896	128	1.00E-51	59	46	(D45894) thiamine-4 [Neurospora crassa]	
18204	ENU01998	ANI61C9802:	72..89	952..972	NAP	g2909465	235	100	2.00E-20	29	96	(AL021930) hypothetical protein Rv0276 [Mycobacterium tuberculosis]	
18205	ENU01999	ANI61C7233:	47..64	930..949	NAP	g4539600	403	88	5.00E-31	52	70	(AL049522) hypothetical protein [Schizosaccharomyces pombe] (L02869) VPS7 [Saccharomyces cerevisiae]	
18206	ENU02000	ANI61C5362:	42..62	931..948	NAP	g173177	577	210	1.00E-53	40	52	Extensin precursor (cell wall hydroxyproline-rich glycoprotein) ; precursor - common tobacco ; (X13885) extensin (AA 1..620) [Nicotiana tabacum]	
18207	ENU02001	ANI61C1208:	1..233	1..233	NAP	g119714	150	53	0.000002	29	33		
			4167..5117										

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Prob	Blast 4.00E-19	% id 39	% cvtg 22	Description
18208	ENU02002	ANI61C1065	43-62	933-952	NAP	g1708797	445	96					[Kluyveromyces marxianus var. lactis] ; (X70373) LET1 [Kluyveromyces lactis]
18209	ENU02003	ANI61C1708:	27-46	924-943	NAP	g3661614	2806	579	e-164	88	41		(AF093142) aconitase [Aspergillus terreus]
18210	ENU02004	ANI61C859:1	70-90	968-987	NAP	g1169587	994	294	6.00E-99	60	65		"fructose-2,6-Bisphosphatase ; fructose-2,6-bisphosphate 2-phosphatase (EC 3.1.3.46) - yeast (Saccharomyces cerevisiae) ; (Z49430) ORF YIL155c [Saccharomyces cerevisiae]"
18211	ENU02005	ANI50C721_ 1:18..977	38-57	936-955	NAP	g2239208	132	4.00E-30	35	30			(Z97209) hypothetical protein [Schizosaccharomyces pombe]
18212	ENU02006	ANI61C9205: 4292..3314	45-64	963-982	NAP	g140459	376	49	4.00E-14	51	74		"hypothetical 30.7 KD protein in RVS161-ADP1 intergenic region ; hypothetical protein YCR010c - yeast (Saccharomyces cerevisiae) ; (X59720) YCR010c, len:283 [Saccharomyces cerevisiae]"
18213	ENU02007	ANI61C1116 1:459..29	46-66	967-986	NAP	g1938424	274	85	3.00E-34	41	21		(U97002) similar to acyl-CoA dehydrogenases and epoxide hydrolases [Caenorhabditis elegans]
18214	ENU02008	ANI61C7920: 1937..949	69-87	994-1015	NAP	g112790	456	199	3.00E-50	33	90		3-dehydroshikimate dehydratase (DHS dehydratase) ; 3-dehydroshikimate dehydratase - Neurospora crassa ; (X14603) DHS dehydratase [Neurospora crassa] ; (M10139) 3-dehydroshikimate dehydratase [Neurospora crassa]
18215	ENU02009	ANI50C1679 9_1:1996..100	39-62	967-986	NAP	g2228748	90	3.00E-17	23	52		(U93867) RNA polymerase III subunit [Homo sapiens]	
18216	ENU02010	ANI61C142:1 893..901	72-94	1002-1022	NAP	g2735428	54	0.000002					(U94913) H-K-ATPase alpha 2b subunit [Rattus norvegicus]

Seq num	Seq id	Contig Source	Primer 3 pos	Primer Basis	Selection	aat	Blast Score	Blast Prob	% id	% cvrg	Description	
			5 pos	NAP	Database Hit	ncbi gi	Score	Prob				
18217	ENU02011	ANI61C5215:	39-58	977-996	g4093186	247	71	2.00E-11	30	91	"(AFI06583) contains similarity to domains present in ubiquitin-regulatory proteins (Pfam: PF00789, Score=79.3, E=7.8e-20, N=1), C2H2-type zinc finger domain (Pfam: PF00096, Score=9.5, E=6.2, N=1) and ubiquitin-associated domains (Pfam: PF00...)" (D83003) ORF(AA 1-1338) [Nicotiana tabacum]	
18218	ENU02012	ANI61C1002	44-64	986-1008	NAP	g1167523	219	62	1.00E-20	26	24	
18219	ENU02013	ANI61C9368:	45-64	1001-1021	NAP	g2497103	512	138	4.00E-39	42	43	"hypothetical 76.1 KD protein in UNG1-OST6 intergenic region; hypothetical protein YML020w - yeast (Saccharomyces cerevisiae); (Z46659) unknown orf, len: 664, CAI: 0.13 [Saccharomyces cerevisiae]"
18220	ENU02014	ANI61C6615:	22-53	982-1001	NAP	g2326188	654	235	5.00E-61	46	92	(U8106) mixed-linked glucanase precursor [Cochliobolus carbonum] vegetative incompatibility protein HET-E-1 ; (L28-25) beta transducin-like protein [Podospora anserina]
18221	ENU02015	ANI61C5217:	49-68	1010-1029	NAP	g3023956	264	90	1.00E-22	33	21	"glutamate decarboxylase, 67 KD isoform (GAD-67) (67 KD glutamic acid decarboxylase); glutamate decarboxylase (EC 4.1.1.15) 1 - cat ; (M18629) glutamic acid decarboxylase [Felis catus]"
18222	ENU02016	ANI61C3697:	40-59	1006-1024	NAP	g416884	658	253	1.00E-66	40	54	splicing factor U2AF homolog - mouse ; (X64587) orf [Mus musculus] putative transcriptional regulatory protein in MKK2-COX11 intergenic region ; hypothetical protein YPL133c - yeast (Saccharomyces cerevisiae); (U43703) Lpi12p [Saccharomyces cerevisiae]
18223	ENU02017	ANI61C6281:	70-90	1045-1065	NAP	g110998	451	178	2.00E-49	42	61	C3H1.06C in chromosome I ; (Z68144) putative major facilitator superfamily transporter [Schizosaccharomyces pombe]
18224	ENU02018	ANI61C3002:	63-82	1041-1061	NAP	g1730882	529	152	5.00E-54	41	69	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]
18225	ENU02019	ANI61C1025	64-83	1044-1063	NAP	g1351690	393	73	2.00E-19	30	55	hypothetical 63.5 KD protein
		4:149..108										
18226	ENU02020	ANI61C1002	44-64	1036-1055	NAP	g1167523	219	62	1.00E-20	26	25	putative major facilitator superfamily transporter [Schizosaccharomyces pombe]
		4:2643..1589										

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat	Blast Score	Blast Prob	% id	% cvg	Description
18227	ENU02021	ANI61C6760:	63-85	NAP	g5338067	1738	217	8.00E-56	36	24	(M77661) putative pol polyprotein [Magnaporthe grisea]		
18228	ENU02022	ANI61C1099	42-61	NAP	g3912972	328	125	9.00E-29	33	94	alcohol dehydrogenase II (ADH 1); (AF008244) alcohol dehydrogenase II [Pichia stipitis]		
18229	ENU02023	ANI61C3608:	44-63	1045-1176..114	NAP	g2408068	769	159	3.00E-77	51	67	(Z99165) hypothetical protein [Schizosaccharomyces pombe]	
18230	ENU02024	ANI61C4301:	42-61	1046-3496..2431	NAP	g2791498	176	111	8.00E-24	35	97	(AL021246) hypothetical protein Rv2458 [Mycobacterium tuberculosis]	
18231	ENU02025	ANI61C8515:	49-66	1054-1422..2488	NAP	g543962	525	173	2.00E-42	45	88	cell division control protein 16; cdc16 protein - fission yeast (Schizosaccharomyces pombe); (X71605) cdc16 [Schizosaccharomyces pombe]; (Z98981) cell division control protein 16 [Schizosaccharomyces pombe]	
18232	ENU02026	ANI61C9037:	39-58	1047-2449..3529	NAP	g2385382	586	116	3.00E-52	42	97	(AJ001428) D-mandelate dehydrogenase [Rhodotorula graminis]; (AJ001429) D-mandelate dehydrogenase [Rhodotorula graminis] putative transporter C11D3.18C; (Z68166) unknown [Schizosaccharomyces pombe]	
18233	ENU02027	ANI61C3359:	70-88	1091-3940..2858	NAP	g1351714	236	81	2.00E-14	27	62	"GNS1" protein ; probable membrane protein YCR034w - yeast (Saccharomyces cerevisiae); (X56909) YCR521 [Saccharomyces cerevisiae]; (S78624) YCR521 [Saccharomyces cerevisiae=yeast, Peptide, 347 aa] [Saccharomyces cerevisiae]; (X59720) YCR34w, len:347 [Saccharomyces cerevisiae]; (AF012655) v-snare bypass mutant [Saccharomyces cerevisiae]" (Z68906) ATP-binding multidrug cassette transporter [Botryotinia fuckeliana]	
18235	ENU02029	ANI61C9101:	63-82	1084-3505..2422	NAP	g3114719	587	109	2.00E-49	43	16		

Seq num	Seq id	Contig	Source	Primer 3 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat	Blast Score	Blast Prob	% id	% cvrg	Description
18236	ENU02030	ANI61C8453:	60-81	3017..1910	1125	NAP	g1352980	846	215	8.00E-85	50	30	ATP-dependent RNA helicase DOB1 (mRNA transport regulator MTR4); SKI2 protein homolog YJL050w - yeast (Saccharomyces cerevisiae); (Z49325) ORF YJL050w	
18237	ENU02031	ANI61C119:1	22-56	1069-55..1263	1088	NAP	g2133335	329	53	0.000003	27	64	[Saccharomyces cerevisiae]; transposase - fungus ( <i>Cochliobolus carbonum</i> )	
18238	ENU02032	ANI61C360:2	60-83	1120-127..3248	1139	NAP	g1293655	589	132	4.00E-30	37	53	(U51327) versicolorin B synthase [Aspergillus parasiticus]; (U51328) versicolorin B synthase [Aspergillus parasiticus]	
18239	ENU02033	ANI61C7661:	58-75	1123-1691..565	1142	NAP	g1658175	809	279	1.00E-86	45	72	(U74468) indole-3-acetaldehyde dehydrogenase [ <i>Ustilago maydis</i> ]	
18240	ENU02034	ANI61C7147:	54-72	1125-2919..4051	1144	NAP	g3122300	1980	602	0	98	82	calcium/calmodulin-dependent protein kinase (CMPK); Ca2+/calmodulin-dependent protein kinase (EC 2.7.1.123) - <i>Emericella nidulans</i> ; (M74120) calmodulin-dependent protein kinase [Emericella nidulans]; (AF054580) calmodulin-dependent protein kinase [Emericella nidulans] stericatocystin-7-O-methyltransferase precursor; (L25835) O-methyltransferase [Aspergillus flavus]; (L25834) O-methyltransferase [Aspergillus parasiticus]; (L22091) O-methyltransferase [Aspergillus parasiticus]	
18241	ENU02035	ANI61C1107	44-63	1117-7:1164..2298	1136	NAP	g2498702	196	109	3.00E-23	33	30	(AL031128) 1-evidence=predicted by content; 1-method=genefinder; 084; 1-method_score=404.95; 1-evidence_end; 2-evidence=predicted by match; 2-match_accession=SWISS-PROT:P46821; 2-match_description=microtubule-associated protein ...	
18242	ENU02036	ANI61C7320:	49-68	1129-123..1264	1148	NAP	g3355742	47	0.0003				(Z25485) ACR1-protein [Saccharomyces cerevisiae]; (Z99165) hypothetical protein [Schizosaccharomyces pombe]	
18243	ENU02037	ANI61C6437:	22-40	1130-3459..2292	1147	NAP	g396595	782	236	7.00E-81	61	96		
18244	ENU02038	ANI61C7645:	22-46	1130-1118..1303	1149	NAP	g2408062	531	164	1.00E-39	35	58		

Seq num	Seq id	Contig Source	Primer 3 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat	Blast Score	Blast Prob	% id	% cvrg	Description
18245	ENU02039	ANI61C2531:	62-81	1179-1202..24	NAP	g2833229	626	116	4.00E-52	36	70	Laccase (benzenediol:oxigen oxidoreductase) (unishiol oxidase) (diphenol oxidase)	
18246	ENU02040	ANI61C6864:	32-51	1151-1215..2395	NAP	g834534	764	184	1.00E-45	45	39	[Saccharomyces cerevisiae] (X87634) oxidative stress resistance [Arabidopsis thaliana]	
18247	ENU02041	ANI61C292:9	70-89	1199-263..8070	NAP	g2833081	416	99	2.00E-28	38	96	"Succinic semialdehyde dehydrogenase ; (Y11192) NAD+ dependent succinic semialdehyde dehydrogenase [Homo sapiens]; (AL031230) dJ73M23.2 (NAD+-dependent succinic semialdehyde dehydrogenase (SSADH, EC 1.12.1.24)) [Homo sapiens]" calcium-transporting ATPase 2 (vacuolar CA2+-ATPase); Ca2+-transporting ATPase (EC 3.6.1.38) - yeast [Saccharomyces cerevisiae]; (U03660) calcium ATPase [Saccharomyces cerevisiae]; (Z72528) ORF YGL006w [Saccharomyces cerevisiae]	
18249	ENU02043	ANI61C1069	39-58	1185-0..2234..1027	NAP	g728904	1065	177	1.00E-43	47	31	(AL022072) possible transmembrane protein [Schizosaccharomyces pombe] Tetraacycline resistance protein (transposon TN4351 / TN4400); NADP-requiring oxidoreductase - Bacteroides fragilis; (M37699) tetracycline resistance protein [Transposon Tn4351] (AL049559) hypothetical protein [Schizosaccharomyces pombe] hypothetical 43.5 KD protein in RPB9- ALG2 intergenic region; hypothetical protein YGL067w - yeast [Saccharomyces cerevisiae]; (Z72589) ORF YGL067w [Saccharomyces cerevisiae]	
18250	ENU02044	ANI61C7104:	51-70	1204-217..431	NAP	g2950489	309	69	8.00E-11	45	53		
18251	ENU02045	ANI61C3347:	44-63	1198-441..3196	NAP	g401172	183	107	2.00E-22	28	96		

Seq num	Seq id	Contig	Source	Primer 3 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat	Blast Score	Blast Prob	% id	% cvrg	Description
18254	ENU02048	ANI61C8681:	45-64	2888..1653	1238	NAP	g2499619	179	68	7.00E-15	32	21		probable serine/threonine-protein kinase YMR216C ; probable membrane protein YMR216c - yeast (Saccharomyces cerevisiae) ; (Z49809)
18255	ENU02049	ANI61C3355:	22-41	2535..3770	1195..1215	NAP	g418150	856	122	1.00E-56				unknown [Saccharomyces cerevisiae] GABA-specific permease (GABA-specific transport protein) ; GABA transport protein yeast (Saccharomyces cerevisiae) ; (X66472)
18256	ENU02050	ANI61C6437:	60-79	5220..6462	1241..1260	NAP	g2497127	440	182	3.00E-45	32	90		GABA-specific permease [Saccharomyces cerevisiae] ; (X99000) GABA transporter protein [Saccharomyces cerevisiae] ; (Z74258) ORF YDL210w [Saccharomyces cerevisiae] ; GABA transport protein [Saccharomyces cerevisiae]
18257	ENU02051	ANI61C1135	69-89	6..3899..2651	1256..1275	NAP	g2213553	595	183	3.00E-45	39	56		hypothetical 48.4 KD protein in ARP9-IMP2 intergenic region ; probable membrane protein YMR034c - yeast (Saccharomyces cerevisiae) ; (Z49213)
18258	ENU02052	ANI61C7225:	64-82	243..1497	1257..1276	NAP	g2497946	1369	279	e-120	62	77		unknown [Saccharomyces cerevisiae] (Z97052) hypothetical protein [Schizosaccharomyces pombe] "PRD protein" ; (U73857) similar to yqiP of <i>B. subtilis</i> [Escherichia coli] ; yqiP of <i>B. subtilis</i> [Escherichia coli] ; (AE000140) orf, hypothetical protein [Escherichia coli]" (AB012140) arylesterase [Acetobacter pasteurianus]
18259	ENU02053	ANI61C4189:	39-59	1681..422	1237..1256	NAP	g2978332	172	57	0.000000	33	51		hypothetical 48.0 KD protein C1B3.08 in chromosome I ; (Z98598)
18260	ENU02054	ANI61C4716:	50-69	2104..841	1252..1271	NAP	g3183362	339	103	3.00E-21	38	74		hypothetical protein [Schizosaccharomyces pombe] (Y10403) RNA-directed RNA polymerase [Lycopersicon esculentum] (AL033391) hypothetical membrane protein [Candida albicans]
18261	ENU02055	ANI61C1046	33-52	7..49..1313	1237..1255	NAP	g4038592	308	154	1.00E-36	30	32		(M20319) aminotriazole resistance protein [Saccharomyces cerevisiae] (AB012604) squalene synthase [Candida utilis]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18265	ENU02059	ANI61C8226:	67..87	1298..	NAP	g4584836	424	150	1.00E-35	33	54	(AJ238009) serine threonine protein kinase [Sclerotinia sclerotiorum]	
18266	ENU02060	ANI61C8226:	67..87	1298..	NAP	g4584836	424	150	1.00E-35	33	54	(AJ238009) serine threonine protein kinase [Sclerotinia sclerotiorum]	
18267	ENU02061	ANI61C1064	47..66	1280..	NAP	g2565329	694	278	7.00E-77	45	88	(AF025290) cAMP-dependent protein kinase catalytic subunit [Ustilago maydis]	
18268	ENU02062	ANI61C4192:	24..43	1261..	NAP	g4160579	227	99	5.00E-20	37	49	(AL035218) hypothetical protein [Schizosaccharomyces pombe]	
18269	ENU02063	ANI61C5216:	48..68	1288..	NAP	g2661608	1696	246	e-118	53	69	(AL009197) hypothetical ctp synthase [Schizosaccharomyces pombe]	
18270	ENU02064	ANI61C2416:	23..43	1296..	NAP	g2239198	636	178	1.00E-62	55	99	(Z97209) putative tricarboxylate transport protein protein	
18271	ENU02065	ANI61C7568:	53..72	1339..	NAP	g1709181	503	136	9.00E-39	34	70	[Schizosaccharomyces pombe] "high affinity methionine permease ; methionine transport protein, high affinity - yeast (Saccharomyces cerevisiae); (U40316) high affinity methionine permease [Saccharomyces cerevisiae]; (Z72840) ORF YGR055w [Saccharomyces cerevisiae]"	
18272	ENU02066	ANI61C1128	23..48	1317..	NAP	g2132491	152	44	5.00E-11	34	68	Probable membrane protein YDR284c - yeast (Saccharomyces cerevisiae); (U51031) Ydr284cp [Saccharomyces cerevisiae]	
18273	ENU02067	ANI61C1016	22..41	1326..	NAP	g1169782	556	206	5.00E-60	37	91	Fusca protein FUS6 ; (L26498) FUS6 [Arabidopsis thaliana]	
18274	ENU02068	ANI61C3255:	44..63	1348..	NAP	g3023683	1913	560	e-180	90	86	Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase) ; 6beta-hydroxyhyoscynamine epoxidase (EC 1.14.11.14) – Aspergillus oryzae ; (D63941) enolase [Aspergillus oryzae] ; (D64113) enolase [Aspergillus oryzae] ; enolase [Aspergillus oryzae] putative taurate transporter ; (U32375) membrane protein [Agrobacterium vitis] (AB018313) KIAA0770 protein [Homo sapiens]	
18275	ENU02069	ANI61C1080	62..81	1389..	NAP	g4033481	233	63	2.00E-21	30	84		
18276	ENU02070	ANI61C7689:	71..90	1408..	NAP	g3882261	375	98	8.00E-25	31	54		

Seq num	Seq id	Contig Source	Primer 3 pos	Primer Basis	Selection Database Hit	aat ncbi gi	Score	Score Prob	% id	% evrg	Description	
18277	ENU02071	ANI61C9422:	40-63	NAP	1379-	1398	214	102	4.00E-21	29	45 (AF131820) Unknown [Homo sapiens]	
18278	ENU02072	ANI61C3006:	40-59	NAP	1388-	1407	g2493484	1127	342	e-110	53	81 glycerol kinase (ATP:glycerol 3-phototransferase) (glycerokinase) (GK); (U48403) glycerol kinase [Mus musculus]
18279	ENU02073	ANI61C6597:	44-63	1393- 4933..6344	1413	NAP	g417699	1559	321	e-171	"histone deacetylase RPD3 (transcriptional regulatory protein RPD3); transcription regulator RPD3-yeast (Saccharomyces cerevisiae); (S66438) RPD3 [Saccharomyces cerevisiae; Peptide, 433 aa]	
18280	ENU02074	ANI61C1223:	24-45	1374- 39..1450	1393	NAP	g3023717	1095	437	e-121	58	86 [Saccharomyces cerevisiae]; (X83226) global transcriptional regulator [Saccharomyces cerevisiae]; (Z71606) ORF YNL330c [Saccharomyces cerevisiae]"
18281	ENU02075	ANI61C1029	69-87	1431-	NAP	g1072104	2199	628	e-180	70	68 ESA1 protein ; hypothetical protein YOR244w – yeast (Saccharomyces cerevisiae); (Z71512) ORF YOR244w [Saccharomyces cerevisiae]	
18282	ENU02076	ANI61C7367:	47-64	1420- 1181..2615	1439	NAP	g2619026	699	153	8.00E-73	43	96 (U39201) acetolactate synthase [Magnaporthe grisea] (AF027868) YoaN [Bacillus subtilis]; (Z99114) similar to hypothetical proteins [Bacillus subtilis] (U73857) galactoside O-acetyltransferase [Escherichia coli] (AL032671) predicted using Genefinder [Caenorhabditis elegans] (AC004473). Contains similarity to goliath protein gb M97204 from D. melanogaster. [Arabidopsis thaliana] Isotrichodermin C-15 hydroxylase (cytochrome P450 65A1); (AF011355) isotrichodermin C-15 hydroxylase [Fusarium sporotrichioides] (AF041050) 4-coumarate:CoA ligase [Populus tremuloides] (Z98529) conserved hypothetical protein [Schizosaccharomyces pombe]
18286	ENU02080	ANI61C1073	41-59	1448- 3..4685..3217	1467	NAP	g3915140	448	73	2.00E-19	33	74
18287	ENU02081	ANI61C8810:	23-40	1443-	NAP	g3258637	442	128	3.00E-50	37	64 (AF041050) 4-coumarate:CoA ligase [Populus tremuloides]	
18288	ENU02082	ANI61C3730:	52-71	1484- 613..19	1501	NAP	g3859776	62	0.000000	41	38 (Z98529) conserved hypothetical protein [Schizosaccharomyces pombe]	

Seq num	Seq id	Contig Source	Primer 3 pos	Primer Basis	Selection	aat	Blast Score	Blast Prob	% id	% cvrg	Description	
			5 pos	Database Hit	ncbi gi	Score	Score	Prob	id	cvrg		
18289	ENU02083	ANI61C3730:	72-91	NAP	g2648302	239	115	6.00E-25	43	49	"(AE000952) 2-hydroxyhepta-2,4-diene-1,7-dioate isomerase [fpcE-2] [Archaeoglobus fulgidus]" (UT5973) NAAG-peptidase; NAALADase; prostate specific membrane antigen; PSM; PSMA [Rattus norvegicus]; (AF040256)	
18290	ENU02084	ANI61C2434:	23-41	1481-	NAP	g1661227	633	234	1.00E-60	32	62	glutamate carboxypeptidase II [Rattus norvegicus]
18291	ENU02085	ANI61C1714:	24-43	1496-3069..1536	NAP	g547880	693	102	7.00E-58	43	78	LYSINE-specific permease ; (U00007) lysine-specific permease [Escherichia coli]; Lys permease [Escherichia coli] (AF017990) Fkb39p
18292	ENU02086	ANI61C5953:	24-43	1512-1675..3225	NAP	g3406742	509	157	2.00E-37	45	72	[Schizosaccharomyces pombe]; (AL035548) Peptidyl Prolyl cis-trans isomerase [Schizosaccharomyces pombe]
18293	ENU02087	ANI61C1758:	24-45	1514-3547..5098	NAP	g464369	566	118	7.00E-26	26	35	phenol 2-monoxygenase (phenol hydroxylase); (L04488) phenol hydroxylase [Trichosporon cutaneum] (X98309) ARI protein [Drosophila melanogaster]; (X98310) ARI protein [Drosophila melanogaster]
18294	ENU02088	ANI61C1052	69-87	1591-1:488..2069	NAP	g2058299	938	317	e-105	44	95	phosphate-repressible phosphate permease ; phosphate-repressible phosphate permease - Neurospora crassa ; (M31364) phosphate permease [Neurospora crassa]
18295	ENU02089	ANI61C3068:	24-43	1582-814..971	NAP	g130117	639	137	3.00E-39	35	80	Dicarboxylic amino acid permease ; dicarboxylic amino acid permease DIP5 - yeast (Saccharomyces cerevisiae); (X95802) dicarboxylic amino acids Dip5 permease [Saccharomyces cerevisiae]; (Z73621) ORF YPL265w [Saccharomyces cerevisiae]
18296	ENU02090	ANI61C4335:	45-64	1624-1165..2805	NAP	g1706439	651	220	1.00E-65	35	81	MLO3 protein ; (L42551) ORF (Z98270) Mlo3p [Schizosaccharomyces pombe]
18297	ENU02091	ANI61C5680:	53-73	1638-3598..1952	NAP	g2498564	186	60	0.000000	39	42	[Schizosaccharomyces pombe]; [Schizosaccharomyces pombe]

Seq num	Seq id	Contig Source	Primer 3 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat	Blast Score	Blast Prob	% id	% cvrg	Description
18298	ENU02092	ANI61C1080	32-51	1618-	NAP	g4033481	233	63	4.00E-22	29	90	putative tartrate transporter ; (U32375)	
18299	ENU02093	ANI61C8511:	53-72	1672-	NAP	g2494913	923	369	e-101	40	98	membrane protein [Agrobacterium vitis]	
18300	ENU02094	ANI61C7716:	34-53	1655-	NAP	g799150	1915	531	e-150	54	69	hypothetical 57.3 KD TRP-ASP repeats containing protein in POM152-	
			2276..594	1674								REC114 intergenic region ; hypothetical protein YMR131c - yeast (Saccharomyces cerevisiae) ; (Z48622)	
18301	ENU02095	ANI61C5161:	53-72	1680-3587..5276	NAP	g2132493	1168	379	e-104	51	86	unknown [Saccharomyces cerevisiae] " (U24701) beta-1,2-D-glucosidase [Septoria lycopersici] ; (U35462) tomatinase [Septoria lycopersici] ; beta2 tomatinase [Septoria lycopersici] "	
18302	ENU02096	ANI61C1048	63-83	1692-7273..36	NAP	g2131317	40	0.04				probable membrane protein YDR294c - yeast [Saccharomyces cerevisiae] ; (U51031) Ydr294cp [Saccharomyces cerevisiae]	
18303	ENU02097	ANI61C5282:	56-74	1705-3209..1499	NAP	g3258635	526	219	3.00E-61	32	99	hypothetical protein YDL037c - yeast (Saccharomyces cerevisiae) ; (Z71781) unknown [Saccharomyces cerevisiae] ; (Z74085) ORF YDL037c [Saccharomyces cerevisiae]	
18304	ENU02098	ANI61C1054	41-60	1693-9:1738..3452	NAP	g2921400	606	257	1.00E-74	33	90	(AF036097) flavocytochrome b subunit [Bos taurus]	
18305	ENU02099	ANI61C154:2	47-66	1713-490..764	NAP	g1405353	614	100	3.00E-55	35	30	(D8686) canalicular multispecific organic anion transporter [Rattus norvegicus]	
18306	ENU02100	ANI61C7473:	71-90	1762-2074..3826	NAP	g2760084	228	126	4.00E-28	31	49	(Y16045) leucine-rich repeat protein [Arabidopsis thaliana]	
18307	ENU02101	ANI61C1883:	68-87	1760-3449..1696	NAP	g2492816	1271	176	e-114	50	84	Uracil permease ; (X98696) uracil permease [Schizosaccharomyces pombe]	
18308	ENU02102	ANI61C1014	68-88	1821-1852	NAP	g3336839	795	100	4.00E-78	40	95	(Y16834) hexose transporter [Candida albicans]	
18309	ENU02103	ANI61C9693:	71-90	1834-5173..3318	NAP	g731909	427	85	2.00E-30	36	31	hypothetical 87.0 KD protein in PAN1- PR1 intergenic region ; hypothetical protein YIR007w - yeast (Saccharomyces cerevisiae)	

Seq num	Seq id	Contig Source	5' pos	Primer 3' pos	Primer Basis	Selection Database Hit	aat	Blast Score	Blast Prob	% id	% cvrg	Description
18310	ENU02104	ANI61C5240:	67-86	1924-755..2676	NAP	g1613878	1680	499	e-140	45	49	(U72236) ModA [Dictyostelium discoideum] (Z74473) predicted using Genefinder [Caenorhabditis elegans]
18311	ENU02105	ANI61C1118:	46-63	1924-11354..10547	NAP	g2877738	122	44	0.003			[AL03..825] putative membrane transport protein
18312	ENU02106	ANI61C5898:	50-69	1995-109..2114	NAP	g3702646	601	135	4.00E-63	34	73	[Schizosaccharomyces pombe] L-amino acid oxidase precursor (LAO) ; L-amino-acid oxidase (EC 1.4.3.2)
18313	ENU02107	ANI61C1125:	52-71	2051-193..2253	NAP	g129307	885	272	e-101	39	93	precursor - Neurospora crassa (AL031261) phosphoserine phosphatase [Schizosaccharomyces pombe]
18314	ENU02108	ANI61C9178:	35-54	2034-4657..6718	NAP	g3417415	462	102	2.00E-48	44	50	hypothetical 51.4 KD protein in RAR1-SCJ1 intergenic region ; hypothetical protein YMR210w - yeast (Saccharomyces cerevisiae) ; (Z49809) unknown [Saccharomyces cerevisiae] probable membrane protein YDL074c-yeast (Saccharomyces cerevisiae) ; (Z74122) ORF YDL074c
18316	ENU02110	ANI61C1122	34-53	2050-9414..2490	NAP	g2132428	356	153	4.00E-36	28	40	[Saccharomyces cerevisiae] (AL034490) hypothetical protein [Schizosaccharomyces pombe] "fatty acid synthase, subunit alpha [contains: EC 1.1.1.100; EC 2.3.1.41]; fatty-acid synthase (EC 2.3.1.85) - Penicillium griseofulvum ; (M37461) FAS2 protein [Penicillium patulum]" "hypothetical 77.5 KD protein in PRP1-STE3 intergenic region ; hypothetical protein YKLJ79c - yeast (Saccharomyces cerevisiae) ; (X74151) previously orf13 and orf14 [2], now merged; homologous to human CENPE [Saccharomyces cerevisiae] ; (Z28179) ORF YKL179c
18317	ENU02111	ANI61C1062	24-45	2080-61866..2040	NAP	g4008552	334	100	4.00E-26	35	57	[Saccharomyces cerevisiae] (AL034490) hypothetical protein [Schizosaccharomyces pombe] "fatty acid synthase, subunit alpha [contains: EC 1.1.1.100; EC 2.3.1.41]; fatty-acid synthase (EC 2.3.1.85) - Penicillium griseofulvum ; (M37461) FAS2 protein [Penicillium patulum]" "hypothetical 77.5 KD protein in PRP1-STE3 intergenic region ; hypothetical protein YKLJ79c - yeast (Saccharomyces cerevisiae) ; (X74151) previously orf13 and orf14 [2], now merged; homologous to human CENPE [Saccharomyces cerevisiae] ; (AL02174) hypothetical protein [Schizosaccharomyces pombe]
18318	ENU02112	ANI61C7956:	63-82	2145-913..2270	NAP	g119830	757	661	0	47	36	
18319	ENU02113	ANI61C4756:	22-57	2132-1265..3436	NAP	g549740	469	113	4.00E-41	28	94	
18320	ENU02114	ANI61C6804:	61-80	2201-3811..6011	NAP	g2842464	260	63	0.000000	26	93	

Seq num	Seq id	Contig	Source	Primer 5 pos	Primer 3 pos	Primer Basis	Selection	Blast gi	aat	Blast Prob	% id	% cvrg	Description
						NAP	Database Hit	ncbi gi	Score	Score	1.00E-16	27	20
18321	ENU02115	ANI61S2760:	43-62	2188-	2188-	NAP	g2072788	89	1.00E-16	27	20	(U64574) cell cycle inhibitor Nifl (AL035065) cell cycle inhibitor nifl.	
316..1				2207									[Schizosaccharomyces pombe]; [Schizosaccharomyces pombe]
18322	ENU02116	ANI61C3865:	38-57	2198-	2217	NAP	g1350600	3129	1186	0	77	88	Ribonucleoside-diphosphate reductase large chain (ribonucleotide reductase); CDC22 protein - fission yeast (Schizosaccharomyces pombe); (Z67998) Cdc22p
3362..5583													[Schizosaccharomyces pombe]
18323	ENU02117	ANI61C2081:	54-73	2213-	2235	NAP	g125935	437	195	1.00E-48	28	70	lactose permease; lactose permease - yeast (Kluyveromyces marxianus var. lactis); (X06997) lactose permease (AA 1-587) [Kluyveromyces lactis] (M59935) negative-acting regulatory protein [Emericella nidulans]; (M77664) repressor protein [Emericella nidulans]
2294..71													[Kluyveromyces marxianus var. lactis]; (X06997) lactose permease (AA 1-587) [Kluyveromyces lactis] (M59935) negative-acting regulatory protein [Emericella nidulans]; (M77664) repressor protein [Emericella nidulans]
18324	ENU02118	ANI61C9003:	63-85	2272-	3491..1222	NAP	g168082	1305	439	e-140	40	78	Maltose permease MAL3T (maltose transport protein MAL3T); maltose transport protein MAL3T - yeast (Saccharomyces cerevisiae); (Z36167) ORF YBR298c [Saccharomyces cerevisiae]
3491..1222				2291									Maltose permease MAL3T (maltose transport protein MAL3T); maltose transport protein MAL3T - yeast (Saccharomyces cerevisiae); (Z36167) ORF YBR298c [Saccharomyces cerevisiae]
18325	ENU02119	ANI61C594:	67-86	2369-	2388	NAP	g585446	772	120	1.00E-83	37	70	hypothetical protein YHR186c - yeast (Saccharomyces cerevisiae); (U00030) Yhr186cp [Saccharomyces cerevisiae] (X86780) polyketide synthase [Streptomyces hygroscopicus]
322..3685													hypothetical protein YHR186c - yeast (Saccharomyces cerevisiae); (U00030) Yhr186cp [Saccharomyces cerevisiae] (X86780) polyketide synthase [Streptomyces hygroscopicus]
18326	ENU02120	ANI61C1055	52-71	2415-	2434	NAP	g731756	867	236	6.00E-79	37	42	probable membrane protein YPL217c - yeast (Saccharomyces cerevisiae); (Z73573) ORF YPL217c
3212..2637													[Saccharomyces cerevisiae]
18327	ENU02121	ANI61C8706:	66-85	2452-	2472	NAP	g987102	493	132	2.00E-62	36	8	"probable glucan 1,3-beta-glucosidase precursor (exo-1,3-beta-glucanase); (Z70721) putative 1,3-beta-D-glucanohydrolase
1514..3962													[Schizosaccharomyces pombe]"
18328	ENU02122	ANI61C1003	72-90	2497-	2516	NAP	g2133002	2342	503	e-141	45	65	"probable membrane protein YPL217c - yeast (Saccharomyces cerevisiae); (Z73573) ORF YPL217c
72-90													[Saccharomyces cerevisiae]
18329	ENU02123	ANI61C1125	72-91	2498-	2516	NAP	g1706727	841	332	7.00E-90	42	48	"probable glucan 1,3-beta-glucosidase precursor (exo-1,3-beta-glucanase); (Z70721) putative 1,3-beta-D-glucanohydrolase
2.685..3171													[Schizosaccharomyces pombe]"

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Primer NAP	Selection Basis	Database Hit	ncbi gi	aat	Blast Score	Blast Prob	% id	% covg	Description
18330	ENU02124	ANI61C1003	72-90	2497-	2516	NAP	g2133002	2342	503	e-141	45	65	probable membrane protein YPL217c-yeast (Saccharomyces cerevisiae); (Z73573) ORF YPL217c	
18331	ENU02125	ANI61C9304:	24-47	2476-	2495	NAP	g2132957	207	51	0.000000	42	14	[Saccharomyces cerevisiae]	
			4815..2302						01					- yeast (Saccharomyces cerevisiae); (Z75286) ORF YOR378w
18332	ENU02126	ANI61C3630:	62-81	2518-	NAP	g1002380		39	0.14					[Saccharomyces cerevisiae]
			2030..1942	2537			g4502897	719	222	1.00E-80	40	47	(U24189) RRM-type RNA binding protein [Caenorhabditis elegans]	
18333	ENU02127	ANI61C648:2	58-77	2698-	NAP	2717								cleft lip and palate associated transmembrane protein 1 ; (AF037338)
			735..34											cleft lip and palate transmembrane protein 1 [Homo sapiens] ; (AF037339) protein 1 [Homo sapiens]
18334	ENU02128	ANI61C7559:	67-86	2707-	NAP	g2853114	361	92	1.00E-17	26	25			(AL021766) hypothetical protein [Schizosaccharomyces pombe]
			126..2828	2727			g3913731	1354	504	e-156	42	82		probable mannosyl-oligosaccharide glucosidase (processing A -glucosidase I); (Z98603) hypothetical protein [Schizosaccharomyces pombe]
18335	ENU02129	ANI61C220:2	49-69	2727-	NAP	2745								(AL035259) putative Ca-calmodulin-dependent serine-threonine-protein kinase [Schizosaccharomyces pombe]
			821..82											Guanyl-specific ribonuclease PB1; ribonuclease T1 (EC 3.1.27.3) - Penicillium brevicompactum; RNase [Penicillium brevicompactum]
18336	ENU02130	ANI61C8057:	45-66	2887-	NAP	g4176548	1115	288	e-109	54	57			cytochrome C oxidase assembly protein COX17; COX17 protein - yeast (Saccharomyces cerevisiae); (L75948) approximately 300 nucleotides distal from helicase gene [Saccharomyces cerevisiae]; (Z73114) ORF YLL009c [Saccharomyces cerevisiae]
18337	ENU02131	ANI61C1412:	66-85	203-223	NAP	g133186	400	111	6.00E-25	71	65			
18338	ENU02132	ANI61C1055	30-50	163-189	NAP	g2493874	127	64	9.00E-11	42	94			
			0..3487..3286											

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database	Hit ncbi	gi	Score	Score	Blast Prob	% id	% cvrg	Description
18339	ENU02133	ANI61C1360:	22-50	164-183	NAP	g2833211	238	46	0.000000	62	50	NADH-ubiquinone oxidoreductase		
		1556..1553										10.5 KD subunit (complex I) (CI);		
												NADH dehydrogenase (ubiquinone)		
												(EC 1.6.5.3) 10.5K chain - Neurospora crassa ; (X69929) NUO-10.5		
18340	ENU02134	ANI61C480:4	55-77	202-222	NAP	g99521	416	137	1.00E-32	91	45	[Neurospora crassa]		
		32..223										nad5 intron 1 protein 459 - Sugar beet mitochondrial (fragment) ; (X55786)		
18341	ENU02135	ANI61C7399:	23-42	172-192	NAP	g1903364	44	0.0002				ORF459 [Beta vulgaris]		
		82..293										(AC000104) EST gb T45093 comes from this gene. [Arabidopsis thaliana] phenol hydroxylase - imperfect fungus (Trichosporon beigelii)		
18342	ENU02136	ANI61C8581:	70-89	232-251	NAP	g102033	98	42	0.0007			"(AE000352) orf, hypothetical protein [Escherichia coli]"		
		4554..4777										"mitochondrial 60S ribosomal protein L33 (YML33); ribosomal protein L33 (YML33); yeast (Saccharomyces cerevisiae); (Z49704) Mrpl33p [Saccharomyces cerevisiae]"		
18343	ENU02137	ANI61C3361:	24-43	187-206	NAP	g1789035	162	62	4.00E-10	46	84	"mitochondrial 60S ribosomal protein L33 (YML33); ribosomal protein L33 (YML33); yeast (Saccharomyces cerevisiae); (Z49704) Mrpl33p [Saccharomyces cerevisiae]"		
		1117..893										"(AE000352) orf, hypothetical protein [Escherichia coli]"		
18344	ENU02138	ANI61C5161:	51-70	215-235	NAP	g1710603	169	62	6.00E-10	38	87	"mitochondrial - yeast (Saccharomyces cerevisiae); (Z49704) Mrpl33p [Saccharomyces cerevisiae]"		
		5997..5772										"mitochondrial 60S ribosomal protein L33 (YML33); ribosomal protein L33 (YML33); yeast (Saccharomyces cerevisiae); (Z49704) Mrpl33p [Saccharomyces cerevisiae]"		
18345	ENU02139	ANI61C3149:	31-49	197-218	NAP	g2507327	156	51	0.000001	44	86	"(AE000352) orf, hypothetical protein [Escherichia coli]"		
		77..306										"(AE000352) orf, hypothetical protein [Escherichia coli]"		
18346	ENU02140	ANI61C7173:	71-90	241-267	NAP	g3395591	176	70	2.00E-12			"(AE000352) orf, hypothetical protein [Escherichia coli]"		
		1312..1550										"(AE000352) orf, hypothetical protein [Escherichia coli]"		
18347	ENU02141	ANI61C4095:	53-72	231-250	NAP	g3647370	210	80	3.00E-15	50	84	"(AE000352) orf, hypothetical protein [Escherichia coli]"		
		457..696										"(AE000352) orf, hypothetical protein [Escherichia coli]"		
18348	ENU02142	ANI61C8881:	59-79	240-259	NAP	g730606	134	56	0.000000	45	88	"DNA-directed RNA polymeraseS I, II, and III 7.7 KD polypeptide (ABC10-alpha) ; DNA-directed RNA polymerase (EC 2.7.7.6) chain ABC10 alpha - yeast (Saccharomyces cerevisiae) ; (U23378) RNA polymerase I, II and III subunit ABC10 alpha [Saccharomyces cerevisiae]; (U10397) Rpb12p: RNA polymerase II subunit [Saccharomyces cerevisiae]"		
		2362..2604										"DNA-directed RNA polymeraseS I, II, and III 7.7 KD polypeptide (ABC10-alpha) ; DNA-directed RNA polymerase (EC 2.7.7.6) chain ABC10 alpha - yeast (Saccharomyces cerevisiae) ; (U23378) RNA polymerase I, II and III subunit ABC10 alpha [Saccharomyces cerevisiae]; (U10397) Rpb12p: RNA polymerase II subunit [Saccharomyces cerevisiae]"		
18349	ENU02143	ANI61C1355:	59-78	230-261	NAP	g1870226	531	187	2.00E-47	98	86	"(AE000352) orf, hypothetical protein [Escherichia coli]"		
		1288..1532										"(AE000352) orf, hypothetical protein [Escherichia coli]"		

શાસ્ત્રીય વિજ્ઞાન  
અધ્યક્ષ પત્રા

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat	Blast Score	Blast Prob	% id	% covg	Description
18350	ENU02144	ANI61S4306:	22-55	190-225	NAP	g2315135	415	166	3.00E-41	100	100	100	(AB003522) beta subunit of coupling factor one [Arabidopsis thaliana]
18351	ENU02145	ANI61C3217:	35-56	215-242	NAP	14..263							[Arabidopsis thaliana]
18352	ENU02146	ANI61C1479:	22-50	215-235	NAP	2010..2265							[Arabidopsis thaliana]
18353	ENU02147	ANI61C7312:	53-76	252-271	NAP	3506..3246							[Arabidopsis thaliana]
18354	ENU02148	ANI61C9353:	39-62	247-266	NAP	3290..3021							[Arabidopsis thaliana]
18355	ENU02149	ANI61C5287:	31-55	234-261	NAP	1745..2017							[Arabidopsis thaliana]
18356	ENU02150	ANI61C1253:	26-49	242-261	NAP	6115..5837							[Arabidopsis thaliana]
18357	ENU02151	ANI61S4051:	22-53	223-258	NAP	117..395							[Arabidopsis thaliana]
18358	ENU02152	ANI61C1068	49-68	270-289	NAP	5..367..649							[Arabidopsis thaliana]
18359	ENU02153	ANI61C563:2	53-72	275-296	NAP	600..2315							[Arabidopsis thaliana]
18360	ENU02154	ANI61C6455:	23-44	249-268	NAP	1510..1223							[Arabidopsis thaliana]
18361	ENU02155	ANI61C3233:	48-69	284-305	NAP	630..331							[Arabidopsis thaliana]
18362	ENU02156	ANI61C1135	26-45	253-284	NAP	8..3396..3096							[Arabidopsis thaliana]

Seq num	Seq id	Contig Source	Primer 3 pos	Primer 3 pos	Selection Basis	Database Hit	nebi gi	aat Score	Blast Prob	% id	% cvrg	Description
18363	ENU02157	AN161C4231:	31-51	264-292	NAP	g3334316	170	59	0.000000	01		"DNA-directed RNA polymeraseS I, II, and III 8.3 KD polypeptide (ABC10-beta); (D89596) RNA polymerase II subunit Rpb10 [Schizosaccharomyces pombe]; (U80219) RNA polymerases I-III common subunit Rpb10 [Schizosaccharomyces pombe]; (AF027818) RNA polymerases I, II and III subunit Rpb10 [Schizosaccharomyces pombe]; (Z98598) dna-directed ma polymerases i, ii, and iii 8.3 kd polypeptide(abc10-beta).dna-directed ma polymerases i, ii, and iii 8.3 kd polypeptide(abc10-beta). [Schizosaccharomyces pombe]" (AC000133) ORF [Emericella nidulans]
18364	ENU02158	AN161C5142:	47-66	289-309	NAP	g1870220	97	41	0.002			suppressor of Ty (S.cereviseiae) 4 homolog 1 ; transcription initiation protein SPT4 homolog 1 ; (U43923) similar to Saccharomyces cerevisiae Spf4; protein has potential N-terminal zinc-finger [Homo sapiens]; (U38818) SUPT4H [Homo sapiens]; (U38817) SUPT4H [Mus musculus]; (U96809) Supt4h [Mus musculus]; chromatin structural protein homolog [Mus musculus]
18365	ENU02159	AN161C2477:	22-57	262-287	NAP	g4507311	92	1.00E-18				ribosomal protein L38 ; 60S ribosomal protein L38 ; ribosomal protein L38 - rat ; ribosomal protein L38 - human ; (X57007) ribosomal protein L38 [Rattus rattus] ; (Z26876) ribosomal protein [Homo sapiens]

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Seq num	Seq id	Contig Source	Primer 3 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat	Blast Score	Blast Prob	% id	% cvrg	Description
18367	ENU02161	ANI61C914:1	22-55	272-291	NAP	g731363	131	57	03	0.000000	PET100 protein precursor ; probable membrane protein YDR079w - yeast (Saccharomyces cerevisiae) ; (X82086)		
			532..1221								1 putative transmembrane spans [Saccharomyces cerevisiae] ; (Z46796)		
											unknown [Saccharomyces cerevisiae] ; (Z74375) ORF YDR079w		
											[Saccharomyces cerevisiae] ; (U91943)		
											cytochrome c oxidase-specific assembly factor [Saccharomyces cerevisiae]		
18368	ENU02162	ANI61C1597:	24-50	271-294	NAP	g2656010	201	76	5.00E-14	29	71	(Z99165) hypothetical protein	
		238..550				g4589971	572	221	1.00E-57	97	98	[Schizosaccharomyces pombe] (AC007195) putative blue copper-binding protein II [Arabidopsis thaliana]	
18369	ENU02163	ANI61C4533:	24-52	267-295	NAP	g417103	338	141	1.00E-33			"Histone H3.2, minor; histone H3.3-like protein - Arabidopsis thaliana ; (X60429) histone H3.3 like protein [Arabidopsis thaliana] ; (X60429) histone H3.3 like protein [Arabidopsis thaliana] ; (U09458) histone H3.2 [Medicago sativa] ; (U09460) histone H3.2 [Medicago sativa] ; (U09461) histone H3.2 [Medicago sativa] ; (U09464) histone H3.2 [Medicago sativa] ; (U09465) histone H3.2 [Medicago sativa] ; (X79714) histone H3 [Lolium temulentum] ; (X83422) histone H3 variant H3.3 [Lycopersicon esculentum] ; (AF024716) histone 3 [Gossypium hirsutum] ; (AB015760) histone H3 [Nicotiana tabacum] ; (AF093633) histone H3 [Oryza sativa] ; (AF109910) histone H3 [Portereria coarctata] ; (AL035708) histone H3.3 [Arabidopsis thaliana] ; (AL035708) Histon H3 [Arabidopsis thaliana]" (AC000133) mt2 [Emericella nidulans]	
18371	ENU02165	ANI61C5625:	23-50	270-295	NAP	g1870224	569	224	2.00E-58	98	99		
		900...586											



Seq num	Seq id	Contig Source	Primer 3 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	Score	Score	Blast Prob	% id	% covg	Description
18382	ENU02176	ANI61C107:1	22-54	286-308	NAP	g1723740	99	50	0.00004	31	82		NAB1A-GPI intergenic region ; hypothetical protein YGR215w - yeast (Saccharomyces cerevisiae) ; (Z73000) ORF YGR215w [Saccharomyces cerevisiae]
18383	ENU02177	ANI61C1034	27-46	292-315	NAP	g586501	138	64	4.00E-10	35	92		hypothetical 13.2 KD protein in ORC2-TIP1 intergenic region ; hypothetical protein YBR062c - yeast (Saccharomyces cerevisiae) ; (Z35931) ORF YBR062c [Saccharomyces cerevisiae]
18384	ENU02178	ANI61C2076:	37-56	295-327	NAP	g3850102	437	161	1.00E-39	67	77		(AL033388) putative golgi membrane protein-sorting protein [Schizosaccharomyces pombe] probable membrane protein YOL026c - yeast (Saccharomyces cerevisiae) ; (Z74768) ORF YOL026c [Saccharomyces cerevisiae]
18385	ENU02179	ANI61C4334:	22-51	297-317	NAP	g2132826	91	56	0.000000	34	93		[Schizosaccharomyces pombe] hypothetical protein YHR004c-a - yeast (Saccharomyces cerevisiae) ; (Z80875) Mrs11p [Saccharomyces cerevisiae] ; (U10555) Mrs11p [Saccharomyces cerevisiae] hypothetical protein SPA.C31A2.08 - C31A2.08 in chromosome 1 ; hypothetical protein SPA.C31A2.08 - fission yeast (Schizosaccharomyces pombe) ; (Z50113) unknown [Schizosaccharomyces pombe] (AC02333) Sm protein F isolog [Arabidopsis thaliana]
18386	ENU02180	ANI61C6137:	35-53	312-331	NAP	g2131721	217	64	1.00E-17	52	91		hypothetical protein YHR004c-a - yeast (Saccharomyces cerevisiae) ; (Z80875) Mrs11p [Saccharomyces cerevisiae] ; (U10555) Mrs11p [Saccharomyces cerevisiae] hypothetical 19.0 KD protein C31A2.08 in chromosome 1 ; hypothetical protein SPA.C31A2.08 - fission yeast (Schizosaccharomyces pombe) ; (Z50113) unknown [Schizosaccharomyces pombe] (AC02333) Sm protein F isolog [Arabidopsis thaliana]
18387	ENU02181	ANI61C4486:	72-92	350-369	NAP	g1175403	164	60	0.000000	36	54		hypothetical 13.4 KD protein C17H9.07 in chromosome 1 ; (Z98597) hypothetical protein [Schizosaccharomyces pombe] Cyanate lyase (cyanate hydrolase) (cyanase) ; (U59481) cyanate lyase [Synchococcus PCC7942] ; (AB00100) cyanase [Synchococcus sp.]
18388	ENU02182	ANI61C5870:	60-79	334-358	NAP	g2281089	152	74	3.00E-13	54	81		
18389	ENU02183	ANI61C3916:	61-88	339-360	NAP	g3183357	41	0.002					
18390	ENU02184	ANI61C3209:	70-89	351-371	NAP	g2498272	267	98	2.00E-20	46	77		
		50..393											

Seq num	Seq id	Contig	Source	5 pos	3 pos	Basis	Database	Hit	ncbi gi	aat Score	blast Score	% id	blast prob	% cvrg	Description
18391	ENU02185	ANI61C8982:	33-51	317-336	NAP	g2983605	238	100	4.00E-21	46	72	(AE000725) ribose 5-phosphate isomerase B [Aequifex aeolicus]			
18392	ENU02186	ANI61C1601:	56-77	115..462	NAP	g1351714	52	0.000002				putative transporter C11D3.18C; (Z68166) unknown			
18393	ENU02187	ANI61C5803:	22-43	2298..1951	NAP	g3183399	125	55	0.000000	28	91	[Schizosaccharomyces pombe] hypothetical protein C2E11.03C in chromosome I; (AL031181) very hypothetical protein [Schizosaccharomyces pombe]; (AL035064) very hypothetical protein [Schizosaccharomyces pombe]			
18394	ENU02188	ANI61C1064	29-54	314-335	NAP	g731777	149	61	1.00E-10	38	97	"hypothetical 11.0 KD protein in FAA3-MA-S3 intergenic region"; hypothetical protein YIL008w - yeast (Saccharomyces cerevisiae); (Z38113) orf, len: 99, CAI=0.21 [Saccharomyces cerevisiae]"			
18395	ENU02189	ANI61C4009:	52-71	342-359	NAP	g2276355	328	101	2.00E-21	60	80	(Z97992) putative small ribonuclear protein [Schizosaccharomyces pombe]			
18396	ENU02190	ANI61C6138:	35-68	562..657	NAP	g1363744	260	41	0.004	38	45	hypothetical protein YLR435w - yeast (Saccharomyces cerevisiae); (U21094) Ylr435wp [Saccharomyces cerevisiae] (AC000133) ORF [Emmericella nidulans]			
18397	ENU02191	ANI61C1127	42-62	329-352	NAP	g1870220	685	234	2.00E-61	98	87	hypothetical 10.7 KD protein C17C9_09C in chromosome I; (Z73099) hypothetical protein [Schizosaccharomyces pombe]			
18398	ENU02192	ANI61C9645:	54-74	1347..993	NAP	g1723568	48	0.00002				small nuclear ribonucleoprotein [Schizosaccharomyces pombe]			
18399	ENU02193	ANI61C1000	26-45	307-339	NAP	g4507129	169	68	2.00E-11			small nuclear ribonucleoprotein polypeptide E ; U1 and U2 small nuclear ribonucleoprotein E (SNRNP-E) ; small nuclear ribonucleoprotein E - human ; (X12466) snRNP E protein (AA 1-92) [Homo sapiens] ; (L19064)			
			4..3168..3523									small nuclear ribonucleoprotein E [Gallus gallus] ; (X65702) SmE protein [Gallus gallus] ; (M37716) small nuclear RNA protein (snRNP E) [Homo sapiens]			

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Primer Basis	Selection	blastn	aat	Blast Score	Blast Prob	% id	% cvrg	Description
18400	ENU02194	ANI61C9311:	44-63	3740..3382	NAP	g1175442	759	138	1.00E-32	58	39		hypothetical protein C22F3.01 in chromosome I ; hypothetical protein SPAC22F3.01 - fission yeast (Schizosaccharomyces pombe) (fragment) ; (Z54285) unknown [Schizosaccharomyces pombe] Lectin precursor (agglutinin); lectin precursor - rice ; (M24504) [lectin [Oryza sativa]]
18401	ENU02195	ANI61C8065:	65-84	364-383	NAP	g113509	78	68	2.00E-11	35	45		60S ribosomal protein L35
18402	ENU02196	ANI61C5436:	34-59	334-353	NAP	g2833359	268	45	0.0002	57	73		"40S ribosomal protein S15 (S12); ribosomal protein S12, cytosolic - Podospora anserina ; (Z23267) cytoplasmic ribosomal protein S12 [Podospora anserina]" (AL035263) weak similarity to chick phosphatidylcholine-site rol acetyltransferase
18403	ENU02197	ANI61C4673:	28-57	329-350	NAP	g464706	506	108	1.00E-37	78	76		
18404	ENU02198	ANI61C7221:	50-72	353-372	NAP	g4176531	1107	89	1.00E-17	34	18		
			1542..1906										
18405	ENU02199	ANI61C9819:	31-56	337-356	NAP	g1351034	167	47	0.000000	52	95		[Schizosaccharomyces pombe] putative protein transport protein SEC61 gamma subunit ; hypothetical protein SPAC4G8.02c - fission yeast (Schizosaccharomyces pombe); (Z56276) putative protein transport protein sec61-gamma subunit
18406	ENU02200	ANI61C3164:	69-88	368-394	NAP	g731437	244	53	2.00E-15	44	81		[Schizosaccharomyces pombe] nuclear transport factor 2 (NTF-2) (nuclear transport factor P10); hypothetical protein YER009w - yeast (Saccharomyces cerevisiae); (UI18778) Ntf2p: Nuclear Transport Factor 2 [Saccharomyces cerevisiae]
18407	ENU02201	ANI61C4957:	60-79	368-393	NAP	g3810851	851	96	1.00E-19	33	15		(AL032664) putative ubiquitin-protein ligase [Schizosaccharomyces pombe]
18408	ENU02202	ANI61C6549:	63-84	378-397	NAP	g3183481	299	92	1.00E-18	51	56		hypothetical 23.0 KD protein in SNF2-CPA1 intergenic region ; hypothetical protein YOR294w - yeast (Saccharomyces cerevisiae); (Z75202) ORF YOR294w [Saccharomyces cerevisiae]

Seq num	Seq id	Contig Source	Primer 3 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat	Blast Score	Blast Prob	% id	% cvrg	Description
18409	ENU02203	ANI61C1235:	2443	341..362	NAP	g114663	685	167	4.00E-41	97	88	"ATP synthase protein 9, mitochondrial precursor (LIPID-binding protein); (M30144) mitochondrial ATP synthase precursor [Emericella nidulans]"	
18410	ENU02204	ANI61C2997:	61-89	381..400	NAP	g1362228	448	161	2.00E-39	60	54	pac2 protein - fission yeast (Schizosaccharomyces pombe); (D43748) Pac2p [Schizosaccharomyces pombe]; (Z98979) camp independent regulatory protein [Schizosaccharomyces pombe] (AJ002026) rAsp f 13 [Aspergillus fumigatus]	
18411	ENU02205	ANI61C7253:	51-70	375..394	NAP	g3005841	341	143	7.00E-34	54	80	(AL031349) 4-nitrophenylphosphatase [Schizosaccharomyces pombe] hypothetical ZINC-type alcohol dehydrogenase-like protein in pre5-FET4 intergenic region ; hypothetical protein YMR318c - yeast (Saccharomyces cerevisiae); (Z54141) unknown [Saccharomyces cerevisiae] (Z97050) hypothetical protein Rv0163 [Mycobacterium tuberculosis] (X99300) unknown epidymal protein [Mus musculus] (Z99259) small nuclear ribonucleoprotein [Schizosaccharomyces pombe] ubiquitin-like protein SMT3; SMT3 protein - yeast (Saccharomyces cerevisiae); (U27233) Sm3p [Saccharomyces cerevisiae]; (U33057) suppressor of MIF2 mutations; CAI: 0.31 [Saccharomyces cerevisiae] hypothetical 14.1 KD protein C31A2.02 in chromosome I;	
18412	ENU02206	ANI61C8384:	67-86	392..411	NAP	g3451473	587	121	2.00E-27	50	41	hypothetical protein SPAC31A2.02 - fission yeast (Schizosaccharomyces pombe); (Z50113) unknown [Schizosaccharomyces pombe] (AC000133) ORF [Emericella nidulans]	
18413	ENU02207	ANI61C6419:	69-88	389..414	NAP	g2492777	314	99	9.00E-21	40	35		
18414	ENU02208	ANI61C1015:	63-91	390..410	NAP	g2213500	173	85	3.00E-16	39	76		
18415	ENU02209	ANI61C2495:	24-55	343..371	NAP	g1430862	90	61	0.000000	26	91		
18416	ENU02210	ANI61C9745:	30-56	358..377	NAP	g2414614	177	43	0.000000	50	60		
18417	ENU02211	ANI61C2576:	22-53	351..370	NAP	g2501450	201	76	7.00E-17	46	94		
18418	ENU02212	ANI61C1557:	55-75	386..406	NAP	g1175395	290	80	5.00E-15	43	84		
18419	ENU02213	ANI61C1098	22-54	349..373	NAP	g1870220	169	81	3.00E-15	39	97		

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18420	ENU02214	ANI61C727:1	45-64	362-397	NAP	g1708982	550	129	1.00E-29	52	23	Ammonium transporter MEP3 - yeast (Saccharomyces cerevisiae); (U40829) Similar to <i>B. subtilis</i> membrane protein NrgA (Swiss Prot accession number Q07429)	
18421	ENU02215	ANI61C7854:	45-72	376-399	NAP	g2828348	362	64	5.00E-10				[Saccharomyces cerevisiae] "(AB007633) Myo3 [Schizosaccharomyces pombe]; (Z98762) SPAC4A.8.05c, myosin heavy chain, len:2104aa, similar eg. to MYS2, DICDI, P08799, myosin ii heavy chain, non muscle, (2116aa), fasta scores, opt: 2488, E(0.0, (29.5% identity in 2167 aa overlap), PS00017 ATP/GTP-bind..."
		785..1181	1057..1454			g3023324	414	133	5.00E-31	48	76		; (AF019223) F1Fo-ATP synthase subunit 7 [Kluyveromyces lactis]" DNA-directed RNA polymerase II 13.3 KD polypeptide (RPB1) (RPB14); (D85818) RNA polymerase II subunit RPB14 [Mus musculus]
18423	ENU02217	ANI61C9131:	54-73	389-411	NAP	g2500634	198	56	3.00E-12	52	70		subunit F [Neurospora crassa] (X89714) rhamnogalacturonan acetyl esterase [Aspergillus aculeatus] (Z28052) ORF YKL053c-a [Saccharomyces cerevisiae]; (Z28054) ORF YKL053c-a [Saccharomyces cerevisiae]
18424	ENU02218	ANI61C6203:	52-73	381-409	NAP	g4426615	398	73	2.00E-15	57	75		(AF099136) vacuolar ATP synthase subunit F [Neurospora crassa] (X89714) rhamnogalacturonan acetyl esterase [Aspergillus aculeatus] (Z28052) ORF YKL053c-a [Saccharomyces cerevisiae]; (Z28054) ORF YKL053c-a [Saccharomyces cerevisiae]
18425	ENU02219	ANI61C5382:	22-50	356-379	NAP	g1004217	840	127	6.00E-31	64	47		(AL031326) putative protein [Arabidopsis thaliana]
18426	ENU02220	ANI61C1044	36-58	374-394	NAP	g2980812	86	37	0.003				"ribosomal protein L11 e.B, cytosolic - yeast (Saccharomyces cerevisiae); (Z72870) ORF YGR085c [Saccharomyces cerevisiae]" [Arabidopsis thaliana]
		2:1486..1886				g3451060	34	0.38					[AC007196] unknown protein [Arabidopsis thaliana]
18427	ENU02221	ANI61C4350:	69-89	408-428	NAP	g71107	635	154	2.00E-42	76	63		[AB011378] MAT-2 protein [Fusarium oxyphorum]
18428	ENU02222	ANI61C9613:	55-77	390-415	NAP	g4582434	207	36	1.00E-11	54	87		
18429	ENU02223	ANI61C1800:	31-50	372-391	NAP	g3168589	206	59	4.00E-19	38	93		
18430	ENU02224	ANI61C7401:	46-65	389-409	NAP								
		1335..930											

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18431	ENU02225	ANI61C6584:	35-56	380-401	NAP	g4322266	1653	245	1.00E-64	82	28	(AF077355) protein phosphatase 2A regulatory B subunit [Neurospora crassa]	
18432	ENU02226	ANI61C5101:	27-51	377-394	NAP	g3676762	443	105	7.00E-32	71	90	(AF087136) RS6/L7A ribosomal protein homolog	
18433	ENU02227	ANI61C4456:	43-62	388-411	NAP	g1082211	148	57	1.00E-10	31	3	[Schizosaccharomyces pombe] "ankyrin 3, long form - human ; (U13616) ankyrin G [Homo sapiens]" Oleate-induced peroxisomal protein POX18 (lipid-transfer protein) (PXP-18) ; POX18 protein - yeast (Candida tropicalis) ; lipid transfer protein - imperfect fungus (Candida tropicalis) ; (X53633) POX18 [Candida tropicalis]; (M24440) peroxisomal protein [Candida tropicalis]	
18435	ENU02229	ANI61C1012	57-76	407-429	NAP	g730548	446	112	1.00E-24	76	55	"probable 60S ribosomal protein L27; e.A. cytosolic - ribosomal protein L27 e.A. cytosolic - yeast (Saccharomyces cerevisiae); (U10400) Rpl27p; Probable 60S ribosomal protein L27 [Saccharomyces cerevisiae]"	
18436	ENU02230	ANI61C7031:	49-68	404-423	NAP	g113701	702	99	1.00E-20			Acetamidase ; amdS protein - Emericella nidulans ; (M16371) acetamidase enzyme [Emericella nidulans]	
18437	ENU02231	ANI61C1047	39-61	395-414	NAP	g3915963	1420	152	9.00E-37	60	8	ATP-dependent bile acid permease ; probable membrane protein YLL048c - yeast (Saccharomyces cerevisiae); (Z73153) ORF YLL048c	
18438	ENU02232	ANI61C3552:	25-44	383-402	NAP	g3249567	200	52	4.00E-14	50	87	[Saccharomyces cerevisiae] (AF047694) glutaredoxin [Vernicia fordii]	
18439	ENU02233	ANI61C8615:	22-40	379-399	NAP	g2833220	579	101	1.00E-32	68	33	hypothetical 35.7 KD protein in DNL4-SLG1 intergenic region ; hypothetical protein YOR006c - yeast (Saccharomyces cerevisiae) ; (U43491) hypothetical protein UND313 [Saccharomyces cerevisiae] ; (Z74914) ORF YOR006c [Saccharomyces cerevisiae]	

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat	Blast Score	Blast Prob	% id	% cvrg	Description	
18440	ENU02234	ANI61C1677:	47-67	396-425	NAP	g418574	520	106	8.00E-23	38	45		mitochondrial carrier protein YMC1 precursor ; (X67122) mitochondrial carrier protein [Saccharomyces cerevisiae]	
18441	ENU02235	ANI61C662:8	26-47	382-406	NAP	g3850125	193	94	6.00E-19	35	27		(AL033391) hypothetical membrane protein [Candida albicans] phosphorylation regulatory protein HP-10 - human	
18442	ENU02236	ANI61C1479:	45-64	405-425	NAP	g627570	180	68	3.00E-11				"putative ATP synthase G chain, mitochondrial ; hypothetical protein YPR020w - yeast (Saccharomyces cerevisiae) ; (Z49919) unknown [Saccharomyces cerevisiae] ; (Z71255) unknown [Saccharomyces cerevisiae]" (AF008220) putative cysteine synthase [Bacillus subtilis] ; (Z99119) similar to cysteine synthase [Bacillus subtilis] (AL022305) mitochondrial import inner membrane translocase subunit precursor [Schizosaccharomyces pombe] (Y08703) SlyA protein [Sinorhizobium meliloti]	
18443	ENU02237	ANI61C3138:	24-52	386-405	NAP	g2493096	103	57	0.000000	30	96		"putative ATP synthase G chain, mitochondrial ; hypothetical protein YPR020w - yeast (Saccharomyces cerevisiae) ; (Z49919) unknown [Saccharomyces cerevisiae] ; (Z71255) unknown [Saccharomyces cerevisiae]" (AF008220) putative cysteine synthase [Bacillus subtilis] ; (Z99119) similar to cysteine synthase [Bacillus subtilis] (AL022305) mitochondrial import inner membrane translocase subunit precursor [Schizosaccharomyces pombe] (Y08703) SlyA protein [Sinorhizobium meliloti]	
18444	ENU02238	ANI61C7858:	60-79	414-441	NAP	g2293314	69	2.00E-11					"putative ATP synthase G chain, mitochondrial ; hypothetical protein YPR020w - yeast (Saccharomyces cerevisiae) ; (Z49919) unknown [Saccharomyces cerevisiae] ; (Z71255) unknown [Saccharomyces cerevisiae]" (AF008220) putative cysteine synthase [Bacillus subtilis] ; (Z99119) similar to cysteine synthase [Bacillus subtilis] (AL022305) mitochondrial import inner membrane translocase subunit precursor [Schizosaccharomyces pombe] (Y08703) SlyA protein [Sinorhizobium meliloti]	
18445	ENU02239	ANI61C394:1	09..533	71-91	434-453	NAP	g3006160	456	165	2.00E-40	51	33		"putative ATP synthase G chain, mitochondrial ; hypothetical protein YPR020w - yeast (Saccharomyces cerevisiae) ; (Z49919) unknown [Saccharomyces cerevisiae] ; (Z71255) unknown [Saccharomyces cerevisiae]" (AF008220) putative cysteine synthase [Bacillus subtilis] ; (Z99119) similar to cysteine synthase [Bacillus subtilis] (AL022305) mitochondrial import inner membrane translocase subunit precursor [Schizosaccharomyces pombe] (Y08703) SlyA protein [Sinorhizobium meliloti]
18446	ENU02240	ANI61C1107	33-53	397-415	NAP	g1926396	33	1.2					"putative ATP synthase G chain, mitochondrial ; hypothetical protein YPR020w - yeast (Saccharomyces cerevisiae) ; (Z49919) unknown [Saccharomyces cerevisiae]" (AF008220) putative cysteine synthase [Bacillus subtilis] ; (Z99119) similar to cysteine synthase [Bacillus subtilis] (AL022305) mitochondrial import inner membrane translocase subunit precursor [Schizosaccharomyces pombe] (Y08703) SlyA protein [Sinorhizobium meliloti]	
18447	ENU02241	ANI61C506:1	28-48	391-411	NAP	g2950478	276	79	1.00E-14	39	82		"putative ATP synthase G chain, mitochondrial ; hypothetical protein YPR020w - yeast (Saccharomyces cerevisiae) ; (Z49919) unknown [Saccharomyces cerevisiae]" (AF008220) putative cysteine synthase [Bacillus subtilis] ; (Z99119) similar to cysteine synthase [Bacillus subtilis] (AL022305) mitochondrial import inner membrane translocase subunit precursor [Schizosaccharomyces pombe] (Y08703) SlyA protein [Sinorhizobium meliloti]	
18448	ENU02242	ANI61C3144:	22-43	385-406	NAP	g140479	260	102	1.00E-21	39	27		"putative ATP synthase G chain, mitochondrial ; hypothetical protein YPR020w - yeast (Saccharomyces cerevisiae) ; (Z49919) unknown [Saccharomyces cerevisiae]" (AF008220) putative cysteine synthase [Bacillus subtilis] ; (Z99119) similar to cysteine synthase [Bacillus subtilis] (AL022305) mitochondrial import inner membrane translocase subunit precursor [Schizosaccharomyces pombe] (Y08703) SlyA protein [Sinorhizobium meliloti]	
18449	ENU02243	ANI61S1388:	58-78	425-444	NAP	g2244709	136	46	0.0001	33	78		"putative ATP synthase G chain, mitochondrial ; hypothetical protein YPR020w - yeast (Saccharomyces cerevisiae) ; (Z49919) unknown [Saccharomyces cerevisiae]" (AF008220) putative cysteine synthase [Bacillus subtilis] ; (Z99119) similar to cysteine synthase [Bacillus subtilis] (AL022305) mitochondrial import inner membrane translocase subunit precursor [Schizosaccharomyces pombe] (Y08703) SlyA protein [Sinorhizobium meliloti]	
18450	ENU02244	ANI61C7468:	39-58	405-426	NAP	g730733	368	83	9.00E-16	50	15		"putative ATP synthase G chain, mitochondrial ; hypothetical protein YPR020w - yeast (Saccharomyces cerevisiae) ; (Z49919) unknown [Saccharomyces cerevisiae]" (AF008220) putative cysteine synthase [Bacillus subtilis] ; (Z99119) similar to cysteine synthase [Bacillus subtilis] (AL022305) mitochondrial import inner membrane translocase subunit precursor [Schizosaccharomyces pombe] (Y08703) SlyA protein [Sinorhizobium meliloti]	

Seq num	Seq id	Contig Source	Primer 3 pos	Primer Basis	Selection Database Hit	aat	Blast Score	Blast Prob	% id	% cvrg	Description	
18451	ENU02245	ANI61C9311:	38-57	NAP	g731668	517	74	6.00E-13	31	31	SSF1 protein ; SSF1 protein - yeast (Saccharomyces cerevisiae) ; (U00061)	
			562..133								Ssf1p [Saccharomyces cerevisiae] ; (U18113) Ssf1p [Saccharomyces cerevisiae]	
18452	ENU02246	ANI61C8081:	67-86	436-455	NAP	g1710760	218	56	4.00E-10	84	73	probable 40S ribosomal protein S28 (S33) ; (Z70691) ribosomal protein S28 [Schizosaccharomyces pombe] ; (AL031545) probable 40s ribosomal protein 28s [Schizosaccharomyces pombe]
			1190..760								(U86782) 26S proteasome-associated pad1 homolog [Homo sapiens]	
18453	ENU02247	ANI61C6597:	72-94	434-461	NAP	g1923256	980	169	1.00E-41	53	46	iucB protein - Escherichia coli ; (X76100) iucB [Escherichia coli] (AF009672) unknown [Acinetobacter sp.] ADP1
			3612..3181								hypothetical 16.2 KD protein in IME2-MEF2 intergenic region ; probable membrane protein YIL104w - yeast (Saccharomyces cerevisiae) ; (X85021) orf 8 [Saccharomyces cerevisiae] ; (Z49379) ORF YJL104w	
18454	ENU02248	ANI61C1463:	50-69	420-440	NAP	g1073534	224	72	8.00E-14	37	40	hypothetical 17.1 KD protein in SAHL-ME14 intergenic region ; hypothetical protein YER044c - yeast (Saccharomyces cerevisiae) ; (U18796) Yer044cp [Saccharomyces cerevisiae] (AL049474) similar to glycosylphosphatidylinositol anchor [Schizosaccharomyces pombe]
			109..541								Lipoic acid synthetase precursor (LIP-SYN) (lipoate synthase) ; lipoic acid synthase (EC 2.8.1.-) precursor - yeast (Saccharomyces cerevisiae) ; (Z75104) ORF YOR196c [Saccharomyces cerevisiae]	
18455	ENU02249	ANI61C1898:	37-64	409-428	NAP	g2271497	316	84	4.00E-16	45	39	hypothetical 16.2 KD protein in IME2-MEF2 intergenic region ; probable membrane protein YIL104w - yeast (Saccharomyces cerevisiae) ; (X85021) orf 8 [Saccharomyces cerevisiae] ; (Z49379) ORF YJL104w
			545..112								(Saccharomyces cerevisiae) ; (Z49379) ORF YJL104w	
18456	ENU02250	ANI61C7592:	25-44	394-416	NAP	g1176485	251	101	3.00E-21	42	96	hypothetical 16.2 KD protein in IME2-MEF2 intergenic region ; probable membrane protein YIL104w - yeast (Saccharomyces cerevisiae) ; (X85021) orf 8 [Saccharomyces cerevisiae] ; (Z49379) ORF YJL104w
			508..75								(Saccharomyces cerevisiae) ; (Z49379) ORF YJL104w	
18457	ENU02251	ANI61C5414:	24-43	381-416	NAP	g731459	168	73	1.00E-12	38	84	hypothetical 17.1 KD protein in SAHL-ME14 intergenic region ; hypothetical protein YER044c - yeast (Saccharomyces cerevisiae) ; (U18796) Yer044cp [Saccharomyces cerevisiae] (AL049474) similar to glycosylphosphatidylinositol anchor [Schizosaccharomyces pombe]
			627..193								Lipoic acid synthetase precursor (LIP-SYN) (lipoate synthase) ; lipoic acid synthase (EC 2.8.1.-) precursor - yeast (Saccharomyces cerevisiae) ; (Z75104) ORF YOR196c [Saccharomyces cerevisiae]	
18458	ENU02252	ANI61C9241:	67-88	430-460	NAP	g4538668	98	45	0.0002	32	73	hypothetical 16.2 KD protein in SAHL-ME14 intergenic region ; hypothetical protein YER044c - yeast (Saccharomyces cerevisiae) ; (U18796) Yer044cp [Saccharomyces cerevisiae] (AL049474) similar to glycosylphosphatidylinositol anchor [Schizosaccharomyces pombe]
			428..863								Lipoic acid synthetase precursor (LIP-SYN) (lipoate synthase) ; lipoic acid synthase (EC 2.8.1.-) precursor - yeast (Saccharomyces cerevisiae) ; (Z75104) ORF YOR196c [Saccharomyces cerevisiae]	
18459	ENU02253	ANI61C1281:	60-79	434-453	NAP	g417254	1206	211	2.00E-54	69	35	hypothetical 16.2 KD protein in SAHL-ME14 intergenic region ; hypothetical protein YER044c - yeast (Saccharomyces cerevisiae) ; (U18796) Yer044cp [Saccharomyces cerevisiae] (AL049474) similar to glycosylphosphatidylinositol anchor [Schizosaccharomyces pombe]
			784..1219								Lipoic acid synthetase precursor (LIP-SYN) (lipoate synthase) ; lipoic acid synthase (EC 2.8.1.-) precursor - yeast (Saccharomyces cerevisiae) ; (Z75104) ORF YOR196c [Saccharomyces cerevisiae]	
18460	ENU02254	ANI61C1100	51-74	410-444	NAP	g1871596	180	78	2.00E-14	29	29	(Z92669) hypothetical protein Rv0223c [Mycobacterium tuberculosis]

Seq num	Seq id	Contig Source	Primer 3 pos	Primer Basis	Selection Database Hit	aat	Blast Score	Blast Prob	% id	% cvrg	Description
18461	ENU02255	ANI61C3253: 92..527	444..465	NAP	g729580	697	200	5.00E-51	61	20	"fructose-bisphosphate aldolase [Neurospora crassa]"
18462	ENU02256	ANI61C426;5 40..103	72..91	441..467	NAP	g729580	697	200	5.00E-51	61	"1,4-alpha-glucan branching enzyme (EC 2.4.1.18) - yeast (Saccharomyces cerevisiae); (UJ18530) 1,4-alpha-glucan branching enzyme [Saccharomyces cerevisiae]"
18463	ENU02257	ANI61C9851: 1250..813	59..80	435..454	NAP	g3128287	134	63	9.00E-10	33	"(AF010496) hypothetical protein [Rhodobacter capsulatus]"
18464	ENU02258	ANI61C2552: 1180..1618	63..82	440..459	NAP	g2131439	192	83	9.00E-16	34	"hypothetical protein YDR348c - yeast (Saccharomyces cerevisiae); (U51032) Ydr348cp [Saccharomyces cerevisiae] thrombospondin 1; (X14787) precursor polypeptide (AA -31 to 1139) [Homo sapiens]"
18465	ENU02259	ANI61C8575: 5652..6090	23..46	400..419	NAP	g4507485	38	0.05			"hypothetical protein C24H6.11C in chromosome I; hypothetical protein SPA.C24H6.11c - fission yeast (Schizosaccharomyces pombe); (Z54142) hypothetical protein [Schizosaccharomyces pombe]"
18466	ENU02260	ANI61C9787: 994..555	53..75	427..449	NAP	g1175439	258	55	3.00E-14	38	"hypothetical 107.1 KD protein C24H6.11C in chromosome I; hypothetical protein SPA.C24H6.11c - fission yeast (Schizosaccharomyces pombe); (Z54142) hypothetical protein [Schizosaccharomyces pombe]"
18467	ENU02261	ANI61C1796: 784..345	38..58	415..435	NAP	g118513	517	155	1.00E-37	54	"Aspartate-semialdehyde dehydrogenase (ASA dehydrogenase) (ASA DH); aspartate-semialdehyde dehydrogenase (EC 1.2.1.11) - yeast (Saccharomyces cerevisiae); (X15649) aspartic semi-aldehyde dehydrogenase (AA 1-365) [Saccharomyces cerevisiae]; (Z50046) Hom2p [Saccharomyces cerevisiae] (Z49149) 100% identity in 135 aa ov with the CSE1 protein from S. cerevisiae. This ORF is incomplete." [Saccharomyces cerevisiae]; HRC135 gene [Saccharomyces cerevisiae] (U58946) transposase [Aspergillus awamori]"
18468	ENU02262	ANI61C9323: 667..1106	62..81	423..459	NAP	g793875	274	111	3.00E-24	42	"with the CSE1 protein from S. cerevisiae. This ORF is incomplete." [Saccharomyces cerevisiae]; HRC135 gene [Saccharomyces cerevisiae] (U58946) transposase [Aspergillus awamori]"
18469	ENU02263	ANI61C1144 8..84..524	69..97	434..467	NAP	g1805251	235	87	8.00E-17	36	"gene [Saccharomyces cerevisiae] (U58946) transposase [Aspergillus awamori]"

Seq num	Seq id	Contig Source	Primer 3 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat	Blast Score	Blast Prob	% id	% cvrg	Description
18470	ENU02264	ANI61C1465:	22-50	399-420	NAP	g133131	116	48	0.00004	37	79	"mitochondrial 60S ribosomal protein L31 precursor (YML31); ribosomal protein Yml31 precursor, mitochondrial - yeast (Saccharomyces cerevisiae); (X15099) precursor rplL31 protein [Saccharomyces cerevisiae]; (Z28138) ORF YKL138c [Saccharomyces cerevisiae]"	
18471	ENU02265	ANI61C6213:	60-81	438-458	NAP	g1723832	368	72	3.00E-17	58	62	hypothetical 15.9 KD protein in OLE1-DUP1 intergenic region ; probable membrane protein YGL054c - yeast (Saccharomyces cerevisiae); (Z72576) ORF YGL054c [Saccharomyces cerevisiae]	
18472	ENU02266	ANI61C3405:	35-59	415-434	NAP	g1170186	200	54	0.000000	34	19	probable ATP-dependent RNA helicase DBP4 (helicase CA4) (helicase UF1); probable RNA helicase CA4 - yeast (Saccharomyces cerevisiae); (Z49308) ORF YJL033w [Saccharomyces cerevisiae]	
18473	ENU02267	ANI61C3640:	71-91	451-472	NAP	g1805251	1188	93	8.00E-19	37	26	(U58946) transposase [Aspergillus awamori]	
18474	ENU02268	ANI61C7618:	63-84	444-464	NAP	g1710803	714	92	1.00E-18	31	23	Retrograde regulation protein 2 ; RTG2 protein - yeast (Saccharomyces cerevisiae); (X94357) ORF NRF588; EMBL:SCR TG2X;M97691; PIR:B44344;B44344 [Saccharomyces cerevisiae]; (M97691) Rtg2p [Saccharomyces cerevisiae]; (Z72774) ORF YGL252c [Saccharomyces cerevisiae]	
18475	ENU02269	ANI61C2182:	38-57	418-440	NAP	g731298	256	105	2.00E-22	37	24	probable transporter SEO1 ; probable membrane protein YAL067c - yeast (Saccharomyces cerevisiae); (U12980) Seo1p: putative membrane protein [Saccharomyces cerevisiae] (U17129) unknown [Rhodococcus erythropolis]	
18476	ENU02270	ANI61C6415:	65-84	449-468	NAP	g3873405	43	0.002					

Seq num	Seq id	Contig Source	5 pos	Primer 3 pos	Primer Basis	Selection	Database	Hit ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18477	ENU02271	ANI61C9683:	71-92	452-475	NAP		g465011	1037	261	1.00E-69	97	43		(EC 1.7.3.3) - Emericella nidulans; (X72210) urate oxidase [Emericella nidulans]
18478	ENU02272	ANI61C3079:	27-53	413-432	NAP		g171183	383	129	1.00E-29	45	34		(M61194) CDC14 [Saccharomyces cerevisiae]
18479	ENU02273	ANI61C7257:	30-49	407-436	NAP		g1723218	294	107	2.00E-23	51	83		hypothetical 19.5 KD protein C3H8.07C in chromosome I; (Z69086) unknown [Saccharomyces pombe]
18480	ENU02274	ANI61C6494:	22-50	409-428	NAP		g1850768	177	88	4.00E-17	47	89		(AB001289) YNL157W homolog [Schizosaccharomyces pombe]
18481	ENU02275	ANI61C4974	31-49	414-438	NAP		g3023637	2950	213	4.00E-55	68	12		probable ATP-dependent RNA helicase HRH1 (DEAH box protein 8); probable RNA helicase 1 - human; (D50487) RNA Helicase (HRH1) [Homo sapiens]
18482	ENU02276	ANI61C1049	39-69	428-447	NAP		g3024439	1855	234	2.00E-61	84	35		26S PROTEASE regulatory subunit 6B homolog; (U15601) 26S proteasome subunit [Aspergillus niger]
18483	ENU02277	ANI61C3576:	26-54	416-435	NAP		g3169068	276	56	5.00E-18	67	84		(AL023704) putative transcription factor IIa small subunit [Schizosaccharomyces pombe]
18484	ENU02278	ANI61C2679:	64-84	443-473	NAP		g2132651	286	127	3.00E-29	42	25		probable membrane protein YLL028w - yeast [Saccharomyces cerevisiae]; (Z73133) ORF YLL028w [Saccharomyces cerevisiae]
18485	ENU02279	ANI61C1083	24-48	403-435	NAP		g3265058	703	165	2.00E-40	91	84		(AF060232) monoubiquitin/carboxy extension protein fusion [Botryotinia fuckeliana]
18486	ENU02280	ANI61C3200:	1304..1757				g1078650	546	136	9.00E-42	81	61		"peptidylprolyl isomerase (EC 5.2.1.8) a, cytosolic - fungus (Fusarium sporotrichioides)"
18487	ENU02281	ANI61C5329:	61-80	451-472	NAP		g131768	605	68	3.00E-11				quinate permease (quinate transporter); quinate transport protein - Emericella nidulans; (X13525) quinate permease [Emericella nidulans]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Primer Database Hit	aat	Blast Score	Blast Prob	% id	% cvrg	Description
18488	ENU02282	ANI61C7023:	22-49	414-434	NAP	g465702	221	83	2.00E-20	42	64	probable ribosomal protein B0303.15 in chromosome III ; ribosomal protein L11 homolog - <i>Caenorhabditis elegans</i> ; (M77697) ribosomal protein L11 [Caenorhabditis elegans] (AC000133) G4P04 [Emeicella nidulans]
18489	ENU02283	ANI61C1355:	60-79	451-473	NAP	g1870214	839	267	4.00E-74	98	68	hypothetical protein YPR100w - yeast (Saccharomyces cerevisiae); (U32445)
18490	ENU02284	ANI61C1024:	26-47	420-440	NAP	g2132281	217	76	2.00E-20	41	94	Note that there is a 357 codon ORF contained within this ORF on the other strand [Saccharomyces cerevisiae] "Lysyl-tRNA synthetase; cytoplasmic (lysine--tRNA ligase) (LYSRS); lysine--tRNA ligase (EC 6.1.1.6) - yeast (Saccharomyces cerevisiae); (J04186) Lysyl-tRNA synthetase [Saccharomyces cerevisiae]; (Z68196) Krs1p [Saccharomyces cerevisiae]; (Z74333) ORF YDR037w [Saccharomyces cerevisiae]"
18491	ENU02285	ANI61C2432:	25-44	421-440	NAP	g135139	698	241	3.00E-63	75	25	"Lysyl-tRNA synthetase; cytoplasmic (lysine--tRNA ligase) (LYSRS); lysine--tRNA ligase (EC 6.1.1.6) - yeast (Saccharomyces cerevisiae); (J04186) Lysyl-tRNA synthetase [Saccharomyces cerevisiae]; (Z68196) Krs1p [Saccharomyces cerevisiae]; (Z74333) ORF YDR037w [Saccharomyces cerevisiae]"
18492	ENU02286	ANI61C1783:	52-72	445-467	NAP	g2492643	621	195	1.00E-49	66	19	(isopropylmalate isomerase) (alpha-IPM isomerase) (IPMI); (D65833) 3-isopropylmalate dehydratase [Rhizopus niveus]; alpha-isopropylmalate isomerase [Rhizopus niveus] (AJ001732) rAsp f4 [Aspergillus fumigatus]
18493	ENU02287	ANI61C4724:	56-78	451-471	NAP	g3005839	485	125	2.00E-28	53	52	(AC004077) putative urease accessory protein [Arabidopsis thaliana]; (AC004481) putative urease accessory protein [Arabidopsis thaliana] (Z81071) predicted using Genefinder; Similarity to Human small nuclear ribonucleoprotein E (SW_P08578); cDNA EST yk375g7.3 comes from this gene; cDNA EST yk375g7.5 comes from this gene; cDNA EST yk435f5.3 comes from this gene; ...
18495	ENU02289	ANI61C9804:	71-95	470-489	NAP	g3876465	129	39	0.0005	63	80	

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat	Blast Score	Blast Prob	% id	% cvrg	Description
18496	ENU02290	ANI61C5930:	24-59	424-443	NAP	g33646479	526	70	1.00E-11	37	91	(AJ010981) putative transposase [Talaromyces stipitatus]	
18497	ENU02291	ANI61C7029:	64-84	464-483	NAP	g1169238	935	169	1.00E-41	56	30	"glutamate decarboxylase (GAD); glutamin-decarboxylase (EC 4.1.1.15), calmodulin-binding - garden petunia ; (L16797) glutamate decarboxylase [Petunia hybrida]; (L16977) glutamate decarboxylase [Petunia hybrida]" (AF079317) unknown [Sphingomonas aromaticivorans]	
18498	ENU02292	ANI61C8332:	33-52	432-452	NAP	g3378330	347	131	4.00E-30	40	79	hypothetical 29.7 KD protein in RSP5-PAK1 intergenic region ; hypothetical protein YER126c - yeast (Saccharomyces cerevisiae); (U18916) Yer126cp [Saccharomyces cerevisiae] (AL035656) hypothetical protein [Arabidopsis thaliana]	
18499	ENU02293	ANI61C9046:	46-66	441-466	NAP	g731511	805	189	1.00E-47	63	58	Prohibitin ; prohibitin - yeast (Saccharomyces cerevisiae); (Z72917) ORF YGR132c [Saccharomyces cerevisiae]	
18500	ENU02294	ANI61C1064	22-46	417-442	NAP	g4490325	104	58	0.000000	25	70	"2,2-dialkylglycine decarboxylase (DGD) ; (I05282) 2,2-dialkylglycine decarboxylase structural protein [Pseudomonas cepacia]" (AL021930) hypothetical protein Rv0276 [Mycobacterium tuberculosis] (AF093540) ribosomal protein L26 [Zea mays]	
18501	ENU02295	ANI61C7541:	928..531	42-61	443-462	NAP	g1730544	909	163	3.00E-53	73	53	Mannose-6-phosphate isomerase (PMI) (phosphomannose isomerase) ; mannose-6-phosphohexomutase ; mannose-6-phosphate isomerase (EC 5.3.1.8) - yeast (Candida albicans) ; (X82024) mannose-6-phosphate isomerase [Candida albicans]
18502	ENU02296	ANI61C3317:	409..870	32-51	433-452	NAP	g729318	784	106	1.00E-28	49	35	hypothetical protein YPR040w - yeast (Saccharomyces cerevisiae) ; (Z68111) unknown [Saccharomyces cerevisiae]; (Z71255) unknown [Saccharomyces cerevisiae]
18503	ENU02297	ANI61C5842:	889..427	68-99	463-488	NAP	g2909465	226	78	3.00E-14			
18504	ENU02298	ANI61C1473:	3926..4389	72-91	471-493	NAP	g3747050	380	115	1.00E-25	68	85	Rv0276 [Mycobacterium tuberculosis] (AF093540) ribosomal protein L26 [Zea mays]
18505	ENU02299	ANI61C2300:	2249..2713	64-83	464-486	NAP	g462565	294	71	3.00E-12	32	31	
18506	ENU02300	ANI61C5903:	2023..1559	33-54	433-455	NAP	g2132260	318	86	2.00E-16	46	37	

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18507	ENU02301	ANI61C7819:	23-42	425-445	NAP	g4235093	357	118	2.00E-27	43	19	(AF108944) beta-xylosidase	
			2..466									[Aspergillus niger]	
18508	ENU02302	ANI61C4975:	68-88	473-492	NAP	g1749584	415	157	6.00E-38	45	74	(D89188) unnamed protein product	
			2990..2524									[Schizosaccharomyces pombe]	
18509	ENU02303	ANI61C2732:	72-94	461-496	NAP	g1722894	465	187	3.00E-47	56	47	"beta-xylosidase (1,4-beta-D-xylan xylohydrolyase) (Xylan 1,4-beta-xylosidase) / alpha-L-	
			1650..1184									arabinofuranosidase (arabinosidase); xylosidase/arabinosidase - Bacteroides ovatus (strain V975); (U04957)	
18510	ENU02304	ANI61C1138:	22-41	428-447	NAP	g1931638	414	145	2.00E-34	42	12	xylosidase/arabinosidase [Bacteroides ovatus]; xylosidase-arabinosidase [Bacteroides ovatus]; xylosidase [Bacteroides ovatus] "	
			8699..9166									(U95973) transcription factor rush-1alpha isolog [Arabidopsis thaliana]	
18511	ENU02305	ANI61C2853:	34-53	436-459	NAP	g731448	70	43	0.001	31	62	hypothetical 18.3 KD protein in GAL83-YPT8 intergenic region ; hypothetical protein YER030w - yeast (Saccharomyces cerevisiae); (U18778) Yer030wp [Saccharomyces cerevisiae]	
			152..619										
18512	ENU02306	ANI61C3640:	67-87	459-493	NAP	g2493387	267	96	1.00E-19	38	27	probable sterigmatocystin biosynthesis P450 monooxygenase STCS (cytochrome P450 59); (U34740) putative p450 monooxygenase	
			5783..5315									[Emericella nidulans]	
18513	ENU02307	ANI61C1140:	48-67	452-474	NAP	g3925776	258	108	3.00E-23	39	94	(AL034353) putative acetyltransferase	
			668..1136									[Schizosaccharomyces pombe]	
18514	ENU02308	ANI61C1115	62-81	470-489	NAP	g2896142	984	85	2.00E-16	40	15	(AF047464) Tpr1	
			5..3351..3820									[Schizosaccharomyces pombe]	
18515	ENU02309	ANI61C2532:	24-46	432-451	NAP	g3006140	622	220	6.00E-57	68	60	(AL022299) ribosomal protein (AJ001133) ribosomal protein L7	
			626..1095									[Schizosaccharomyces pombe]	
18516	ENU02310	ANI61C8155:	64-84	468-492	NAP	g1572791	63	42	0.003			(U70852) weak similarity to neutral endopeptidases [Caenorhabditis elegans]	
			2369..2839									(AF095903) unknown [Sinorhizobium meliloti]	
18517	ENU02311	ANI61C5147:	69-100	477-498	NAP	g4580321	36	0.12					

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat	Blast Score	Blast Prob	% id	% cvrg	Description
18518	ENU02312	ANI61C8277:	68-87	478-497	NAP	g134975	495	101	3.00E-31	52	23	Heat shock protein STI1 ; stress-induced protein STI1 - yeast (Saccharomyces cerevisiae) ; (M28486)	
18519	ENU02313	ANI61C4165:	22-55	432-452	NAP	5..478	g548437	364	146	7.00E-35	47	18	STI1 heat shock protein [Saccharomyces cerevisiae] ; (X87331) ORF YOR027w [Saccharomyces cerevisiae]
18520	ENU02314	ANI61C102:1	28-46	435-460	NAP	415..1889	g2865437	214	83	1.00E-15			OSH1 protein ; SWH1 protein (version 1) - yeast [Saccharomyces cerevisiae] ; (L28920) Osh1p [Saccharomyces cerevisiae] (AF039376) polyprotein [Arabidopsis arenosa]
18521	ENU02315	ANI61C1075	23-44	435-455	NAP	2..1531..1057	g1351700	696	137	7.00E-42	57	46	hypothetical 34.1 KD protein C11D3.03C in chromosome 1 ; (Z68166) unknown [Schizosaccharomyces pombe] CUT8 protein ; (D31772) ORF [Schizosaccharomyces pombe] (Z73099) protein kinase [Schizosaccharomyces pombe] (AC05397) putative 3-methyl-2-oxobutanoate hydroxy-methyl-transferase [Arabidopsis thaliana] hypothetical zinc finger protein ZK686.4 in chromosome III ; ZK686.4 protein - Caenorhabditis elegans ; (L17337) coded for by C. elegans cDNAs GenBank:M88869 and T01933; putative [Caenorhabditis elegans] (Z97050) hypothetical protein Rv0163 [Mycobacterium tuberculosis] (AL023859) putative tRNA splicing endonuclease gamma subunit [Schizosaccharomyces pombe] (AF079317) unknown [Sphingomonas aromaticivorans]
18522	ENU02316	ANI61C8453:	59-81	464-491	NAP	1035..561	g729231	249	108	2.00E-23	33	60	
18523	ENU02317	ANI61C2468:	54-74	461-486	NAP	374..848	g3702336	566	134	4.00E-31	46	45	
18524	ENU02318	ANI61C2736:	35-60	448-467	NAP	518..44	g466044	150	72	2.00E-12	28	37	

Seq num	Seq id	Contig Source	5 pos	Primer 3 pos	Primer Basis	Selection Database Hit	aat	Blast Score	Blast Prob	% id	% cvrg	Description
18528	ENU02322	ANI61C1087	63-85	475-497	NAP	g1934614	269	109	1.00E-23	36	14	(U93874) cytochrome P450 102 [Bacillus subtilis]; (Z99117) similar to cytochrome P450 / NADPH-
18529	ENU02323	ANI61C35:18	41-60	456-475	NAP	g2498971	502	66	2.00E-10			cytochrome P450 reductase [Bacillus subtilis]
			1..657									putative sterigmatocystin biosynthesis monooxygenase STCW ; (U34740) putative FAD-containing
18530	ENU02324	ANI61C8224:	66-84	467-501	NAP	g1072179	109	40	0.009			"(U40939) Similar to dihydroflavonol-4-reductase (maize, petunia, tomato). [Caenorhabditis elegans]" (U61841) cutinase G-box binding protein [Fusarium solani f. sp. pisi] "(AF125459) contains similarity to enoyl-CoA hydratases/isomerasases (Pfam:PF00378, Score=59.1, E=3.3e-16, N=1) [Caenorhabditis elegans]" (Z95556) fadD35 [Mycobacterium tuberculosis]
18531	ENU02325	ANI61C2974:	51-70	464-486	NAP	g1438949	424	69	1.00E-18	42	28	"(AF125459) contains similarity to enoyl-CoA hydratases/isomerasases (Pfam:PF00378, Score=59.1, E=3.3e-16, N=1) [Caenorhabditis elegans]" (Z95556) fadD35 [Mycobacterium tuberculosis]
18532	ENU02326	ANI61C3312:	30-49	447-466	NAP	g4226133	34	0.00006				"(AF125459) contains similarity to enoyl-CoA hydratases/isomerasases (Pfam:PF00378, Score=59.1, E=3.3e-16, N=1) [Caenorhabditis elegans]" (Z95556) fadD35 [Mycobacterium tuberculosis]
18533	ENU02327	ANI61C7634:	40-68	458-477	NAP	g2113938	551	105	2.00E-30	51	25	"(AF125459) contains similarity to enoyl-CoA hydratases/isomerasases (Pfam:PF00378, Score=59.1, E=3.3e-16, N=1) [Caenorhabditis elegans]" (Z95556) fadD35 [Mycobacterium tuberculosis]
18534	ENU02328	ANI61C2961:	62-81	480-499	NAP	g2649635	292	124	4.00E-28	40	61	"(AF125459) contains similarity to enoyl-CoA hydratases/isomerasases (Pfam:PF00378, Score=59.1, E=3.3e-16, N=1) [Caenorhabditis elegans]" (Z95556) fadD35 [Mycobacterium tuberculosis]
18535	ENU02329	ANI61C9447:	63-82	481-501	NAP	g2499624	662	187	4.00E-47	68	12	"(AF125459) contains similarity to enoyl-CoA hydratases/isomerasases (Pfam:PF00378, Score=59.1, E=3.3e-16, N=1) [Caenorhabditis elegans]" (Z95556) fadD35 [Mycobacterium tuberculosis]
18536	ENU02330	ANI61C7555:	46-66	455-485	NAP	g3025275	375	102	2.00E-38	59	94	"(AF125459) contains similarity to enoyl-CoA hydratases/isomerasases (Pfam:PF00378, Score=59.1, E=3.3e-16, N=1) [Caenorhabditis elegans]" (Z95556) fadD35 [Mycobacterium tuberculosis]
			3253..3734									hypothetical 16.9 KD protein in ALD6-PDR12 intergenic region ; hypothetical protein YPL059w - yeast (Saccharomyces cerevisiae); (U39205) Lpe13p [Saccharomyces cerevisiae]

Seq num	Seq id	Contig Source	Primer Basis	Primer 3 pos	Selection Database Hit	aat	Blast Score	Blast Prob	% id	% cvrg	Description	
18537	ENU02331	ANI61C465:6	NAP	51..70	467..491	g4557817	1328	187	5.00E-47	57	30	3-oxoacid CoA transferase precursor; succinyl-CoA:3-ketoacid-CoA transferase precursor ; succinyl-CoA:3-ketoacid-CoEnzyme A transferase precursor (succinyl COA:3-oxoacid COA-transferase) (OXCT1); (U62961) succinyl CoA:3-oxoacid CoA transferase precursor [Homo sapiens]
18538	ENU02332	ANI61C1508:	NAP	42..62	458..482	g1363392	267	113	8.00E-25	36	24	beta-glucosidase/xylosidase - <i>Erwinia chrysanthemi</i> (AL031349) conserved hypothetical protein [Schizosaccharomyces pombe "Carboxy-cis,cis-muconate cyclase (3-carboxy-cis,cis-muconate lactonizing enzyme) (CMLE); carboxy-cis,cis-muconate cyclase (EC 5.5.1.5) - <i>Neurospora crassa</i> ; (L27538) 3-carboxy-cis,cis-muconate cyclase [Neurospora crassa] "
18541	ENU02335	ANI61C323:4	NAP	22..41	444..463	g549686	238	119	1.00E-26	39	16	Manganese resistance protein ; hypothetical protein YKL064w - yeast ( <i>Saccharomyces cerevisiae</i> ) ; (X75781) B969 [Saccharomyces cerevisiae]; (Z28064) ORF YKL064w [Saccharomyces cerevisiae] ; ORF [Saccharomyces cerevisiae]
18542	ENU02336	ANI61C1029	NAP	60..79	482..501	g4586458	163	85	2.00E-16	35	55	(AB025252) reverse transcriptase [Magnaporthe grisea] (D87924) ORF 6 [Actinomadura hibisca]
18543	ENU02337	ANI61C1099	NAP	3..1728..1245	446..466	g2580447	86	2.00E-16				(AL031743) conserved hypothetical protein [Schizosaccharomyces pombe tuberosus sclerosis protein 2 - human
18544	ENU02338	ANI61C2925:	NAP	666..183	70..89	g3650394	157	75	2.00E-13	33	80	(AL031540) uroporphyrin methyltransferase
18545	ENU02339	ANI61C349:7	NAP	145..6662	23..53	g631482	273	68	4.00E-11			[ <i>Schizosaccharomyces pombe</i> ] (AL031180) putative 2-hydroxyacid dehydrogenase [Schizosaccharomyces pombe]
18546	ENU02340	ANI61S1334:	NAP	61..82	484..503	g3581882	492	197	5.00E-50	59	32	
18547	ENU02341	ANI61C9558:	NAP	65..84	488..507	g3395556	695	156	8.00E-38	50	48	
		6029..6513										

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18548	ENU02342	ANI61C1812:	46-67	468-488	NAP	g2440206	412	122	2.00E-27	42	20	(Z99532) putative integral membrane protein [Schizosaccharomyces pombe]	
18549	ENU02343	ANI61C5509:	519..35	27-46	NAP	g140400	1065	201	3.00E-51	65	50	"hypothetical 37.2 KD protein in CHA1-PRD1 intergenic region ; hypothetical protein YCL059c - yeast (Saccharomyces cerevisiae); (X59720) YCL059c, len:316 [Saccharomyces cerevisiae]"	
18550	ENU02344	ANI61C6930:	26-46	450-469	NAP	g2160183	316	47	0.000000	47	42	"(AC000132) identical to A. thaliana U2 SnRNP-specific A' protein (gb X69137). ESTs gb ATTS0705, gb ATTS0339 come from this gene. [Arabidopsis thaliana]"	
18551	ENU02345	ANI61C9624:	43..530	22-57	446-466	NAP	g2842472	174	83	1.00E-15	31	65	(AL021747) preg-like protein. [Schizosaccharomyces pombe] "probable 60S ribosomal protein YIL052C ; ribosomal protein L34.e.B, cytosolic - yeast (Saccharomyces cerevisiae); (Z38060) spliced ribosomal protein, len: 121, CAI: 0.77, RL34_RAT P11250 60S ribosomal protein L34 [Saccharomyces cerevisiae]"
18552	ENU02346	ANI61C1031	8:1335..1135	22-56	445-466	NAP	g731810	335	92	2.00E-18	65	94	"(D89220) similar to Saccharomyces cerevisiae glutathion-dependent formaldehyde dehydrogenase, SWISS-PROT Accession Number P32771 [Schizosaccharomyces pombe]" hypothetical 66.4 KD protein in SMC3-MRPL8 intergenic region ; hypothetical protein YIL069c - yeast (Saccharomyces cerevisiae); (Z34288) HRE594 [Saccharomyces cerevisiae]; (X88851) hypothetical protein [Saccharomyces cerevisiae]; (Z49344) ORF YIL069c [Saccharomyces cerevisiae]
18553	ENU02347	ANI61C6624:	815..1301	68-87	491-512	NAP	g1749648	32	2.5				

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	atc.ncbi gi	Blast Score	Blast Prob	% id	% cvrg	Description
18555	ENU02349	ANI61C1036	50-69	462-495	NAP	g128478	171	93	1.00E-18	38	75	Nodulation protein L ; nodulation protein nodL - Rhizobium leguminosarum bv. viciae plasmid pRL1II ; (Y00548) nodL [Rhizobium leguminosarum] ; (X1755) nodL [Rhizobium leguminosarum] ; (Z99295) hypothetical protein [Schizosaccharomyces pombe]
18556	ENU02350	ANI61C7084:	30-53	455-475	NAP	g2414606	252	81	4.00E-15			"splicing factor, arginine/serine-rich 2; splicing factor, arginine/serine-rich 2; (splicing factor SC35) (SC-35) (splicing component, 35 KD) (PR264 protein); splicing factor SC35 - human ; (M90104) splicing factor [Homo sapiens]"
18557	ENU02351	ANI61C4309:	43-63	469-488	NAP	g4506899	173	53	0.000001	42	68	hypothetical 27.7 KD protein in UME3-HDA1 intergenic region ; probable membrane protein YNL024c - yeast (Saccharomyces cerevisiae) ; (Z71300) ORF YNL024c [Saccharomyces cerevisiae]
18558	ENU02352	ANI61C9255:	57-86	472-502	NAP	g1730714	220	86	1.00E-16	37	66	(U94183) unknown [Glomerella cingulata] [Z28283] ORF YKR057w [Saccharomyces cerevisiae] hypothetical 48.0 KD protein in MRPL37-RIF1 intergenic region ; probable membrane protein YBR271w - yeast (Saccharomyces cerevisiae) ; (Z36140) ORF YBR271w [Saccharomyces cerevisiae] (U62933) multidrug resistance protein 1 [Aspergillus fumigatus] ; (U62934) multidrug resistance protein 1 [Aspergillus fumigatus]
18562	ENU02356	ANI61C1090	35-54	463-482	NAP	g2673951	1172	247	3.00E-65	89	10	

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Primer NAP	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18563	ENU02357	ANI50C1_11	66-86	484-514	NAP		g2493561		117	2.00E-33				Cytosine deaminase (cytosine aminohydrolase); hypothetical protein [Saccharomyces cerevisiae]; (Z49219) unknown [Saccharomyces cerevisiae]; (Z71255) unknown [Saccharomyces cerevisiae]; (U55193) cytosine deaminase [Saccharomyces cerevisiae]; (AF005261) cytosine deaminase [Saccharomyces cerevisiae]
18564	ENU02358	ANI61C2752:	40-59	469-488	NAP		g2493540	965	314	3.00E-85	99	22		catalase B; (U80672) catalase [Emeticella nidulans]
18565	ENU02359	ANI61C6673:	27-49	447-476	NAP		g731886	189	88	3.00E-17	32	83		"hypothetical 22.0 KD protein in FOX3-UBP7 intergenic region; probable membrane protein YIL157c - yeast (Saccharomyces cerevisiae); (Z38059) orf; len 197, CAI: 0.19 [Saccharomyces cerevisiae]"
18566	ENU02360	ANI61C1188:	42-63	471-491	NAP		g729839	985	240	4.00E-79	89	41		ketol-acid reductoisomerase precursor (acetohydroxy-acid reductoisomerase) (alpha-keto-beta-hydroxylacil reductoisomerase); alpha-keto-beta-hydroxylacyl reductoisomerase - Neurospora crassa; (M84189) alpha-keto-beta-hydroxylacyl reductoisomerase [Neurospora crassa] (AF035619) pyridoxine biosynthesis protein [Cercospora nicotianae] (AL031540) short chain dehydrogenase [Schizosaccharomyces pombe]
18567	ENU02361	ANI61C9579:	45-65	473-494	NAP		g2979688	923	169	1.00E-41	73	46		Probable nicotinate phosphoribosyltransferase (NAPRTASE); probable nicotinate phosphoribosyltransferase (EC 2.4.2.11) - yeast (Saccharomyces cerevisiae); (Z75117) ORF YOR209c [Saccharomyces cerevisiae]
18568	ENU02362	ANI61C6739:	37-56	467-486	NAP		g3581884	362	58	3.00E-17	46	50		Coatomer beta subunit (beta-coat protein) (beta-COP); beta-COP protein - rat; (X57228) beta COP [Rattus norvegicus]
18569	ENU02363	ANI61C8503:	71-90	500-520	NAP		g2507262	786	64	4.00E-21	42	33		
18570	ENU02364	ANI61C5428:	23-42	446-474	NAP		g116923	715	222	9.00E-58	62	17		
		2..495												

Seq num	Seq id	Contig Source	Primer 3 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat	Blast Score	Blast Prob	% id	% cvrg	Description
18571	ENU02365	ANI61C4891:	22-47	455-474	NAP	g2132942	275	110	7.00E-24	36	31	probable membrane protein YOR306c-yeast (Saccharomyces cerevisiae); (Z75214) ORF YOR306c-[Saccharomyces cerevisiae]	
18572	ENU02366	ANI61C8291:	70-89	500-523	NAP	g548818	283	85	1.00E-25	57	85	"DNA-directed RNA polymeraseS I, II, and III 15 KD polypeptide (RPABC6); (L00597) RNA polymerase small common phosphorylated subunit [Schizosaccharomyces pombe]; (L25592) RNA polymerase [Schizosaccharomyces pombe]; (AL023518) dna-directed RNA polymerase [Schizosaccharomyces pombe]"	
18573	ENU02367	ANI61C2932:	64-83	499-518	NAP	g3850092	819	149	9.00E-50	72	32	(AL033389) argininosuccinate lyase [Schizosaccharomyces pombe]	
18574	ENU02368	ANI61C8403:	48-69	483-502	NAP	g1353060	439	185	1.00E-46	58	89	"3-hydroxyanthranilateE 3,4-dioxygenase (3-HAO) (3-hydroxyanthranilic acid dioxygenase); (3-hydroxyanthranilate oxyxygenase); hypothetical protein YIR075c - yeast (Saccharomyces cerevisiae); (Z49525) ORF YJR025c [Saccharomyces cerevisiae]; (X87297) J1550 (U60989) putative transposase [Saccharomyces cerevisiae]"	
18575	ENU02369	ANI61C171:1	24-54	452-478	NAP	g1408257	305	117	6.00E-26	35	29	[Magnaporthe grisea]	
18576	ENU02370	ANI61C7500:	54-73	489-509	NAP	g1706568	140	85	3.00E-16	34	64	putative enoyl-CoA hydratase; (Z73101) echA6 [Mycobacterium tuberculosis]	
18577	ENU02371	ANI61C6450:	57-77	492-512	NAP	g1351658	351	131	4.00E-30	54	79	Adaptin complex small chain homolog C30D11.05 ; hypothetical protein SPAC30D11.05 - fission yeast (Schizosaccharomyces pombe); (Z67961) adaptin complex small chain homolog [Schizosaccharomyces pombe] (U77369) transcription factor dMax	
18578	ENU02372	ANI61C7324:	28-48	455-483	NAP	g1763539	77	55	0.000000	32	67	[Drosophila melanogaster]	

Seq num	Seq id	Contig Source	5 pos	3 pos	Primer Basis	Primer NAP	Selection	Blast ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18579	ENU02373	ANI61C5863:	29-51	466-485				g1169869	267	50	0.00001			"eukaryotic translation initiation factor 3 gamma subunit (EIF-3 gamma) (EIF3, P62) (translation initiation factor EIF3, P62 subunit) (GCD10 protein); GCD10 protein - yeast (Saccharomyces cerevisiae); (X83511) Gedl0p [Saccharomyces cerevisiae]; (Z71338) ORF YNL062c [Saccharomyces cerevisiae]; (UJ2141) Gedl0p [Saccharomyces cerevisiae]"
18580	ENU02374	ANI61C3397:	27-47	453-483	NAP			g4206286	1929	173	5.00E-43	52	16	(AF043332) p1asma membrane H(+)-ATPase [Emericella nidulans] (AL022103) hypothetical protein
18581	ENU02375	ANI61C1097	24-52	461-480	NAP			g2956778	409	80	2.00E-28	51	32	[Schizosaccharomyces pombe] cyclin-dependent kinaseS regulatory subunit (cell division control protein CKS1) ; protein kinase CDC28 complex subunit CKS1 - yeast (Saccharomyces cerevisiae); (M26033) protein kinase [Saccharomyces cerevisiae]; (X75891) CKS1 [Saccharomyces cerevisiae]; (Z36004) ORF YBR135w [Saccharomyces cerevisiae]; CKS1 gene [Saccharomyces cerevisiae]
18582	ENU02376	ANI61C3024:	67-86	503-523	NAP			g116484	296	87	8.00E-26			
18583	ENU02377	ANI61C1300:	23-44	459-480	NAP			g2501011	453	77	9.00E-14	28	16	
18584	ENU02378	ANI61C6297:	58-77	497-516	NAP			g465677	196	109	1.00E-23	37	60	[Synechocystis sp.] hypothetical 30.5 KD protein C30A5.3 (isoleucyl-tRNA synthetase) (ILERS); (D90907) isoleucyl-tRNA synthetase [Synechocystis sp.]
18585	ENU02379	ANI61C2983	65-85	504-523	NAP			g3192023	220	79	2.00E-14	32	33	in chromosome III ; C30A5 protein - Caenorhabditis elegans ; (L10990) putative [Caenorhabditis elegans] (AL023794) putative proline oxidase precursor [Schizosaccharomyces pombe]

Seq num	Seq id	Contig Source	Primer 3 pos	Primer Basis	Selection Database Hit	aat	Blast Score	Blast Prob	% id	% cvrg	Description	
18586	ENU02380	ANI61C462:6	39..58	478..497	NAP	g4504799	837	127	2.00E-34	63	32	isovaleryl Coenzyme A dehydrogenase ; isovaleryl-CoA dehydrogenase precursor (IVD) ; isovaleryl-CoA dehydrogenase (EC 1.3.99.10) precursor - human ; (M34192) isovaleryl-coA dehydrogenase (IVD) [Homo sapiens]
18587	ENU02381	ANI61C9323:	38..59	477..497	NAP	g1077341	137	50	0.000000	40	88	"hypothetical protein YLR281c - yeast (Saccharomyces cerevisiae); (U17243) This gene is in the -2 reading frame. There are also overlapping ORFs in the -3 reading frame, and in the +1 reading (on the other strand). The longest ORF was arbitrarily chosen as L8003.11 [Saccharomyces cerevisiae]" (U89492) arylsulfatase [Neurospora crassa]
18589	ENU02383	ANI61C9179:	56..75	494..515	NAP	g2873363	212	108	4.00E-23	37	23	Antiranilate synthase component I; antiranilate synthase (EC 4.1.3.27) component I - yeast (Saccharomyces cerevisiae); (X68327) antiranilate synthase (component 1) [Saccharomyces cerevisiae]; (U18839) Trp2p; antiranilate synthase component I [Saccharomyces cerevisiae]
18590	ENU02384	ANI61C6172:	70..89	511..530	NAP	g3169083	279	81	6.00E-15	36	49	(AL023705) hypothetical protein [Schizosaccharomyces pombe] hypothetical 43.3 KD protein in EVGS GLK intergenic region ; (AE000325) putative enzyme [Escherichia coli] probable peptidyl-l-prolyl cis-trans isomerase C57A10.03 ; (Z94864) peptidyl-prolyl cis-trans isomerase [Schizosaccharomyces pombe]
18592	ENU02386	ANI61C6376:	46..65	486..506	NAP	g3219935	546	215	6.00E-56	70	92	
			4221..4723									

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Prob	% id	% cvrg	Description
18593	ENU02387	ANI61C2093:	42-62	484-503	NAP	g1711596	231	91	5.00E-18	40	16		putative sulfate transporter YPR003C; probable membrane protein YPR003c; yeast (Saccharomyces cerevisiae); (Z48951) unknown [Saccharomyces cerevisiae]; (U31900) Lpz3p
18594	ENU02388	ANI61C2410:	22-43	462-484	NAP	g1710602	192	73	9.00E-13	30	57		[Saccharomyces cerevisiae]; (Z71255) unknown [Saccharomyces cerevisiae] "mitochondrial 60S ribosomal protein L30 precursor (YML30); ribosomal protein Yml30 precursor, mitochondrial - yeast (Saccharomyces cerevisiae); (X96722) ORF N0864 [Saccharomyces cerevisiae]; (Z71528) ORF YNL252c [Saccharomyces cerevisiae]" hypothetical 47.3 KD protein C17G8.13C in chromosome I; (Z69795) unknown [Schizosaccharomyces pombe] alpha-glucosidase (EC 3.2.1.20) M6L62 - yeast (Candida albicans); (M94674) alpha-glucosidase [Candida albicans]
18596	ENU02390	ANI61C8016:	59-78	483-522	NAP	g3223015	1408	118	3.00E-26	37	29		(AL02377) ma binding protein [Schizosaccharomyces pombe] 40S ribosomal protein S17; (M13933) ribosomal protein S17 [Cricetulus griseus]; (D25213) ribosomal protein S17 [Mus musculus]
18597	ENU02391	ANI61C7458:	22-45	462-485	NAP	g3184100	327	145	2.00E-34	43	61		sorbitol dehydrogenase (L-iditol 2-dehydrogenase); L-iditol 2-dehydrogenase (EC 1.1.1.14) precursor - mouse ; (U27014) sorbitol dehydrogenase precursor [Mus musculus domesticus]
18598	ENU02392	ANI61C1126:	66-89	511-530	NAP	g133820	334	92	1.00E-31	62	91		hypothetical 45.7 KD protein in RPS3-PSD1 intergenic region ; hypothetical protein YNL175c - yeast (Saccharomyces cerevisiae); (Z71451) ORF YNL175c [Saccharomyces cerevisiae]
18599	ENU02393	ANI61C4302:	34-63	477-498	NAP	g2492773	574	96	1.00E-19	37	41		
18600	ENU02394	ANI61C879:5	46-68	491-510	NAP	g1730806	196	87	6.00E-17	31	36		
			66..1072										

Seq num	Seq id	Contig Source	Primer 3 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18601	ENU02395	ANI61C631:1	53-73	489-517	NAP	g2497216	123	62	0.000000	28	22	003	CAT8 intergenic region ; hypothetical protein YMR277w - yeast (Saccharomyces cerevisiae) ; (Z49704) unknown [Saccharomyces cerevisiae] (U34346) unknown [Paracoccus denitrificans] (AB01288) ribosomal protein S23 homolog [Schizosaccharomyces pombe]
18602	ENU02396	ANI61C8419:	34-54	470-498	NAP	g1002864	555	198	2.00E-50	53	85	(AB023235) KIAA1018 protein [Homo sapiens]	
18603	ENU02397	ANI61C2838:	45-64	488-510	NAP	g1850766	614	144	1.00E-56	86	86	(AB01288) ribosomal protein S23 homolog [Schizosaccharomyces pombe]	
18604	ENU02398	ANI61C4555:	47-79	491-512	NAP	g4589686	210	100	1.00E-20	33	16	(AB023235) KIAA1018 protein [Homo sapiens]	
18605	ENU02399	ANI61C7287:	45-66	492-511	NAP	g1176711	137	59	0.000000	22	89	hypothetical 21.6 KD protein F37A4.2 in chromosome III ; F37A4.2 protein - Caenorhabditis elegans ; (U00032) F37A4.2 gene product [Caenorhabditis elegans]	
18606	ENU02400	ANI50C1_10	40-59	480-506	NAP	g131056	237	4.00E-62	69	60	Aspergilllopepsin II precursor (acid protease A) (protease A) ; aspergilllopepsin II (EC 3.4.23.19) precursor - Aspergillus niger (var. macrosporus) ; (M68871) acid proteinase A [Aspergillus niger] ; acid protease A [Aspergillus niger] ; macrosporus]		
18607	ENU02401	ANI61C5560:	53-73	501-520	NAP	g1353046	190	45	0.0003	37	22	hypothetical 65.3 KD protein in pre-3-SAG1 intergenic region ; hypothetical protein YJR001w - yeast (Saccharomyces cerevisiae) ; (X87611) ORF YJR83.4 [Saccharomyces cerevisiae] ; (Z49501) ORF YJR001w [Saccharomyces cerevisiae]	
18608	ENU02402	ANI61C9150:	26-50	464-493	NAP	g1911486	388	90	4.00E-34	51	52	"(S80872) putative Tc1-mariner class transposase/IS630-Tc1 homolog [Aspergillus niger, chlorate-resistant mutant 46, transposon Ant1, Peptide Transposon, 325 aa] [Aspergillus niger]"	

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18609	ENU02403	ANI61C8849:	72-93	520-539	NAP	g2497193	499	152	2.00E-36	44	33	hypothetical 56.2 KD protein in ERG8-UBP8 intergenic region ; probable membrane protein YMR221c - yeast (Saccharomyces cerevisiae) ; (Z49939)	
18610	ENU02404	ANI61C6707:	62-81	508-530	NAP	g3451464	370	111	1.00E-35	59	88	(AL031349) N-acetyltransferase [Schizosaccharomyces pombe] (Y15278) cytochrome P450	
18611	ENU02405	ANI61C5252:	65-90	505-533	NAP	g3549891	562	102	2.00E-21	46	28	monoxygenase [Gibberella fujikuroi] sugar transporter STL1 ; sugar transport protein STP1 - yeast (Saccharomyces cerevisiae) ; (U33057)	
18612	ENU02406	ANI61C4094:	22-47	472-491	NAP	g1711561	283	110	6.00E-24	34	29	St1p; plasma membrane sugar transporter; CAI: 0.19 [Saccharomyces cerevisiae]	
18613	ENU02407	ANI61C3490:	22-45	472-491	NAP	g3851164	163	62	0.000000	23	32	(AF097181) tuftelin-interacting protein 10 [Mus musculus]	
18614	ENU02408	ANI61C7357:	70-96	521-540	NAP	g34204901	215	71	7.00E-12	38	66	(U57100) orf256; putative triose phosphate isomerase [Brucella abortus]	
18615	ENU02409	ANI61C5347:	46-65	495-516	NAP	g3929399	96	1.00E-19				proline-specific permease (proline transport protein); (X79797) proline permease [Emericella nidulans]	
18616	ENU02410	ANI61C6339:	34-54	480-506	NAP	g1352881	180	66	2.00E-10	37	94	hypothetical 15.7 KD protein in NUP85-SSC1 intergenic region ; probable membrane protein YJR044c - yeast (Saccharomyces cerevisiae) ; (Z49544) ORF YJR044c [Saccharomyces cerevisiae] ; (L36344) ORF; putative [Saccharomyces cerevisiae]	
18617	ENU02411	ANI61C6057:	60-79	512-533	NAP	g4150918	288	113	7.00E-28	50	70	(Z50728) putative acetyltransferase [Schizosaccharomyces pombe]	

Seq num	Seq id	Contig Source	Primer 3 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	Score	Blast Score	Blast Prob	% id	% cvrg	Description
18618	ENU02412	ANI61C3771:	22-41	470-496	NAP	g417274	407	181	3.00E-45				mitochondrial import inner membrane translocase subunit TIM23 (mitochondrial protein import protein 3) (mitochondrial protein import protein MAS6) (membrane import machinery protein MIM23); mitochondrial inner membrane protein MIM23 - yeast (Saccharomyces cerevisiae); (X71633) MAS6 [Saccharomyces cerevisiae]; (Z71632) ORF YNR017w (AF048992) ribonuclease H1 [Saccharomyces pombe] (AL031535) transcription initiation factor tfIID 60 kd subunit [Schizosaccharomyces pombe] (X96943)
18619	ENU02413	ANI61C9517:	44-63	500-519	NAP	g2911504	332	94	4.00E-25	44	55		[Schizosaccharomyces pombe] (Y15277) cytochrome P450 monooxygenase [Gibberella fujikuroi] hypothetical 63.0 KD protein in PYC2- PDB1 intergenic region ; probable membrane protein YBR220c - yeast (Saccharomyces cerevisiae); (Z36088) ORF YBR220c [Saccharomyces cerevisiae]
18620	ENU02414	ANI61C1044	44-63	500-519	NAP	g3560272	594	84	7.00E-16	38	36		(AL031535) transcription initiation factor tfIID 60 kd subunit [Schizosaccharomyces pombe] (X96943)
18621	ENU02415	ANI61C1050	36-55	491-512	NAP	g1524045	459	132	1.00E-30	42	38		Geranylgeranylpyrophosphate Synthetase [Gibberella fujikuroi] (AL033391) hypothetical membrane protein [Candida albicans]
18622	ENU02416	ANI61C3996:	23-44	480-499	NAP	g3850125	542	115	2.00E-25	41	32		(Y15277) cytochrome P450 monooxygenase [Gibberella fujikuroi] hypothetical 63.0 KD protein in PYC2- PDB1 intergenic region ; probable membrane protein YBR220c - yeast (Saccharomyces cerevisiae); (Z36088) ORF YBR220c [Saccharomyces cerevisiae]
18623	ENU02417	ANI61C8551:	32-54	489-508	NAP	g3549879	436	88	1.00E-22	40	28		(AL033396) putative alcohol phosphatidyl transferase [Candida albicans]
18624	ENU02418	ANI61C1086	60-79	520-539	NAP	g586338	913	126	9.00E-29	43	26		"Cleavage and polyadenylation specificity factor, 160 KD subunit (CPSF 160 KD subunit); (U37012) cleavage and polyadenylation specificity factor [Homo sapiens]"
18625	ENU02419	ANI61C4950:	27-58	486-506	NAP	g3850144	198	75	1.00E-17	36	60		
18626	ENU02420	ANI61C9832:	22-57	483-502	NAP	g1706102	133	77	7.00E-14	32	11		

Seq num	Seq id	Contig Source	Primer 3 pos	Primer 3 pos	Selection Basis	Database Hit	blast gi	aat	Blast Score	Blast Prob	% id	% cvrg	Description
18627	ENU02421	ANI61C6709:	23-46	472-503	NAP	g2500360	157	64	6.00E-15	38	60	60	60S ribosomal protein L14 ; ribosomal protein L14 [Rattus norvegicus]
18628	ENU02422	ANI61C5035:	40-60	499-521	NAP	g1723738	548	164	4.00E-40	43	34	34	hypothetical 55.1 KD protein in TRX1. RTA1 intergenic region ; hypothetical protein YGR211w - yeast (Saccharomyces cerevisiae) ; (Z72996) ORF YGR211w [Saccharomyces cerevisiae] ; (AF019769) zinc finger protein [Saccharomyces cerevisiae] (U81509) urease [Coccidioides immitis]
18629	ENU02423	ANI61C1400:	36-55	497-517	NAP	g2580518	3042	136	5.00E-39	66	15	15	[Cochliobolus heterostrophus] (U68040) polyketide synthase (U61840) sodium transport ATPase FST [Fusarium solani f. sp. pisi] (X96943)
18630	ENU02424	ANI61C1002	29-48	489-510	NAP	g1546072	1185	68	5.00E-11	29	6	6	Synthetase [Gibberella fujikuroi] (AE000952) methylmalonyl-CoA decarboxylase, biotin carboxyl carrier subunit (mmdC) [Archaeoglobus fulgidus]" (AE000855) endonuclease III [Methanobacterium thermoautotrophicum]
18631	ENU02425	ANI61C1767:	53-74	510-534	NAP	g1438947	697	272	1.00E-72	67	35	35	"CAT5 protein (ubiquinone biosynthesis protein COQ7); CAT5 protein - yeast (Saccharomyces cerevisiae) ; (X82930) CAT5 [Saccharomyces cerevisiae] ; (X90518) putative [Saccharomyces cerevisiae] ; (X94335) YOR3284c [Saccharomyces cerevisiae] ; (Z75033) ORF YOR125c [Saccharomyces cerevisiae] ; (S81938) COQ7 [Saccharomyces cerevisiae, Peptide, 272 aa] [Saccharomyces cerevisiae]" (AE000352) putative transport protein [Escherichia coli]
18633	ENU02427	ANI61C2430:	22-53	474-504	NAP	g2648307	127	59	0.000000	32	99	99	
18634	ENU02428	ANI61C8832:	54-73	516-536	NAP	g2621854	84	52	0.000002	29	52	52	
18635	ENU02429	ANI61C303;9	28-48	491-510	NAP	g1168783	381	118	1.00E-34				
18636	ENU02430	ANI61C3361:	34-53	498-517	NAP	g1789036	257	61	0.000000	33	56	56	
		637..112					008						

Seq num	Seq id	Contig Source	Primer 3 pos	Primer 3 pos	Selection Basis	Database Hit	nebi gi	aat	Blast Score	Blast Prob	% id	% cvrg	Description
18637	ENU02431	ANI61C9483:	32-51	484-515	NAP	g133887	234	94	8.00E-19	54	96	"mitochondrial ribosomal protein S24; ribosomal protein S16, mitochondrial - Neurospora crassa ; (X06360) cyt-21; [Neurospora crassa] ; (J03533)	
		965..1490											ribosomal protein S-24 [Neurospora crassa]"
18638	ENU02432	ANI61C2362:	48-67	510-531	NAP	gg699196	316	104	4.00E-22				(U15181) 4-coumarate-coA ligase
		805..1330											[Mycobacterium leprae]
18639	ENU02433	ANI61C9152:	63-82	525-546	NAP	g133336	145	53	1.00E-12				DNA-directed RNA polymerase II 32 KD polypeptide (B32) ; DNA-directed RNA polymerase (EC 2.7.7.6) II chain RPB4 - yeast (Saccharomyces cerevisiae) ; (X58099) RPB4
		6161..6686											[Saccharomyces cerevisiae] ; (M27253) RNA polymerase II subunit RPB4
18640	ENU02434	ANI61C2487:	61-82	525-544	NAP	g2983039	285	132	2.00E-30	41	30	[Saccharomyces cerevisiae] ; (Z49415) ORF YJL40w [Saccharomyces cerevisiae]	
		2519..1994											[Aquifex aeolicus]
18641	ENU02435	ANI50C3497	28-47	492-512	NAP	g462739	109	2.00E-23	38	26			NPL4 protein ; NPL4 protein - yeast (Saccharomyces cerevisiae) ; (X72224) NPL4 [Saccharomyces cerevisiae] ; (X74437) open reading frame YBR12.31 [Saccharomyces cerevisiae] ; (Z36039) ORF YBR170c
		5..1:867..341											[Saccharomyces cerevisiae]
18642	ENU02436	ANI61C383:5	61-80	526-545	NAP	g399112	199	91	6.00E-18	33	16	beta-galactosidase (lactase) ; beta-galactosidase (EC 3.2.1.23) - yeast (Kluyveromyces marxianus var. lactis) ; (M84410) beta-D-galactosidase [Kluyveromyces lactis]	
		5..581											(Z82062) cDNA EST yk415c12.5 comes from this gene [Caenorhabditis elegans]
18643	ENU02437	ANI61C6528:	28-49	488-513	NAP	g3880440	190	69	2.00E-11	32	96		
		2573..3100											

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18644	ENU02438	ANI61C6109:	23-43	482-509	NAP	g3123100	351	99	6.00E-33	50	99	"hypothetical 15.9 KD protein C4A8.02C in chromosome 1; (Z98762) SPAC4A.8.02C, unknown, len:[42aa, similar eg. to YJBQ_ECOLI, P32698, hypothetical 15.7 kd protein, ([138aa), fast a scores, opt:403, E0: 2.4e-32, (41.0% identity in 134 aa overlap) [Schizosaccharomyces pombe]"	
18645	ENU02439	ANI61C5925: 1611..1083	38-57	504-524	NAP	g2543649	245	86	2.00E-21	53	91	hypothetical protein 133 - Rhodococcus erythropolis (fragment); (D14454) P47K protein [Rhodococcus erythropolis]; ORF P47K [Rhodococcus erythropolis]	
18646	ENU02440	ANI61C7364: 2988..3517	22-50	490-509	NAP	g2585656	249	86	2.00E-16			Pyridoxamine 5'-phosphate oxidase (PNP/PMP oxidase); pyridoxamine- phosphatase oxidase (EC 1.4.3.5) - yeast (Saccharomyces cerevisiae); (X76992) pyridoxamine-phosphate oxidase [Saccharomyces cerevisiae]; (X76078) YBR0321 [Saccharomyces cerevisiae]; (Z35904) ORF YBR035c [Saccharomyces cerevisiae]; ORF YBR0321 [Saccharomyces cerevisiae] (AL023554) zinc finger protein [Schizosaccharomyces pombe] (AF034090) MAPKK kinase [Neurospora crassa]	
18647	ENU02441	ANI61C137:1	22-42	484-510	NAP	g3133097	114	48	0.00005	30	35	SAP1 protein ; hypothetical protein YER047c - yeast (Saccharomyces cerevisiae); (UJ8796) Yer047cp [Saccharomyces cerevisiae] (AJ000084) putative acetyl transferase [Proteus mirabilis]	
18648	ENU02442	ANI61C132:1: 82..612	23-47	490-511	NAP	g2654103	751	250	4.00E-66	67	25	sterigmatocystin 7-O-methyltransferase precursor ; (L25836) O-methyltransferase [Aspergillus flavus] hypothetical 59.3 KD protein C17C9.16C in chromosome 1; (Z73099) hypothetical protein [Schizosaccharomyces pombe]	
18649	ENU02443	ANI61C799: 555..23	27-55	496-516	NAP	g731461	793	138	4.00E-41	57	19		
18650	ENU02444	ANI61C817: 61-81	531-550	NAP		g3395518	124	60	0.000000	28	88		
18651	ENU02445	ANI61C3627: 3038..3570	4238..3705	525-546	NAP	g2498701	127	63	0.000000	33	37		
18652	ENU02446	ANI61C8243: 920..388	41-62	507-531	NAP	g1723574	549	74	8.00E-13	33	33		

Seq num	Seq id	Contig Source	Primer 3 pos	Primer Basis	Selection Database Hit	aat.ncbi gi	Blast Score	Blast Prob	% id	% cvrg	Description
18653	ENU02447	ANI61C8767:	2848	NAP	g3334833	66	2.00E-10				(AJ007932) ketoreductase [Streptomyces argillaceus]
18654	ENU02448	ANI61C4182:	35-54	NAP	g2330829	826	182	2.00E-45	52	11	(Z98530) hypothetical protein [Schizosaccharomyces pombe]
18655	ENU02449	ANI61C7614:	13..544	NAP	g118066	259	104	5.00E-22	35	32	cyclohexanone monooxygenase ; (M19029) cyclohexanone monooxygenase [Acinetobacter sp.]
18656	ENU02450	ANI61C6208:	32-51	NAP	g1350839	257	114	5.00E-25	52	60	RIBOSE 5-phosphate isomerase [phosphoRIBOisomerase] ; (L35034) ribose 5-phosphate isomerase [Mus musculus]
18657	ENU02451	ANI61C8852:	60-79	NAP	g2832629	60	0.000000				(AL021711) 4-coumarate-CoA ligase - like [Arabidopsis thaliana]
18658	ENU02452	ANI61C1084:	1907..1371	NAP	g2131743	361	129	0.00E-29	52	85	hypothetical protein YLR009w - yeast (Saccharomyces cerevisiae) ; (Z73181) ORF YLR009w [Saccharomyces cerevisiae]
18659	ENU02453	ANI61C1271:	116..653	NAP	g1729996	667	228	2.00E-59	62	60	TOXD protein ; (X92391) unique to isolates that make the cyclic peptide HC-toxin [Cochliobolus carbonum] Lipase (EC 3.1.1.3) (Triacylglycerol Acylhydrolase)
18660	ENU02454	ANI61C1190:	4015..3476	NAP	g999873	616	106	9.00E-23	49	51	hypothetical 62.6 KD protein C29E6.02 in chromosome I ; (Z66525) unknown [Schizosaccharomyces pombe]
18661	ENU02455	ANI61C1070	6..4348..4887	NAP	g1351617	728	138	4.00E-32	45	31	Benzaldehyde lyase (benzoin aldolase) (BL) (BZL) ; (U04048) benzaldehyde lyase [Pseudomonas fluorescens] putative sterigmatocystin biosynthesis monoxygenase STCW ; (U34740) putative FAD-containing monooxygenase [Emericella nidulans] (AL023796) hypothetical protein [Schizosaccharomyces pombe]
18662	ENU02456	ANI61C2194:	524-543	NAP	g1705519	153	68	3.00E-12	31	31	
18663	ENU02457	ANI61C3754:	1807..1268	NAP	g2498971	574	110	8.00E-24	32	36	
18664	ENU02458	ANI61C9710:	487-520	NAP	g3192040	147	48	0.00004	28	98	
		559..1099									

Seq num	Seq id	Contig Source	Primer 3 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18665	ENU02459	ANI61C7140:	2948	54..594	NAP	g4505495	239	104	6.00E-22				8-oxoguanine DNA glycosylase ; (Y11731) DNA glycosylase/AP lyase [Homo sapiens] ; (Y11838) 8-oxoguanine DNA glycosylase homolog 1 [Homo sapiens] ; (AB000410) hOGG1 [Homo sapiens] ; (AF003595) 8-oxoguanine DNA glycosylase 1 [Homo sapiens] ; (U88527) 8-hydroxyguanine glycosylase/lyase [Homo sapiens]
18666	ENU02460	ANI61C3964:	40-59	515-538	NAP	g2492754	582	76	1.00E-18	42	57		sorbitol utilization protein SOU1 ; (AF002134) Sou1p [Candida albicans] hypothetical 56.2 KD protein in UME3-HDA1 intergenic region ; hypothetical protein YNL022c - yeast (Saccharomyces cerevisiae) ; (Z71298) ORF YNL022c [Saccharomyces cerevisiae]
18667	ENU02461	ANI61C2208:	61-80	540-559	NAP	g1730712	372	78	4.00E-14	29	35		(M2988) DNA mismatch repair protein [Saccharomyces cerevisiae] (AF026523) manganese superoxide dismutase; Mn-SOD [Penicillium chrysogenum] ; (AF026790) manganese superoxide dismutase [Penicillium chrysogenum] (U62028) negative acting factor [Fusarium solani f. sp. pisi]
18670	ENU02464	ANI61C8484:	52-71	532-551	NAP	g1470090	92	50	0.00001	27	38		

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Primer NAP	Database Hit	ncbi gi	aat	Blast Score	Blast Prob	% id	% cvrg	Description
18671	ENU02465	ANI61C1889:	41-61	516-540	NAP		g1346554		42	0.000000		1		probable myosin regulatory light chain ; (Z46793) similar to myosin regulatory light chain 2; cDNA EST EMBL:T01273 comes from this gene; cDNA EST EMBL:C09382 comes from this gene; cDNA EST EMBL:C07858 comes from this gene; cDNA EST yk404h11.3 comes from this gene; cDN... ; (Z34801) similar to myosin regulatory light chain 2; cDNA EST EMBL:T01273 comes from this gene; cDNA EST EMBL:C09382 comes from this gene; cDNA EST EMBL:C07858 comes from this gene; cDNA EST yk404h11.3 comes from this gene; cDN...
18672	ENU02466	ANI61C7908:	50-69	526-550	NAP		g3929362	397	97	3.00E-24	41	29		Pisatin demethylase (cytochrome P450 57A1) ; pisatin demethylase - fungus ( <i>Nectria haematococca</i> ) ; (L20976) pisatin demethylase [ <i>Nectria haematococca</i> mpV1]
18673	ENU02467	ANI61C2918:	49-68	526-550	NAP		g118572	180	59	0.000000	007			Granaticin polyketide synthase putative ketoacyl reductase 2 (ORF6) ; granaticin-producing polyketide synthase chain 6 - <i>Streptomyces violaceoruber</i> ; (X16144) ketoacyl reductase (AA 1-289) [ <i>Streptomyces violaceoruber</i> ] ; (X16300) ORF 6 (AA 1-249) [ <i>Streptomyces violaceoruber</i> ] ; (AJ011500) gra-orf6 [ <i>Streptomyces violaceoruber</i> ]
18674	ENU02468	ANI61C6924:	34-53	516-535	NAP		g4503609	375	50	3.00E-19				"electron-transfer-flavoprotein, beta polypeptide ; electron transfer flavoprotein beta-subunit (beta-ETF) ; electron transfer flavoprotein beta chain - human ; Chain B, Three-Dimensional Structure Of Human Electron Transfer Flavoprotein To 2.1 A Resolution ; (X71129) electron transfer flavoprotein beta subunit [Homo sapiens]"

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database	Hit ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18675	ENU02469	ANI61C1036	37-56	521-540	NAP	g3560474	209	80	2.00E-19	32	51	(U81312) S-adenosyl-methionine-7,900..1447	[Nicotiana tabacum]
18676	ENU02470	ANI61C1112	72-93	556-575	NAP	g450864	536	198	2.00E-50	54	32	(L2793) alkaline phosphatase [Neurospora crassa]	2,63..608
18677	ENU02471	ANI61C4008:	32-56	512-535	NAP	g731922	414	130	8.00E-30	43	64	"hypothetical oxidoreductase in LYS1-HYR1 intergenic region ; probable membrane protein YIR035c - yeast (Saccharomyces cerevisiae); (Z38061)	89..634
18678	ENU02472	ANI61C2566:	53-77	533-557	NAP	g2497980	772	203	6.00E-75	83	51	[Saccharomyces cerevisiae]" "ADP,ATP carrier protein (ADP/ATP translocase) (adenine nucleotide translocator) (ANT); (Z49974) adenine nucleotide carrier	547..1
18679	ENU02473	ANI61C3960:	23-51	503-529	NAP	g1351687	108	49	0.00002	28	98	[Schizosaccharomyces pombe]; (AL023634) adppatp translocase [Schizosaccharomyces pombe]" hypothetical 17.2 KD protein C3H1.03 in chromosome 1; (Z68144)	1663..2211
18680	ENU02474	ANI61C8321:	50-76	536-556	NAP	g3023267	658	212	6.00E-65	66	18	[Schizosaccharomyces pombe] alpha-glucosidase precursor (maltase); (D45356) alpha-glucosidase [Aspergillus niger]	87..635
18681	ENU02475	ANI61C6620:	43-64	531-551	NAP	g2916970	194	33	1.3			(AL0222002) hypothetical protein Rv1672c [Mycobacterium tuberculosis]	826..1376
18682	ENU02476	ANI61C3952:	72-91	560-580	NAP	g124205	193	62	0.000000	003		eukaryotic translation initiation factor 2 beta subunit (EIF-2-beta); translation initiation factor eIF-2 beta chain - yeast (Saccharomyces cerevisiae); (M21813) translation initiation factor eIF2 beta- subunit [Saccharomyces cerevisiae]; (Z67751) SUI3 [Saccharomyces cerevisiae]; (Z73594) ORF YPL237w [Saccharomyces cerevisiae]	556..331
18683	ENU02477	ANI61C5937:	31-53	520-539	NAP	g2950465	215	76	3.00E-18	38	39	(AL022071) fructosyl amine [Schizosaccharomyces pombe]	1283..733

Seq num	Seq id	Contig Source	Primer 3 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat	Blast Score	Blast Score	% id	% cvrg	Description
18684	ENU02478	ANI61C8339:	25-44	512-533	NAP	g1730644	243	100	1.00E-20	28	27	27	hypothetical 73.4 KD protein in ERG24-MET2 intergenic region ; probable membrane protein YNL279w -yeast (Saccharomyces cerevisiae) ; (Z71555) ORF YNL279w [Saccharomyces cerevisiae] (AL032681) putative hydroxyacylglutathione hydrolase
18685	ENU02479	ANI61C1708:	22-51	509-530	NAP	g3810866	60	0.000000	01				[Schizosaccharomyces pombe] "beta-galactosidase precursor (lactase); (L06037) beta-D-galactosidase [Aspergillus niger]; (S37150) beta-galactosidase [Aspergillus niger, Peptide, 1006 aa] [Aspergillus niger]; beta galactosidase [Aspergillus niger]" (AL035064) queuine tma-ribosyltransferase
18686	ENU02480	ANI61C1532:	39-58	518-548	NAP	g461623	823	146	1.00E-34	53	17		[Schizosaccharomyces pombe] "beta-galactosidase precursor (lactase); (L06037) beta-D-galactosidase [Aspergillus niger]; (S37150) beta-galactosidase [Aspergillus niger, Peptide, 1006 aa] [Aspergillus niger]; beta galactosidase [Aspergillus niger]" (AL035064) queuine tma-ribosyltransferase
18687	ENU02481	ANI61C9801:	23-45	513-532	NAP	g4106673	413	153	6.00E-37	54	38		[Schizosaccharomyces pombe] Rodlet protein precursor ; Rodletless protein - Emericella nidulans ; (M61113) rodlet peptide [Emericella nidulans] (AL022590) amino acid permease [Schizosaccharomyces pombe] hypothetical 61.8 KD peptidase in MPR1-GCN20 intergenic region ; probable membrane protein YFR006w -yeast (Saccharomyces cerevisiae) ; (D50617) YFR006w [Saccharomyces cerevisiae]
18688	ENU02482	ANI61C1130:	65-84	555-574	NAP	g133264	313	66	4.00E-14	59	81		[X76302] nucleic acid binding protein [Homo sapiens] (AF029913) unknown [Cochliobolus heterostrophus] ; (AF027687) unknown [Cochliobolus heterostrophus] hypothetical 27.3 KD protein in REF2-CBS2 intergenic region ; hypothetical protein YDR196c - yeast (Saccharomyces cerevisiae) ; (Z48784) unknown [Saccharomyces cerevisiae]
18689	ENU02483	ANI61C1027	69-88	560-579	NAP	g3136040	706	142	2.00E-33	39	34		
18690	ENU02484	ANI61C9766:	47-66	535-557	NAP	g1175977	465	136	1.00E-31	37	34		
			32..584										

Seq num	Seq id	Contig Source	Primer 3 pos	Primer Basis	Selection	aat	Blast Score	Blast Prob	% id	% cvrg	Description
					Database Hit	ncbi gi					
18694	ENU02488	ANI61C3516:	29-48	NAP	g3687456	303	127	8.00E-30	44	97	(AL031798) hypothetical protein [Schizosaccharomyces pombe]
18695	ENU02489	ANI50C392_-	22-50	NAP	g2144770	209	1.00E-53	65	59	"acidic ribosomal protein P0.e, cytosolic - yeast [Saccharomyces cerevisiae]; (M37326) ribosomal protein L10e [Saccharomyces cerevisiae]; (M26506) L10e protein [Saccharomyces cerevisiae]; (M26506)	
18696	ENU02490	ANI61C7084:	24-43	518-537	NAP	g2414606	252	104	6.00E-22	46	94
18697	ENU02491	ANI61C7236:	27-48	522-541	NAP	g548420	373	84	6.00E-31	54	90
		3666..4222									
18698	ENU02492	ANI61C7717:	68-87	550-583	NAP	g4456822	352	141	5.00E-33	42	100
		2362..2919									
18699	ENU02493	ANI61C4632:	68-87	564-583	NAP	g2351250	325	89	3.00E-17	43	25
18700	ENU02494	ANI61C1096	71-97	554-587	NAP	g2498530	198	100	9.00E-21	40	56
		43.004..2446									
18701	ENU02495	ANI61C1484:	50-83	546-567	NAP	g2708305	766	154	2.00E-43	47	35
		714..154									
18702	ENU02496	ANI61C3181:	42-65	537-559	NAP	g1054845	1435	159	2.00E-57	62	39
		1268..1827									
18703	ENU02497	ANI61C9072:	72-94	569-589	NAP	g1764098	178	31	0.000003	37	20
		149..708									
18704	ENU02498	ANI61C2133:	66-88	562-584	NAP	g1877327	60	0.000000	01		[Mycobacterium tuberculosis]
		927..1487									

Seq num	Seq id	Contig	Source	Primer 3 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat	Blast Score	Blast Prob	% id	% cvrg	Description
18705	ENU02499	ANI61C884:7	2949	528-547	NAP		g2500493	324	98	3.00E-27	66	97		putative 40S ribosomal protein in SNF2-CPA1 intergenic region ; ribosomal protein S10.e.A - yeast (Saccharomyces cerevisiae); (Z75201) ORF YOR293w [Saccharomyces cerevisiae]
18706	ENU02500	ANI61C8267:	45-66	543-564	NAP		g481285	342	130	9.00E-30	38	26		NADPH--ferrithemoprotein reductase (EC 1.6.2.4) - Aspergillus niger; (Z26938) NADPH cytochrome P450 oxidoreductase [Aspergillus niger]; NADPH cytochrome P450 reductase [Aspergillus niger] (AJ223998) PCZA361.9 [Amycolatopsis orientalis] (AL023592) putative
18707	ENU02501	ANI61C8414:	48-67	548-567	NAP		g2894160	229	71	4.00E-18	38	59		phosphatidylinositol-glycan-class c protein [Schizosaccharomyces pombe] myoSIN-2 isoform ; myosin myo2 - yeast (Saccharomyces cerevisiae); (M35532) myosin I isoform (myo2) [Saccharomyces cerevisiae]; (Z75234) ORF YOR326w [Saccharomyces cerevisiae]
18708	ENU02502	ANI61C9773:	22-44	523-542	NAP		g3136049	270	129	2.00E-29	40	56		Deoxyribose-phosphate aldolase (phosphodeoxyribaldolase) (deoxyribaldolase); deoxyribose aldolase (deoC) homolog - Haemophilus influenzae (strain Rd KW20); (U32791) deoxyribose-phosphate aldolase (deoC) [Haemophilus influenzae Rd] hypothetical protein YOR171c - yeast (Saccharomyces cerevisiae); (U55021) O3615p [Saccharomyces cerevisiae]; (Z75078) ORF YOR171c [Saccharomyces cerevisiae] (AF027979) carnitine acetyl transferase [Magnaporthe grisea] (Z97210) hypothetical protein [Schizosaccharomyces pombe]
18709	ENU02503	ANI61C8325:	54-75	553-574	NAP		g127736	322	62	4.00E-18	43	9		
18710	ENU02504	ANI61C3214:	56-76	557-576	NAP		g1169268	326	108	2.00E-23	43	81		
18711	ENU02505	ANI61C1078	44-65	546-565	NAP		g2132075	519	117	5.00E-26	30	30		
18712	ENU02506	ANI61C8080:	31-59	533-552	NAP		g2688966	991	259	1.00E-68	64	30		
18713	ENU02507	ANI61C1189:	41-60	539-563	NAP		g2239219	194	46	0.000000	34	79		
			10..573					005						



Seq num	Seq id	Contig Source	Primer 3 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	Score	Score	Blast Prob	% id	% cvrg	Description
18721	ENU02515	ANI61C1211:	35-65	541-560	NAP	g4506439	556	129	4.00E-47				retinoblastoma-binding protein 7; histone acetyltransferase type B subunit 2 (retinoblastoma binding protein P46) (retinoblastoma-binding protein 7); retinoblastoma-binding protein RbAp46 - human ; (X72841) IEF 7442 [Homo sapiens] ; (U35143) retinoblastoma-binding protein RbAp46 [Homo sapiens] ; (AF090306) retinoblastoma binding protein [Rattus norvegicus]; retinoblastoma-binding protein [Homo sapiens]
18722	ENU02516	ANI61C4036:	50-69	559-576	NAP	g729327	166	41	0.0006	25	47	glucose 1-dehydrogenase IV (GLCDH-IV); glucose 1-dehydrogenase (EC 1.1.1.47) - Bacillus megaterium ; (D10626) glucose dehydrogenase [Bacillus megaterium]	
18723	ENU02517	ANI61C3865:	60-81	566-586	NAP	g4387575	251	109	1.00E-23	39	59	"(AC006550) Belongs to PF01121 Uncharacterized protein family UPF0038 containing ATP/GTP binding domain. ESTs gblAA585719, gblAA728503 and gblT22272 come from this gene. [Arabidopsis thaliana]" (U8827) 8 kDa cytoplasmic dynein light chain [Emeticella nidulans] (D85924) myosin [Mus musculus]	
18724	ENU02518	ANI61C6288:	48-68	551-574	NAP	g4099025	316	62	2.00E-16	84	97	[Schizosaccharomyces pombe] casein kinase I homolog HHPI ; hhpl protein - fission yeast	
18725	ENU02519	ANI61C7365:	46-65	549-572	NAP	g1945080	48	0.00005				(Schizosaccharomyces pombe)	
18726	ENU02520	ANI61C1062	30-51	538-558	NAP	g2842503	301	80	5.00E-27	43	75	(AL021748) hypothetical protein [Schizosaccharomyces pombe]	
18727	ENU02521	ANI61C6548:	44-63	553-572	NAP	g729712	1373	225	2.00E-58			(Schizosaccharomyces pombe) ; casein kinase-1 homolog hhpl - Yeast (Schizosaccharomyces pombe); (X78871) Hhp1 protein kinase [Schizosaccharomyces pombe]; (UJ0863) casein kinase-1 [Schizosaccharomyces pombe]; (AL031261) casein kinase i homologue [Schizosaccharomyces pombe]	

Seq num	Seq id	Contig Source	Primer 3 pos	Primer Basis	Selection Database Hit	aat ncbi gi	Score	Prob	% id	% cvrg	Description	
18728	ENU02522	ANI61C1038	43-68	NAP	553-572	g2842501	81	7.00E-15	(AL021748) putative quinone oxidoreductase [Schizosaccharomyces pombe]			
18729	ENU02523	ANI61C7455:	23-42	NAP	533-552	g4506235	165	69	2.00E-11	36	73	"proteasome (prosome, macropain) 26S subunit, non-ATPase, 9 ; 26S proteasome regulatory subunit P27 ; (AB003177) proteasome subunit p27 [Homo sapiens]"
18730	ENU02524	ANI61C1020	61-80	NAP	561-591	g3929392	633	201	4.00E-62	82	57	vacuolar ATP synthase subunit D (V-ATPase D subunit) ; (AF052320) vacuolar ATPase subunit D [Neurospora crassa]
18731	ENU02525	ANI50C1	10	26-46	538-557	NAP	g416837	84	6.00E-16	34	40	cytochrome P450-TERP (cytochrome P450 108) ; cytochrome P450terp - Pseudomonas sp. ; (M91440) P450terp [Pseudomonas sp.]
18732	ENU02526	ANI61C8486:	42-64	NAP	554-574	g3560214	806	207	5.00E-53	67	30	(AL031536) tma splicing protein [Schizosaccharomyces pombe]
18733	ENU02527	ANI61C9210:	62-83	NAP	378-952	g126192	739	106	2.00E-22			2-isopropylmalate synthase (alpha-isopropylmalate synthase) (alpha-IPM synthetase) ; 2-isopropylmalate synthase (EC 4.1.3.12) - yeast (Saccharomyces cerevisiae) ; (M12893) alpha-isopropylmalate synthase (EC 4.1.3.12), long form [Saccharomyces cerevisiae] ; (Z50161) 2-Isopropylmalate Synthase [Saccharomyces cerevisiae] ; (Z71380) ORF YNL104c [Saccharomyces cerevisiae]
18734	ENU02528	ANI61C6322:	55-73	NAP	569-588	g3873823	169	59	0.000000	39	72	(Z73422) predicted using Genefinder [Caenorhabditis elegans]
18735	ENU02529	ANI61C5608:	71-91	NAP	581-604	g173624	114	65	3.00E-10	27	36	(U34744) cytochrome P450 [Phalaenopsis sp. "hybrid SM9108"]
18736	ENU02530	ANI61C8209:	43-62	NAP	557-577	g3114281	437	186	9.00E-47	46	84	"Chain M, Crystal Structure Of The 20s Proteasome From Yeast At 2.4 Angstroms Resolution ; Chain 1, Crystal Structure Of The 20s Proteasome From Yeast At 2.4 Angstroms Resolution "

Seq num	Seq id	Contig Source	Primer 3 pos	Primer 3 pos	Selection Basis	Database Hit	nebi gi	Score	Score Prob	% id	% cvrg	Description
18737	ENU02531	ANI61C1107	22-44	536-556	NAP	g1730718	297	140	8.00E-33	43	31	probable membrane protein YNL029c - yeast (Saccharomyces cerevisiae); (Z71305) ORF YNL029c [Saccharomyces cerevisiae]
18738	ENU02532	ANI61C1137	56-75	563-591	NAP	g731738	596	122	3.00E-27	37	12	DNA replication helicase DNA2; probable purine nucleotide-binding protein YHR164c - yeast (Saccharomyces cerevisiae); (U00027) Dna2pp: DNA replication helicase [Saccharomyces cerevisiae]
18739	ENU02533	ANI61C2857:	24-59	533-559	NAP	g2130462	205	100	7.00E-21	36	30	poly A polymerase (EC 2.7.7.-) - fission yeast (Schizosaccharomyces pombe); (X79705) polymerase [Schizosaccharomyces pombe]; (AL035216) poly A polymerase [Schizosaccharomyces pombe] DNA-directed RNA polymerase II 14.2 KD polypeptide (B12.6); DNA-directed RNA polymerase (EC 2.7.7.6) II chain RPB9 - yeast (Saccharomyces cerevisiae); (M73060) RNA polymerase II subunit RPB9 [Saccharomyces cerevisiae]; (Z72592) ORF YGL070c [Saccharomyces cerevisiae]
18740	ENU02534	ANI61C3020:	34-54	543-569	NAP	g133341	289	91	6.00E-18	51	96	hypothetical 74.4 KD protein C30D11.09 in chromosome I; hypothetical protein SPA-C30D11.09 - fission yeast (Schizosaccharomyces pombe); (Z67961) hypothetical protein [Schizosaccharomyces pombe] (Z99111) similar to glucose 1-dehydrogenase [Bacillus subtilis] (AF008220) yteR [Bacillus subtilis]; (Z99119) similar to hypothetical proteins [Bacillus subtilis]
18741	ENU02535	ANI61C2411:	53-72	570-589	NAP	g1351662	660	205	2.00E-52	48	30	hypothetical 74.4 KD protein C30D11.09 in chromosome I; hypothetical protein SPA-C30D11.09 - fission yeast (Schizosaccharomyces pombe); (Z67961) hypothetical protein [Schizosaccharomyces pombe] (Z99111) similar to glucose 1-dehydrogenase [Bacillus subtilis] (AF008220) yteR [Bacillus subtilis]; (Z99119) similar to hypothetical proteins [Bacillus subtilis]
18742	ENU02536	ANI61C9242:	36-57	553-573	NAP	g2633748	305	94	6.00E-19	38	76	
18743	ENU02537	ANI61C8858:	23-45	536-560	NAP	g2293194	303	99	3.00E-20			
		580..1										

Seq num	Seq id	Contig Source	Primer 3 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat	Blast Score	Blast Prob	% id	% cvrg	Description
18744	ENU02538	ANI61C508:2	28-56	545-565	NAP	g1077558		33	0.005				hypothetical protein YDR063w - yeast (Saccharomyces cerevisiae); (X84162) unknown [Saccharomyces cerevisiae]; (Z49209) unknown [Saccharomyces cerevisiae]; (Z74359) ORF YDR063w [Saccharomyces cerevisiae]
18745	ENU02539	ANI61C749:8: 22-52	540-559	NAP	81..660	g2465148	135	75	4.00E-13	32	45		(Z99753) hypothetical protein [Schizosaccharomyces pombe]
18746	ENU02540	ANI61C464:7 45-73	556-582	NAP	084..7663	g1708006	215	105	2.00E-22	37	95		probable gluconokinase (gluconate kinase); (Z69727) probable glucokinase [Schizosaccharomyces pombe]
18747	ENU02541	ANI61C1052 23-49	534-561	NAP	9.4702..5282	g3873699	160	94	1.00E-18	44	85		(Z73102) predicted using Genefinder; Similarity to viral non-structural proteins (SW:POLN_EEVV3); cDNA EST EMBL:D65747 comes from this gene; cDNA EST D69295 comes from this gene; cDNA EST EMBL:C10380 comes from this gene;
18748	ENU02542	ANI61C784: 38-57	557-577	NAP	1359..778	g1705999	291	123	1.00E-27	33	37		Coatomer delta subunit (delta-coat protein) (delta-COP); (X94265) coat protein delta-cop [Bos primigenius] (Z99168) putative heat shock transcription factor
18749	ENU02543	ANI61C2563: 65-85	584-604	NAP	2203..1622	g3327019	230	89	1.00E-18	41	28		[Schizosaccharomyces pombe] "fructose-bisphosphate aldolase" (Y11135) fructose-1,6-bisphosphate aldolase type II [Bacillus stearothermophilus]"
18750	ENU02544	ANI61C939: 47-66	555-586	NAP	721..1303	g4033506	206	86	2.00E-16	35	60		probable calcium-binding protein ALG-2 (PMP41) (ALG-257); (U49112) ALG-2 [Mus musculus] sterigmatocystin biosynthesis regulatory protein ; sterigmatocystin synthesis transcriptional regulator affR - Emmericella nidulans ; (U34740) pathway specific transcription factor [Emmericella nidulans] (L07492) sugar transport protein [Saccharomyces cerevisiae]
18751	ENU02545	ANI61C984: 37-56	544-576	NAP	222..303	g2506252	340	145	2.00E-34	39	97		
18752	ENU02546	ANI61C970: 66-87	586-605	NAP	52..634	g1703202	228	67	1.00E-10	35	44		
18753	ENU02547	ANI61C537:8 36-55	543-575	NAP	55..274	g409547	138	45	0.0006	38	24		

Seq num	Seq id	Contig Source	Primer 3 pos	Primer Basis	Selection Database Hit	aat ncbi gi	blast Score	blast Prob	% id	% cvrg	Description
18754	ENU02548	ANI61C9833:	2746	NAP	g3877351	308	75	9.00E-18			(Z66520) similar to ERG-3 like protein
18755	ENU02549	ANI61C215.8	2241	543-562	NAP	g3881138	159	85	5.00E-16	38	96 [Caenorhabditis elegans] (AL023846) Y52B11C.1
18756	ENU02550	ANI61C1039	72-92	596-615	NAP	g280470	64	0.000000			[Caenorhabditis elegans] (AF043701) contains similarity to ankyrin repeats and protein kinases
18757	ENU02551	ANI61C3473:	42-61	556-585	NAP	g465713	216	71	9.00E-18	32	67 [Caenorhabditis elegans]
			1214..1386								hypothetical 30.3 KD protein in APE1/LAP4-CWP1 intergenic region ; hypothetical protein YKL099c - yeast
18758	ENU02552	ANI61C1071	27-47	551-570	NAP	g4506617	391	102	1.00E-27	59	67 (Saccharomyces cerevisiae) ; (X71133) YKL449 [Saccharomyces cerevisiae]; (Z28099) ORF YKL099c
			3..86..671								[Saccharomyces cerevisiae]
18759	ENU02553	ANI61C8712:	58-77	577-602	NAP	g2498702	79	48	0.00007	34	38 ribosomal protein L17 ; 60S ribosomal protein L17 - human ; (X53777) putative ribosomal protein (AA 1-184) [Homo sapiens]
			1686..1480								sterigmatocystin 7-O-methyltransferase precursor ; (L25835) O-methyltransferase [Aspergillus flavus] ; (L25834) O-methyltransferase [Aspergillus parasiticus] ; (L22091) O-methyltransferase [Aspergillus parasiticus]
18760	ENU02554	ANI61C2827:	31-60	556-575	NAP	g114988	1001	363	e-100	98	16 Kinesin-like protein BIMC ; kinesin-related protein bimC - Emericella nidulans ; (M32075) kinesin-like protein (bimC) [Emericella nidulans]
18761	ENU02555	ANI61C9570:	44-63	568-589	NAP	g1084581	396	118	4.00E-36	50	89 hypothetical protein YER007c-a - yeast (Saccharomyces cerevisiae) ; (U18778) Yel007c-ap [Saccharomyces cerevisiae]
18762	ENU02556	ANI61C7729:	31-50	557-576	NAP	g2231082	1314	100	8.00E-21	37	19 (Y07891) dynamin-related protein [Schizosaccharomyces pombe]
18763	ENU02557	ANI61C4165:	69-95	591-614	NAP	g3264834	1030	187	4.00E-47	50	55 (AF072541) xylitol dehydrogenase; XDH [Galactocandida mastotermitis]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Primer Basis	Selection	Blast gi	aat Score	Blast Score	% id	% cvrg	Description
						Database Hit	ncbi gi	580	131	1.00E-48		
18764	ENU02558	ANI61C8730:	71-90	594-616	NAP	g130879						Proteasome component PUP1 precursor (macropain subunit PUP1) (proteinase YSCE subunit PUP1) (multicatalytic endopeptidase complex subunit PUP1) ; probable multicatalytic endopeptidase complex (EC 3.4.99.46) chain PUP1 - yeast (Saccharomyces cerevisiae); (X61189) PUP1 [Saccharomyces cerevisiae]; (U55020) Pup1p [Saccharomyces cerevisiae]; (Z75065) ORF YOR157c [Saccharomyces cerevisiae]
18765	ENU02559	ANI61C1935:	52-71	576-598	NAP	g2117760	802	92	1.00E-25	50	33	"aspartate transaminase (EC 2.6.1.1), cytosolic - yeast (Saccharomyces cerevisiae); (Z73199) ORF YLR027c [Saccharomyces cerevisiae]" (AL023780) zinc finger protein [Schizosaccharomyces pombe] (L48797) toxin pump [Cochliobolus carbonum]
18766	ENU02560	ANI61C6513:	22-47	545-568	NAP	g3184113	116	66	2.00E-10	35	30	Autophagy serine/threonine-protein kinase APG1 ; probable membrane protein YGL180w - yeast (Saccharomyces cerevisiae); (X91489) putative ser/thr protein kinase [Saccharomyces cerevisiae]; (Z72702) ORF YGL180w [Saccharomyces cerevisiae]; (D29991) Apg1p [Saccharomyces cerevisiae]
18767	ENU02561	ANI61C886:	1 40-59	565-587	NAP	g1063421	252	84	6.00E-16	28	34	yeast (Saccharomyces cerevisiae); (X61189) PUP1 [Saccharomyces cerevisiae]; (U55020) Pup1p [Saccharomyces cerevisiae]; (Z75065) ORF YOR157c [Saccharomyces cerevisiae]
18768	ENU02562	ANI61C5484:	72-92	590-619	NAP	g1730043	222	77	2.00E-17	39	19	
18769	ENU02563	ANI61C4438:	68-86	594-615	NAP	g730759	197	49	0.000000	33	71	
18770	ENU02564	ANI61C7200:	48-70	571-596	NAP	g3834684	121	66	2.00E-10	30	86	(AF100925) mating type protein MAT-1-3 [Gibberella fujikuroi]
18771	ENU02565	ANI61C1125	59-78	584-607	NAP	g464786	235	94	1.00E-26	34	28	SPT10 protein ; regulatory protein SPT10 - yeast (Saccharomyces cerevisiae); (L244435) SPT10 [Saccharomyces cerevisiae]; (Z49402) ORF YJL127c [Saccharomyces cerevisiae]

Seq num	Seq id	Contig Source	Primer 3 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat	Blast Score	Blast Prob	% id	% cvrg	Description
18772	ENU02566	ANI61C8336:	59-88	589-608	NAP	g3722	816	258	2.00E-68	63	32	(X52633) GAP1 protein (AA 1-601)	
18773	ENU02567	ANI61C7975:	36-55	566-585	NAP	g4056551	666	154	9.00E-57	62	33	[Saccharomyces cerevisiae] (AL024583) putative elongation initiation factor subunit	
18774	ENU02568	ANI61C1803:	65-100	582-615	NAP	g1805251	273	101	4.00E-21	35	34	[Schizosaccharomyces pombe] (U58946) transposase [Aspergillus awamori]	
18775	ENU02569	ANI61C1115	53-73	584-603	NAP	g1723280	354	106	1.00E-22	43	52	hypothetical 34.8 KD protein C4H3.04C in chromosome I; (Z69380) unknown [Schizosaccharomyces pombe]	
18776	ENU02570	ANI61C8494:	59-80	589-610	NAP	g3913497	637	84	3.00E-33	54	58	putative carboxymethyl/enebutenolidase (dienelactone hydrolase) (DLH); hypothetical protein YDL086w - yeast (Saccharomyces cerevisiae); (Z74134) ORF YDL086w [Saccharomyces cerevisiae]	
18777	ENU02571	ANI61C6927:	47-66	563-599	NAP	g729230	652	191	1.00E-64	82	12	chromosome segregation protein CUT3 ; cut3 protein - fission yeast (Schizosaccharomyces pombe); (D30788) cut3 protein [Schizosaccharomyces pombe]	
18778	ENU02572	ANI61C4306:	37-57	553-589	NAP	g2132076	302	64	2.00E-18	33	44	hypothetical protein YOR173w - yeast (Saccharomyces cerevisiae); (U55021) O3625p [Saccharomyces cerevisiae]; (Z75081) ORF YOR173w [Saccharomyces cerevisiae] (AF039838)	
18779	ENU02573	ANI61C6203:	62-81	582-615	NAP	g4322563	441	103	3.00E-40	60	91	phosphatidylglycerol/phosphatidylinositol transfer protein [Aspergillus oryzae] (AB04537) hypothetical 47.4KD protein in SHP1-SEC17 intergenic region [Schizosaccharomyces pombe] peroxisomal assembly protein 5 - yeast (Picta pastoris)	
18780	ENU02574	ANI61C1145	71-94	605-624	NAP	g2257524	619	127	2.00E-41	56	62		
18781	ENU02575	ANI61C941:9	28-46	560-581	NAP	g539079	440	147	2.00E-37	54	14		
			7..692										

Seq num	Seq id	Contig Source	Primer 3 pos	Primer 5 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18782	ENU02576	ANI61C3194:	23-43	547-577	NAP	g133371	207	74	7.00E-18				III 16 KD polypeptide (AC19) ; DNA-directed RNA polymeraseS I and directed RNA polymerase (EC 2.7.7.6)
													I/III chain AC19 - yeast
													(Saccharomyces cerevisiae) ; (M64991)
													AC19 RNA polymerase subunit [Saccharomyces cerevisiae] ; (Z69382)
													Subunit of RNA polymerase I and III [Saccharomyces cerevisiae] ; (Z71390)
													ORF YNL113w [Saccharomyces cerevisiae]
18783	ENU02577	ANI61C8284:	40-59	573-595	NAP	g461540	796	171	7.00E-57				"phospho-2-dehydro-3-deoxyheptonate aldolase, tyrosine-inhibited (phospho-2-keto-3-deoxyheptonate aldolase) (DAHP synthetase) (3-deoxy-D-arabino-heptulosonate 7-phosphate synthase) ; 2-dehydro-3-deoxyphosphoheptonate aldolase (EC 4.1.2.15) ARO4 - yeast (Saccharomyces cerevisiae) ; (L20296) homology with DAHP-synthase (ARO4) gene [Saccharomyces cerevisiae] ; (X61107) phospho-2-dehydro-3-deoxyheptonate aldolase [Saccharomyces cerevisiae] ; (Z36118) ORF YBR249c [Saccharomyces cerevisiae]"
													(AL035260) dna-directed rna polymerase iii subunit [Schizosaccharomyces pombe]
18785	ENU02579	ANI61C3975:	66-86	587-622	NAP	g1351702	337	76	2.00E-13	31	36		hypothetical 61.1 KD protein C11D3.05 in chromosome I ; (Z68166) unknown [Schizosaccharomyces pombe]
													(AL022245) ser/thr protein kinase [Schizosaccharomyces pombe] ; (AL031603) protein kinase.
18786	ENU02580	ANI61C9713:	63-86	594-619	NAP	g2995375	924	212	4.00E-59	66	46		[Schizosaccharomyces pombe] ; (AL023781) hypothetical protein [Schizosaccharomyces pombe]
18787	ENU02581	ANI61C3218:	70-89	606-626	NAP	g3184080	394	68	4.00E-11	60	85		
													1079..1677

Seq num	Seq id	Contig Source	Primer 3 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18788	ENU02582	ANI61C1056	46-65	578-602	NAP	g1722905	157	66	3.00E-14	34	26	"endo-1,4-beta-xylanase D precursor (xylanase D) (XYLD); endo-1,4-beta-xylanase (EC 3.2.1.8) D - Cellulomonas fimi; (X76729) endo-1,4-beta-xylanase [Cellulomonas fimi]"	
18789	ENU02583	ANI61C1120	72-91	610-629	NAP	g3184056	56	0.000000					(AL023776) hypothetical protein [Schizosaccharomyces pombe]
18790	ENU02584	ANI61C8956:	25-46	555-582	NAP	g2598037	257	60	3.00E-17	31	43	(AJ001272) manganese resistance 1 protein [Saccharomyces cerevisiae]	
18791	ENU02585	ANI61C7700:	22-55	561-580	NAP	g133264	341	73	7.00E-21	52	96	Rodlet protein precursor ; Rodletless protein - Emericella nidulans ; (M61113) rodlet peptide [Emericella nidulans]	
18792	ENU02586	ANI61C5260:	44-63	581-602	NAP	g1710503	609	161	3.00E-46	69	85	"probable 60S ribosomal protein L18 (RP28); ribosomal protein L18.e, cytosolic - fission yeast (Schizosaccharomyces pombe); (AL031528) 60S ribosomal protein 118 [Schizosaccharomyces pombe]"	
18793	ENU02587	ANI61C3974:	48-79	583-607	NAP	g120609	630	199	4.00E-53			Uracil phosphoribosyltransferase (UMP pyrophosphorylase)	
		733..1334										(UPRTASE); uracil phosphoribosyltransferase (EC 2.4.2.9) chain FUR1 - yeast (Saccharomyces cerevisiae); (M36485) uracil phosphoribosyltransferase (FUR1) [Saccharomyces cerevisiae]; (U10398) Furlp: Uracil phosphoribosyltransferase [Saccharomyces cerevisiae]; (X79811) FUR1 [Saccharomyces cerevisiae]	
18794	ENU02588	ANI61C1048	27-46	564-586	NAP	g2132237	287	112	2.00E-24	48	93	hypothetical protein YPL225w - yeast (Saccharomyces cerevisiae); (Z73581) ORF YPL225w [Saccharomyces cerevisiae]	
18795	ENU02589	ANI61C7255:	30-49	565-589	NAP	g4007771	210	100	1.00E-20	29	30	(AL034433) hypothetical protein [Schizosaccharomyces pombe] (X78082) NADH:ubiquinone oxidoreductase (complex I)	
18796	ENU02590	ANI61C8977:	33-54	570-592	NAP	g577597	347	138	3.00E-32	49	79	[Neurospora crassa]	
603..2													

Seq num	Seq id	Contig Source	Primer 3 pos	Primer 610-629	Selection Basis	Database Hit	ncbi gi	aat	Blast Score	Blast Prob	% id	% cvrg	Description
18797	ENU02591	ANI61C7354:	5 pos 69-88	NAP		g586551	490	87	8.00E-17	35	53		hypothetical 33.5 KD protein in MRPSS-YSW1 intergenic region ; probable membrane protein YBR147w - yeast ( <i>Saccharomyces cerevisiae</i> ) ; (Z36016) ORF YBR147w
18798	ENU02592	ANI61C8993:	22-53	564-582	NAP		g1170922	293	101	1.00E-30	39	37	[ <i>Saccharomyces cerevisiae</i> ] Ammonium transporter MEP2 ; ammonium transport protein MEP2 - yeast ( <i>Saccharomyces cerevisiae</i> ) ; (X83608) ammonium transporter [Saccharomyces cerevisiae] ; (Z46843) NH3 permease [ <i>Saccharomyces cerevisiae</i> ] ; (Z71418) ORF YNL142w [ <i>Saccharomyces cerevisiae</i> ] (X60381) ORF2 [ <i>Saccharomyces cerevisiae</i> ] hypothetical 26.9 KD protein in BTN1-PEP8 intergenic region ; hypothetical protein YIL055w - yeast ( <i>Saccharomyces cerevisiae</i> ) ; (Z49330) ORF YIL055w [ <i>Saccharomyces cerevisiae</i> ] hypothetical protein in DFR1 3'region
18799	ENU02593	ANI61C8845:	22-49	563-582	NAP		g388249	198	106	2.00E-22	39	60	[ <i>Saccharomyces cerevisiae</i> ] ; (Z46843) NH3 permease [ <i>Saccharomyces cerevisiae</i> ] ; (Z71418) ORF YNL142w [ <i>Saccharomyces cerevisiae</i> ] (X60381) ORF2 [ <i>Saccharomyces cerevisiae</i> ] hypothetical 26.9 KD protein in BTN1-PEP8 intergenic region ; hypothetical protein YIL055w - yeast ( <i>Saccharomyces cerevisiae</i> ) ; (Z49330) ORF YIL055w [ <i>Saccharomyces cerevisiae</i> ] hypothetical protein in DFR1 3'region
18800	ENU02594	ANI61C3564:	39-58	578-600	NAP		g1352984	365	114	6.00E-25	42	68	[ <i>Saccharomyces cerevisiae</i> ] ; (Z46843) NH3 permease [ <i>Saccharomyces cerevisiae</i> ] ; (Z71418) ORF YNL142w [ <i>Saccharomyces cerevisiae</i> ] (X60381) ORF2 [ <i>Saccharomyces cerevisiae</i> ] hypothetical 26.9 KD protein in BTN1-PEP8 intergenic region ; hypothetical protein YIL055w - yeast ( <i>Saccharomyces cerevisiae</i> ) ; (Z49330) ORF YIL055w [ <i>Saccharomyces cerevisiae</i> ] hypothetical protein in DFR1 3'region
18801	ENU02595	ANI61C3979:	43-62	585-604	NAP		g1352982	52	0.00004				-Arabidopsis thaliana ; (U18675) 4-coumarate-CoA ligase (EC 6.2.1.12) [Arabidopsis thaliana] (AL023589) membrane transporter [ <i>Schizosaccharomyces pombe</i> ] hypothetical zinc metalloproteinase T16A9.4
18802	ENU02596	ANI61C1076:	32-51	574-593	NAP		g1361982	354	167	5.00E-41	44	34	[ <i>Saccharomyces cerevisiae</i> ] ; (Z46843) NH3 permease [ <i>Saccharomyces cerevisiae</i> ] ; (Z71418) ORF YNL142w [ <i>Saccharomyces cerevisiae</i> ] hypothetical 26.9 KD protein in BTN1-PEP8 intergenic region ; hypothetical protein YIL055w - yeast ( <i>Saccharomyces cerevisiae</i> ) ; (Z49330) ORF YIL055w [ <i>Saccharomyces cerevisiae</i> ] hypothetical protein in DFR1 3'region
18803	ENU02597	ANI61C3755:	34-53	577-596	NAP		g3135990	322	97	1.00E-25	45	30	(AL023589) membrane transporter [ <i>Schizosaccharomyces pombe</i> ] hypothetical zinc metalloproteinase T16A9.4
18804	ENU02598	ANI61C5967:	35-55	576-597	NAP		g2499919	494	134	3.00E-31	45	20	coumarate--coenzyme A ligase [ <i>Saccharomyces cerevisiae</i> ] ; (Z46843) NH3 permease [ <i>Saccharomyces cerevisiae</i> ] ; (Z71418) ORF YNL142w [ <i>Saccharomyces cerevisiae</i> ] hypothetical 26.9 KD protein in BTN1-PEP8 intergenic region ; hypothetical protein YIL055w - yeast ( <i>Saccharomyces cerevisiae</i> ) ; (Z49330) ORF YIL055w [ <i>Saccharomyces cerevisiae</i> ] hypothetical protein in DFR1 3'region
18805	ENU02599	ANI61C4286:	23-50	559-587	NAP		g1083278	163	87	1.00E-16	33	27	cytochrome P450 3A13 - mouse ; (X65023) cytochrome P-450IIA [ <i>Mus musculus</i> ] ; cytochrome P450 Cyp3a-13 [ <i>Mus musculus</i> ] ; (Z46843) NH3 permease [ <i>Saccharomyces cerevisiae</i> ] ; (Z71418) ORF YNL142w [ <i>Saccharomyces cerevisiae</i> ] hypothetical 26.9 KD protein in BTN1-PEP8 intergenic region ; hypothetical protein YIL055w - yeast ( <i>Saccharomyces cerevisiae</i> ) ; (Z49330) ORF YIL055w [ <i>Saccharomyces cerevisiae</i> ] hypothetical protein in DFR1 3'region

Seq num	Seq id	Contig Source	Primer 3 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat	Blast Score	Blast Prob	% id	% cvrg	Description
18806	ENU02600	ANI61C197.6	25-46	566-589	NAP	g1911486	466	102	2.00E-21	49	61	"(S80872) putative Tc1-mariner class transposase/[S630-Tc1 homolog [Aspergillus niger; chlorate-resistant mutant 46, transposon Ant1. Peptide Transposon, 325 aa] [Aspergillus niger]"	
18807	ENU02601	ANI61C9009:	45-64	589-609	NAP	g2619026	435	155	3.00E-37	43	46	(AF027868) YoaN [Bacillus subtilis]; (Z99114) similar to hypothetical proteins [Bacillus subtilis]	
18808	ENU02602	ANI61C6045:	34-53	570-598	NAP	g1749484	203	76	1.00E-13	41	47	"(D89138) similar to Saccharomyces cerevisiae ORF YGL208W, EMBL Accession Number Z72730	
18809	ENU02603	ANI61C1111	5:817..210	28-49	570-593	NAP	g2498970	485	157	6.00E-38	40	73	[Schizosaccharomyces pombe] "putative sterigmatocystin biosynthesis protein STCQ ; (U34740) similar to A. parasiticus putative aflatoxin biosynthesis protein [Emericella nidulans]
18810	ENU02604	ANI61C1209:	55-78	600-621	NAP	g2132284	367	91	1.00E-36	39	89	hypothetical protein YPR107c - yeast (Saccharomyces cerevisiae); (U32445) P8283:17 gene product	
18811	ENU02605	ANI61C4438:	68-86	612-634	NAP	g730759	197	49	0.000000	35	74	[Saccharomyces cerevisiae] nuclear protein SNF7 ; SNF7 protein - yeast (Saccharomyces cerevisiae); (Z73197) ORF YLR025w	
18812	ENU02606	ANI61C5883:	1197..1805	564-595	NAP	g731875	437	148	3.00E-35	39	65	[Saccharomyces cerevisiae] "mitochondrial FAD carrier protein FLX1 ; carrier protein FLX1, inner membrane - yeast (Saccharomyces cerevisiae) ; (Z38059) orf, len: 311, CAI: 0.12, similar to peroxisomal membrane protein and mitochondrial carrier protein [Saccharomyces cerevisiae] ; (L41168) inner membrane carrier protein [Saccharomyces cerevisiae]"	
18813	ENU02607	ANI61C7524:	66-86	614-633	NAP	g128337	1671	324	2.00E-88	98	29	G2-specific protein kinase NIMA (never in mitosis) ; probable protein kinase nima (EC 2.7.1.-) - Eméricella nidulans ; (M20249) never in mitosis protein [Emericella nidulans]	

Seq num	Seq id	Contig Source	Primer 3 pos	Primer Basis	Selection	Blast gi	aat	Blast Score	Prob	% id	% cvrg	Description	
18814	ENU02608	ANI61C1107	24..42	NAP	565..591	g2879805	600	131	3.00E-30	37	12	(AL021813) hypothetical protein	
18815	ENU02609	ANI61C8051:	36..55	NAP	585..604	g1706087	910	173	7.00E-43	50	37	[Schizosaccharomyces pombe] cytochrome P450-DIT2 (cytochrome P450 56); cytochrome P450 56 - yeast (Saccharomyces cerevisiae); (U32274) Dlt2p; cytochrome P450; CAI: 0.13 [Saccharomyces cerevisiae]	
18816	ENU02610	ANI61C757:1	22..46	NAP	571..590	541..251	g126597	577	203	8.00E-59	58	87	"N,O-diacyl)muramidase (lysozyme CH); lysozyme (EC 3.2.1.17) - fungus (Chalara sp.)"
18817	ENU02611	ANI61C8231:	61..81	NAP	1762..1152	g130117	813	110	9.00E-24	49	27	phosphate-repressible phosphate permease ; phosphate-repressible phosphate permease - Neurospora crassa ; (M31364) phosphate permease [Neurospora crassa]	
18818	ENU02612	ANI61C3107:	43..62	NAP	769..1380	g730334	405	108	3.00E-23	32	35	putative polyketide biosynthesis protein PKSj ; (U11039) unknown [Bacillus subtilis] ; (Z99112) pksj [Bacillus subtilis] ; (Z99113) pksj [Bacillus subtilis]	
18819	ENU02613	ANI61C7361:	63..82	NAP	452..1063	g3687462	370	100	5.00E-29	45	91	(A1031798) coatomer zeta subunit [Schizosaccharomyces pombe]	
18820	ENU02614	ANI61C9833:	42..61	NAP	2306..2917	g1723488	87	61	0.000000	42	8	hypothetical 104.0 KD protein C32A11.03C in chromosome I ; (Z69796) unknown	
18821	ENU02615	ANI61C8431:	72..92	NAP	242..853	g2914565	413	141	1.00E-36	48	70	[Schizosaccharomyces pombe] "Chain A, Yeast Chorismate Mutase, T226s Mutant, Complex With Trp"	

Seq num	Seq id	Contig Source	Primer 3 pos	Primer 3 pos Basis	Selection	Database Hit	ncbi gi	aat	Blast Score	Blast Prob	% id	% cvrg	Description
18822	ENU02616	ANI61C3868:	22-45	572-593	NAP	g47817	409	176	1.00E-43				protein-S-isoprenylcysteine O-methyltransferase (isoprenylcysteine carboxylmethyltransferase); farnesylcysteine carboxyl-methyltransferase - yeast (Saccharomyces cerevisiae); (L07952) farnesyI cysteine carboxyl-methyltransferase [Saccharomyces cerevisiae]; (L15442) isoprenyl(cysteine carboxyl methyltransferase [Saccharomyces cerevisiae]; (U33007) Ste14p; farnesyI cysteine carboxyl-methyltransferase; YDR410C; CAI: 0.12 [Saccharomyces cerevisiae]
18823	ENU02617	ANI61C3365:	53-72	592-624	NAP	g3116144	110	54	0.000001	27	64		(AL023290) hypothetical protein [Schizosaccharomyces pombe] hypothetical protein ZK757.3 - Caenorhabditis elegans EPD1 protein precursor ; (AB005130) EPD1 [Candida maltosa] (AF110494) mitochondrial precursor protein import receptor tom70 [Neurospora crassa]
18824	ENU02618	ANI61C502:6	49-72	596-621	NAP	g482219	290	113	8.00E-25	38	20		
18825	ENU02619	ANI61C1027	72-93	620-644	NAP	g2494676	1242	123	7.00E-28	38	36		
18826	ENU02620	ANI61C1166:	44-67	597-616	NAP	g4330327	890	205	2.00E-80	79	30		
18827	ENU02621	ANI61C8770:	70-89	623-642	NAP	g1710055	788	148	2.00E-35	44	44		RDS1 protein ; rds1 protein - fission yeast [Schizosaccharomyces pombe]; (X77328) rds1 [Schizosaccharomyces pombe]
18828	ENU02622	ANI61C293:2	30-50	583-602	NAP	g1929333	120	61	0.000000	26	97		(Z93167) ywrF [Bacillus subtilis] (Z99122) ywrF [Bacillus subtilis]
18829	ENU02623	ANI61C5354:	65-83	619-638	NAP	g464725	689	249	2.00E-65	69	91		"40S ribosomal protein S8 (S14) (YS9) (R19) ; ribosomal protein S8, e, cytosolic - yeast (Saccharomyces cerevisiae); (Z26879) ribosomal protein S8 [Saccharomyces cerevisiae]; (Z35833) ORF YBL072c [Saccharomyces cerevisiae]; (U18839) Rps8bp: Ribosome protein, small subunit [Saccharomyces cerevisiae]" (U13050) pectate lyase D [Fusarium solani f. sp. pisii]
18830	ENU02624	ANI61C3563:	58-77	611-631	NAP	g1526987	450	183	7.00E-46	54	77		

Seq num	Seq id	Contig Source	Primer 3 pos	Primer Basis	Selection Database Hit	nebi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18831	ENU02625	ANI61C8909:	30-49	NAP	g2773042	750	105	3.00E-22	41	17	(AF038440) phospholipase D2 [Homo sapiens]	
18832	ENU02626	ANI61C1583:	22-45	NAP	g1723912	78	50	0.00002	33	11	hypothetical 73.5 KD protein in SCS3-SUP44 intergenic region ; hypothetical protein YGL124c - yeast	
			81..697									[Saccharomyces cerevisiae]; (Z77646) ORF YGL124c [Saccharomyces cerevisiae]; (X94106) G2839
18833	ENU02627	ANI61C1141	71-97	626-645	NAP	g83699	1733	264	5.00E-70	98	57	[Saccharomyces cerevisiae] dehydroshikimate dehydratase (EC 4.2.1.-) ; Emericella nidulans ; (M77665) dehydroshikimate dehydratase [Emericella nidulans]
18834	ENU02628	ANI61C915:2	43-62	591-617	NAP	g799150	179	98	7.00E-20	40	14	"(U24701) beta-1,2-D-glucosidase [Septoria lycopersici] ; (U35462) tomatinase [Septoria lycopersici] ; beta2 tomatinase [Septoria lycopersici]"
			2..639									
18835	ENU02629	ANI61C5294:	22-45	576-598	NAP	g730717	400	117	1.00E-31	50	90	"signal sequence processing protein SEC11 ; signal peptidase (EC 3.4.99.-) SEC11 - yeast (Saccharomyces cerevisiae) ; (Z38061) sec11, len: 167, CAI: 0.17 SC11_yeast PI5367 signal sequence processing protein [Saccharomyces cerevisiae]"
18836	ENU02630	ANI61C4039:	60-79	610-636	NAP	g132172	699	154	5.00E-37	38	38	PIM1 protein ; pim1l hypothetical protein - fission yeast (Schizosaccharomyces pombe)
18837	ENU02631	ANI61C3092:	22-53	580-599	NAP	g3219941	318	77	5.00E-25	34	94	hypothetical 24.7 KD protein C3A12.04C in chromosome 1 ; (Z95395) conserved hypothetical protein [Schizosaccharomyces pombe]
18838	ENU02632	ANI61C6403:	52-82	609-629	NAP	g586394	356	134	4.00E-31			hypothetical 98.1 KD TRP-ASP repeats containing protein in PAF1-MRPL27 intergenic region ; hypothetical protein YBR281c - yeast (Saccharomyces cerevisiae) ; (X76053) YBR2018-ORF [Saccharomyces cerevisiae] ; (Z36150) ORF YBR281c [Saccharomyces cerevisiae] ; ORF YBR2018
			97..716									[Saccharomyces cerevisiae]

Seq num	Seq id	Contig Source	Primer 3 pos	Primer Basis	Selection Database Hit	aat	Blast Score	Blast Prob	% id	% cvrg	Description	
18839	ENU02633	ANI61C8982:	52-71	NAP	g3170178	71	5.00E-12				(AF039689) antigen NY-CO-7 [Homo sapiens]	
18840	ENU02634	ANI61C3314:	48-67	NAP	g3004934	801	189	2.00E-47	46	43	(AF036871) annexin XIV [Neurospora crassa]	
18841	ENU02635	ANI61C748:1	38-58	NAP	g2132293	228	75	3.00E-21	38	53	hypothetical protein YPR128c - yeast (Saccharomyces cerevisiae); (U40829)	
			7..638								Similar to mitochondrial ADP/ATP carrier protein (Swiss Prot, accession number P12235) and mitochondrial phosphate carrier protein (Swiss Prot, accession number Q00325)	
18842	ENU02636	ANI61C7556:	41-62	601-620	NAP	g2624417	384	126	1.00E-28	53	88	[Saccharomyces cerevisiae] (AJ002959) Ubiquitin carrier protein [Zea mays]
18843	ENU02637	ANI61C9743:	23-42	581-603	NAP	g2492754	518	127	5.00E-29	44	63	sorbitol utilization protein SOU1; (AF002134) Soulip [Candida albicans] (AB016218) unknown; similar to human GA17 protein
18844	ENU02638	ANI61C8297:	70-89	630-650	NAP	g3327876	189	87	8.00E-17	35	47	[Schizosaccharomyces pombe] (AL031852) u-snmp-associated cyclophilin [Schizosaccharomyces pombe]
18845	ENU02639	ANI61C7885:	22-53	575-602	NAP	g3738142	459	80	1.00E-45	57	99	(U00036) R151.6 gene product [Caenorhabditis elegans]
18846	ENU02640	ANI61C8732:	22-50	573-602	NAP	g459002	392	118	2.00E-32	42	78	2-deoxy-D-gluconate 3-dehydrogenase (2-keto-3-deoxygluconate oxidoreductase); (U29581) ORF_F253 [Escherichia coli]; (AE000368) 2-deoxy-D-gluconate 3-dehydrogenase [Escherichia coli]
18847	ENU02641	ANI61C1042	68-87	630-649	NAP	g1730032	250	52	2.00E-14	35	66	(AL022019) conserved hypothetical protein [Schizosaccharomyces pombe]
			3,907..1529								Acetamidase ; amdS protein - Emericella nidulans ; (M16371) acetamidase enzyme [Emericella nidulans]	
18848	ENU02642	ANI61C5330:	68-87	631-650	NAP	g2924501	390	43	0.001	30	23	
18849	ENU02643	ANI61C172:3	47-71	610-630	NAP	g113701	203	50	4.00E-14	42	27	

Seq num	Seq id	Contig Source	Primer 3 pos	Primer 3 pos Basis	Selection Database Hit	aat ncbi gi	Score	Score Prob	% id	% cvrg	Description	
18850	ENU02644	ANI61C9290:	49-68	NAP	g549626	261	102	2.00E-21	36	92	hypothetical 22.0 KD protein in LAS1-CCP1 intergenic region ; hypothetical protein YKR065c - yeast	
		1992..1366									(Saccharomyces cerevisiae) ; (Z28290) ORF YKR065c [Saccharomyces cerevisiae]	
18851	ENU02645	ANI61C5915:	33-53	598-617	NAP	g586521	369	153	9.00E-37	43	26	hypothetical 86.4 KD protein in PHO5-VPS15 intergenic region ; hypothetical protein YBR094w - yeast
		732..106									(Saccharomyces cerevisiae) ; (X78993) hyp. protein [Saccharomyces cerevisiae] ; (Z35963) ORF YBR094w (AL035216) nucleolar protein involved in pre-RNA processing	
18852	ENU02646	ANI61C1650:	23-42	588-607	NAP	g4160346	1532	218	3.00E-56	65	38	[Saccharomyces cerevisiae] [Schizosaccharomyces pombe] 3-hydroxy-3-methylglutaryl-Coenzyme A reductase (HMG-COA reductase) ; (X94307) HMG-CoA-reductase [Gibberella fujikuroi] quinate permease (quinate transporter); quinate transport protein - Neurospora crassa ; (X14603) quinate transporter [Neurospora crassa]
18853	ENU02647	ANI61C995:8	56-75	621-640	NAP	g2495263	743	248	3.00E-65	56	21	7alpha-hydroxysteroid dehydrogenase [Eubacterium sp. VPI 12708] "hypothetical 42.5 KD protein in TSM1-ARE1 intergenic region ; probable membrane protein YCR044c-yeast (Saccharomyces cerevisiae) ; (X59720) YCR044c, len:357 [Saccharomyces cerevisiae]"
18854	ENU02648	ANI61C3926:	55-74	621-640	NAP	g131761	220	112	3.00E-24	30	38	7alpha-hydroxysteroid dehydrogenase (EC 1.1.1.159) - Eubacterium sp. (strain VPI 12708) ; (M58473) 7-alpha-hydroxysteroid dehydrogenase [Eubacterium sp. VPI 12708]
18855	ENU02649	ANI61C5699:	46-69	611-631	NAP	g98747	248	116	2.00E-25	30	78	"hypothetical 42.5 KD protein in TSM1-ARE1 intergenic region ; probable membrane protein YCR044c-yeast (Saccharomyces cerevisiae) ; (X59720) YCR044c, len:357 [Saccharomyces cerevisiae]"
18856	ENU02650	ANI61C2043:	34-53	600-620	NAP	g140496	284	136	2.00E-31	36	55	(Saccharomyces cerevisiae) ; (Z48179) unknown [Saccharomyces cerevisiae] (AF010138) transcription factor [Mus musculus]
18857	ENU02651	ANI61C7025:	28-50	595-615	NAP	g1077536	260	109	2.00E-23	40	77	
18858	ENU02652	ANI61C2654:	40-59	608-627	NAP	g2281697	434	57	0.000000	28	17	
		467..761			1							

Seq num	Seq id	Contig Source	Primer 3 pos	Primer 3 pos Basis	Selection Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18859	ENU02653	ANI61C6471:	22-55	590-610	NAP	g4538667	391	126	8.00E-29	65	85	(AL049474) clathrin coat assembly protein [Schizosaccharomyces pombe]
18860	ENU02654	ANI61C2906:	22-53	583-610	NAP	g762850	299	76	2.00E-13	40	100	(L41166) p21 protein [Schizosaccharomyces pombe]; (Z99262) p21 protein; cell cycle regulatory protein; interacts with cdc2 in the control of the M-G1 transition
18861	ENU02655	ANI61C7933:	37-56 217..847	606-625	NAP	g1077514	302	114	5.00E-25	46	76	[Schizosaccharomyces pombe] hypothetical protein YDR013w - yeast (Saccharomyces cerevisiae); (Z48008) unknown [Saccharomyces cerevisiae]; (X95966) orf:PZA208 [Saccharomyces cerevisiae]; (Z74309) ORF YDR013w [Saccharomyces cerevisiae]
18862	ENU02656	ANI61C9492:	46-65 4333..4965	616-635	NAP	g1723848	277	89	4.00E-17	46	85	"putative mitochondrial 60S ribosomal protein L7/L12 precursor; probable ribosomal protein L12, mitochondrial - yeast (Saccharomyces cerevisiae); (Z72591) ORF YGL068w [Saccharomyces cerevisiae]"
18863	ENU02657	ANI61C6172:	38-57 17..648	608-627	NAP	g3169083	279	111	6.00E-24	37	61	(AL023705) hypothetical protein [Schizosaccharomyces pombe]
18864	ENU02658	ANI61C6638:	28-52 1269..1900	598-617	NAP	g3915558	169	92	3.00E-18	29	62	hypothetical 36.5 KD protein in GBSA-TLBP intergenic region; (Z99119) similar to hypothetical proteins [Bacillus subtilis]
18865	ENU02659	ANI61C1015	56-77 5.610..1241	625-645	NAP	g2131385	270	87	1.00E-16	40	33	hypothetical protein YDR145w - yeast (Saccharomyces cerevisiae); (Z50046) unknown [Saccharomyces cerevisiae]; (Z95395) putative membrane transport protein [Schizosaccharomyces pombe]
18866	ENU02660	ANI61C1039	44-63 9..994..362	613-634	NAP	g2104422	323	113	1.00E-24	42	26	DNA binding protein - Emericella nidulans; (Z47081) DNA binding protein [Emericella nidulans]
18867	ENU02661	ANI61C7015:	22-42 7160..7005	591-613	NAP	g1078629	1199	309	1.00E-83	97	31	(Z56279) beta-xylo-glucosidase [Thermoanaerobacter brockii]
18868	ENU02662	ANI61C3159:	25-44 747..114	585-616	NAP	g1749831	731	165	2.00E-40	45	26	[Mycobacterium tuberculosis]
18869	ENU02663	ANI50C7416	23-42 _1:82..716	596-615	NAP	g1781180	47	0.0001	32	29		

Seq num	Seq id	Contig Source	Primer 3 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18870	ENU02664	ANI61C3242:	42-61	604-634	NAP	g1173168	299	139	2.00E-32	40	75	hypothetical 31.5 KD protein ; (U05664) homologous to Swiss-Prot Accession Number P20435;	
			178..812										Saccharomyces cerevisiae RNA polymerase subunit RPO26 [Sulfolobus acidocaldarius]
18871	ENU02665	ANI61C4376:	45-66	620-639	NAP	g23347143	660	224	4.00E-58	55	89	(U48234) spU2AF23	
			881..1482										[Schizosaccharomyces pombe]
18872	ENU02666	ANI61C9847:	71-96	646-666	NAP	g117619	704	131	4.00E-30	36	34	choline transport protein ; choline transport protein - yeast (Saccharomyces cerevisiae); (I05603)	
			8262..7625										choline transport protein [Saccharomyces cerevisiae]; (Z72599) ORF YGL077c [Saccharomyces cerevisiae]
18873	ENU02667	ANI61C6047:	22-45	598-617	NAP	g729998	505	174	6.00E-43	45	49	"mRNA capping enzyme (mRNA guanylyltransferase) (GTP--RNA guanylyltransferase); (U16143) GTP:RNA guanylyltransferase [Schizosaccharomyces pombe]; (U18811) GTP--RNA guanylyltransferase [Schizosaccharomyces pombe]; (Z97211) mma capping enzyme, mma guanylyltransferase [Schizosaccharomyces pombe]"	
			138..775										eukaryotic initiation factor 4A (EIF-4A); (X80796) translation initiation factor eIF-4A [Schizosaccharomyces pombe]; (L40627) cell cycle control protein eIF-4A [Schizosaccharomyces pombe] (Z66499) T01B7.8 [Caenorhabditis elegans]
18874	ENU02668	ANI61C1029	60-86	633-655	NAP	g1708418	1571	354	2.00E-97	86	54	hypothetical protein YOL071w - yeast (Saccharomyces cerevisiae); (Z74813) ORF YOL071w [Saccharomyces cerevisiae]	
18875	ENU02669	ANI61C8590:	22-41	593-617	NAP	g3879236	36	0.25					
18876	ENU02670	ANI61C352:9	52-75	623-648	NAP	g2132007	181	79	2.00E-14	40	89		
			224..9862										

Seq num	Seq id	Contig Source	Primer 3 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	Score	Score Prob	% id	% cvrg	Description
18877	ENU02671	ANI61C1805:	40-64	618-637	NAP	g728904	335	95	5.00E-19	41	15	calcium-transporting ATPase 2 (vacuolar CA2+-ATPase); Ca2+-transporting ATPase (EC 3.6.1.38) - yeast [Saccharomyces cerevisiae]; (U03060) calcium ATPase [Saccharomyces cerevisiae]; (Z72528) ORF YGL006w [Saccharomyces cerevisiae]
18878	ENU02672	ANI61C9127:	44-63	622-641	NAP	g2959364	326	146	1.00E-34	39	78	(AL022117) putative o-methyltransferase [Schizosaccharomyces pombe]
18879	ENU02673	ANI61C3023:	40-63	617-637	NAP	g1083278	114	55	4.00E-11	32	35	cytochrome P450 3A13 - mouse; (X63023) cytochrome P-450IIA [Mus musculus]; cytochrome P450 Cyp3a-13 [Mus musculus]
18880	ENU02674	ANI61C3023:	40-63	617-637	NAP	g1083278	114	55	4.00E-11	32	35	cytochrome P450 3A13 - mouse; (X63023) cytochrome P-450IIA [Mus musculus]; cytochrome P450 Cyp3a-13 [Mus musculus]
18881	ENU02675	ANI61C8458:	63-85	641-660	NAP	g3885836	51	5.00E-14				(AF091042) putative cercosporin transporter [Cercospora kikuchii] HAP3 protein - Emericella nidulans; (U35341) HapC[Emericella nidulans]; (U70043) NsdD[Emericella nidulans]; (U70044) DNA binding protein NsdD [Emericella nidulans]
18882	ENU02676	ANI61C8439:	68-103	649-668	NAP	g2133270	576	100	5.00E-53	91	78	(AL022103) histidyl-tRNA synthetase [Schizosaccharomyces pombe] MPV17 protein ; mpv17 protein - mouse ; (M36411) Mpv17 [Mus musculus]
18883	ENU02677	ANI61C9069:	27-46	609-628	NAP	g1617552	2322	229	4.00E-78	97	38	(U70044) DNA binding protein NsdD [Emericella nidulans]
18884	ENU02678	ANI61C2652:	66-87	634-667	NAP	g2956779	556	194	4.00E-49	53	38	(AL022103) histidyl-tRNA synthetase [Schizosaccharomyces pombe] MPV17 protein ; mpv17 protein - mouse ; (M36411) Mpv17 [Mus musculus]
18885	ENU02679	ANI61C2281:	22-41	604-623	NAP	g127297	124	53	0.000001			(AC000133) ORF [Emericella nidulans]
18886	ENU02680	ANI61C1422:	22-52	604-623	NAP	g1870230	1304	436	e-122	99	81	(Z99262) hypothetical protein [Schizosaccharomyces pombe] (AL023064) putative ubiquinone biosynthesis protein [Schizosaccharomyces pombe] (AL021748) hypothetical protein [Schizosaccharomyces pombe]
18887	ENU02681	ANI61C1079	62-83	642-664	NAP	g4033573	239	85	5.00E-23	43	88	
18888	ENU02682	ANI61C843:7	22-52	603-624	NAP	g4106666	421	171	5.00E-42	44	71	
18889	ENU02683	ANI61C66:29	36-56	611-638	NAP	g2842509	416	101	9.00E-41	44	38	
		64..2320										

Seq num	Seq id	Contig Source	Primer 3 pos	Primer Basis	Selection Database Hit	aat ncbi gi	Score 377	Blast Score 164	Prob 4.00E-40	% id 43	% cvrg 89	Description
18890	ENU02684	ANI61C2870:	64-84	NAP	g1723479	377	164	4.00E-40	43	89	C17G8.07 in chromosome I; (Z69795) unknown [Schizosaccharomyces pombe]	
18891	ENU02685	ANI61C7394:	68-87 86..733	NAP	g1723879	252	95	5.00E-19	37	73	hypothetical 32.1 KD protein in MAD1-SCY1 intergenic region ; probable membrane protein YGL085w - yeast (Saccharomyces cerevisiae); (Z72607) ORF YGL085w [Saccharomyces cerevisiae]	
18892	ENU02686	ANI61C7972:	55-75 2692..2045	NAP	g1351612	274	113	7.00E-28	40	61	hypothetical oxidoreductase C23D3.11 in chromosome I ; hypothetical protein SPAC23D3.11 - fission yeast (Schizosaccharomyces pombe)	
18893	ENU02687	ANI61C1056	22-47 9:1845..1198	NAP	g2132491	274	75	1.00E-25	40	61	probable membrane protein YDR284c-yeast (Saccharomyces cerevisiae); (U51031) Ydr284cp [Saccharomyces cerevisiae]	
18894	ENU02688	ANI61C5718:	51-74 705..1354	NAP	g731073	251	48	0.00006			Uracil phosphoribosyltransferase (UMP pyrophosphorylase) (UPRTASE) ; uracil phosphoribosyltransferase - Bacillus subtilis ; (Z38002) uracil phosphoribosyltransferase [Bacillus subtilis] ; (Z99122) uracil phosphoribosyltransferase [Bacillus subtilis] ; uracil phosphoribosyltransferase [Bacillus subtilis] ubiquitin-like protein 9 - Arabidopsis thaliana	
18895	ENU02689	ANI61C3229:	24-52 1057..1705	NAP	g1362010	267	117	3.00E-28	70	30	(AL049559) riboflavin synthase alpha chain [Schizosaccharomyces pombe] (AE000314) putative racemase [Escherichia coli] ; (D90856) similar to [SwissProt Accession Number P31458] [Escherichia coli]	
18896	ENU02690	ANI61C1148	69-88 0:1225..576	NAP	g4581523	425	178	3.00E-44	53	87	(AB010901) ribosomal protein L21 homolog [Schizosaccharomyces pombe]	
18897	ENU02691	ANI61C8540:	71-90 653..1303	NAP	g1788580	657	146	9.00E-35	40	52		
18898	ENU02692	ANI61C7170:	42-62 4254..4905	NAP	g2865171	478	118	3.00E-38	69	90		

Seq num	Seq id	Contig Source	Primer 3 pos	Primer 3 pos	Selection Basis	Database Hit	nebi gi	aat	Blast Score	Blast Prob	% id	% cvrg	Description
18899	ENU02693	ANI50C6324	71..95	661..680	NAP	g465873		63	0.000000	25	33		hypothetical 59.1 KD protein F22B7.6 in chromosome III; f22b7.6 protein - Caenorhabditis elegans ; (L12018)
18900	ENU02694	ANI61C5149:	48..67	63..658	NAP	g3183389	540	153	8.00E-37	39	23		putative [Caenorhabditis elegans] hypothetical 98.3 KD protein C9G1.06C in chromosome I ; (Z98763)
			2171..2823										hypothetical src homology domain containing protein
18901	ENU02695	ANI61C8056:	50..69	641..660	NAP	g3688090	189	59	2.00E-13	43	86		[Schizosaccharomyces pombe] (AC005757) R32611_2 [Homo sapiens]
18902	ENU02696	ANI61C5061:	23..42	603..634	NAP	g3560144	370	145	3.00E-34	41	38		(AL031534) putative asparagine synthase [Schizosaccharomyces pombe]
18903	ENU02697	ANI61C5317:	29..48	619..642	NAP	g1346878	585	141	3.00E-33	39	51		PSI protein ; DNAJ-like protein homolog - fission yeast (Schizosaccharomyces pombe); (L37753) Psi protein
			1951..2606										[Schizosaccharomyces pombe]; Dnal-like protein [Schizosaccharomyces pombe]
18904	ENU02698	ANI61C2530:	45..64	637..658	NAP	g2492825	298	89	3.00E-17	29	52		"N"-carbamyl-L-amino acid amidohydrolase ; N-carbamyl-L-amino acid amidohydrolase (EC 3.5.-.-)-Bacillus stearothermophilus (strain NS1122A) ; (S67784) N'-carbamyl-L-amino acid amidohydrolase [Bacillus stearothermophilus, NS1122A, Peptide, 409 aal] [Bacillus stearothermophilus]" (AL022634) hypothetical protein
18905	ENU02699	ANI61C3258:	38..57	633..652	NAP	g3150262	564	146	1.00E-34	38	61		[Schizosaccharomyces pombe]
18906	ENU02700	ANI61C1430:	65..84	660..679	NAP	g2133013	401	93	1.00E-18	34	51		probable membrane protein YPL264c - yeast (Saccharomyces cerevisiae); (Z73620) ORF YPL264c
18907	ENU02701	ANI61C6665:	45..67	634..660	NAP	g1723253	130	61	0.000000	01			[Saccharomyces cerevisiae] hypothetical 29.3 KD protein C3F10.08C in chromosome I; (Z69369) hypothetical protein [Schizosaccharomyces pombe]

Seq num	Seq id	Contig Source	Primer 3 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat	Blast Score	Blast Prob	% id	% cvrg	Description
18908	ENU02702	ANI61C6366:	25-56	619-640	NAP	g1352984	390	132	1.00E-39	46	81	hypothetical 26.9 KD protein in BTNI-PEP8 intergenic region ; hypothetical protein YJL055w - yeast	
18909	ENU02703	ANI61C718:4	33-55	618-648	NAP	g3150116	754	191	4.00E-48	45	39	(Saccharomyces cerevisiae) ; (Z49330) ORF YJL055w [Saccharomyces cerevisiae]	
18910	ENU02704	ANI61C5178:	40-60	636-655	NAP	g1730641	299	79	3.00E-14	29	30	[Schizosaccharomyces pombe] hypothetical 65.0 KD protein in MET2-SEC2 intergenic region ; probable membrane protein YNL275w - yeast (Saccharomyces cerevisiae) ; (Z71551) ORF YNL275w [Saccharomyces cerevisiae]	
18911	ENU02705	ANI61C6874:	49-69	643-664	NAP	g3043428	670	174	1.00E-66	68	97	(AJ005346) 40S ribosomal protein S5 [Cicer arietinum]	
18912	ENU02706	ANI61C1298:	66-86	663-682	NAP	g2492997	438	98	2.00E-33	62	68	probable succinyl-COA:3-ketoacid-Coenzyme A transferase subunit B (succinyl COA:3-OXOacid COA-transferase) (OXCT B) ; (Z95556) scoB [Mycobacterium tuberculosis] (L35053) homolog of retroviral gag genes; putative [Magnaporthe grisea] (Z50728) putative acetyltransferase [Schizosaccharomyces pombe]	
18913	ENU02707	ANI61C3599:	22-44	620-639	NAP	g522301	535	160	8.00E-39	41	46	"mitochondrial inner membrane protease subunit 2 ; proteinase 2 precursor, mitochondrial inner membrane - yeast (Saccharomyces cerevisiae) ; (Z49213) Imp2p [Saccharomyces cerevisiae]"	
18914	ENU02708	ANI61C1083	72-92	670-689	NAP	g4150918	302	113	1.00E-24	40	81	(AL033391) conserved hypothetical protein [Candida albicans]	
18915	ENU02709	ANI61C8998:	31-51	627-648	NAP	g1170551	183	88	7.00E-17	37	96	phosphate-repressible phosphate permease ; phosphate-repressible phosphate permease - Neurospora crassa ; (M31364) phosphate permease [Neurospora crassa]	
18916	ENU02710	ANI61C6525:	53-72	651-670	NAP	g3850129	585	16	2.00E-40	56	85		
18917	ENU02711	ANI61C7950:	70-89	668-687	NAP	g130117	1210	96	1.00E-54	58	30		
			6601..5942										

Seq num	Seq id	Contig Source	Primer 3 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	Score	Score Prob	% id	% cvrg	Description
18918	ENU02712	ANI61C3150:	59-80	658-677	NAP	g2492777	537	155	7.00E-39	55	52	hypothetical ZINC-type alcohol dehydrogenase-like protein in pref-FET4 intergenic-region ; hypothetical protein YMR318c - yeast
18919	ENU02713	ANI61C1022	33-53	629-651	NAP	g3298472	38	0.088				(Saccharomyces cerevisiae) ; (Z54141) unknown [Saccharomyces cerevisiae] (AB012725) zinc finger protein [Mus musculus]
18920	ENU02714	ANI61C8624:	23-50	619-642	NAP	g731611	247	110	1.00E-23	35	89	hypothetical 25.4 KD protein in GUT1-RIM1 intergenic region ; hypothetical protein YHL031c - yeast
18921	ENU02715	ANI61C8624:	23-50	619-642	NAP	g731611	247	110	1.00E-23	35	89	[Saccharomyces cerevisiae] hypothetical 25.4 KD protein in GUT1-RIM1 intergenic region ; hypothetical protein YHL031c - yeast
18922	ENU02716	ANI61C8082:	57-76	659-678	NAP	g2144564	606	151	9.00E-61	61	61	[Saccharomyces cerevisiae] phosphoribosylaminoimidazolesuccinocarboxamide synthase (EC 6.3.2.6) - yeast (Saccharomyces cerevisiae) ; (M67445) phosphoribosyl-amino-imidazolesuccinocarboxamide synthetase [Saccharomyces cerevisiae] ; (L22015) Ade1p: phosphoribosyl amino imidazolesuccinocarboxamide synthetase [Saccharomyces cerevisiae] ORM1 protein ; probable membrane protein YGR038w - yeast
18923	ENU02717	ANI61C9181:	28-47	622-649	NAP	g1723661	472	169	1.00E-49	59	76	(Saccharomyces cerevisiae) ; (Z72823) ORF YGR038w [Saccharomyces cerevisiae]

Seq num	Seq id	Contig Source	Primer 3 pos	Primer 3 pos	Selection Basis	Database Hit	nebi gi	aat	Blast Score	Blast Score	% id	% cvrg	Description
			5 pos	NAP	gi30880	799	167	6.00E-41					"Proteasome component Y7 (macropain subunit 7) (proteinase YSCE subunit 7) (multicatalytic endopeptidase complex subunit Y7); multicatalytic endopeptidase complex (EC 3.4.99.46) chain Y7 - yeast (Saccharomyces cerevisiae); Chain B, Crystal Structure Of The 20S Proteasome From Yeast At 2.4 Angstroms Resolution ; Chain P, Crystal Structure Of The 20S Proteasome From Yeast At 2.4 Angstroms Resolution ; (X56731) proteasome Y7 subunit [Saccharomyces cerevisiae]; (Z46660) proteasome component Y gene, len: 250, CAI:0.15, PRCX_yeast P23639 [Saccharomyces cerevisiae]"
18925	ENU02719	ANI50C3665	47-66	649-669	NAP	g2995341	121	5.00E-27	41	39			[AL022244] hypothetical protein [Schizosaccharomyces pombe]
18926	ENU02720	$\bar{0}$ ..1:1418..754 ANI61C3667:	33-56	632-656	NAP	g120593	319	74	8.00E-13				L-fucose permease ; fucose permease - Escherichia coli ; (X50225) fucP ORF (AA 1-438) [Escherichia coli]; (U29581) L-fucose permease [Escherichia coli] ; (AE000364) fucose permease [Escherichia coli] (Z98601) mitochondrial 40s ribosomal protein mfp4. [Schizosaccharomyces pombe]
18927	ENU02721	ANI61C1677:	22-49	626-645	NAP	g4038620	521	186	1.00E-46	51	83		Elongation factor 2 (EF-2) ; (D83975) elongation factor 2 (EF-2) ; (D83976) elongation factor 2 [Schizosaccharomyces pombe] ; [Schizosaccharomyces pombe] (D83976) elongation factor 2 [Schizosaccharomyces pombe] (AC000133) ORF [Emericella nidulans]
18929	ENU02723	ANI61C5502:	27-47	617-652	NAP	g1870209	961	265	e-104	86	40		(AL035065) protein translation factor sui1. [Schizosaccharomyces pombe]
18930	ENU02724	520..1187 ANI61C6250:	54-74	655-679	NAP	g4106682	245	59	7.00E-11	59	82		

Seq num	Seq id	Contig Source	Primer 3 pos	Primer Basis	Selection Database Hit	aat	Blast Score	Blast Prob	% id	% cvrg	Description	
18931	ENU02725	ANI61C9933:	61-80	NAP	g1175363	S35	198	3.00E-50	44	70	hypothetical protein HI1014;	
			144..812								Haemophilus influenzae (strain Rd KW20); (U32782) conserved hypothetical protein [Haemophilus influenzae Rd]	
18932	ENU02726	ANI61C8405:	22-43	623-649	NAP	g3925782	333	146	1.00E-34	48	91	(AL034353) putative 60s ribosomal protein [Schizosaccharomyces pombe] (AF120278) proline dehydrogenase; PRODH [Homo sapiens]
18933	ENU02727	ANI61C205:1	45-66	633-672	NAP	g4581877	144	92	3.00E-18	30	40	(U82513) random slug cDNA25 protein [Dictyostelium discoideum] (U00063) weakly similar to R. rickettsii protein P34 [Caenorhabditis elegans]
18934	ENU02728	ANI61C3750:	33-54	640-660	NAP	g2367392	873	118	4.00E-26	34	30	(D63703) isobutene-forming enzyme and benzoate 4-hydroxylase [Rhodotorula minuta]
18935	ENU02729	ANI61C1118	32-52	641-660	NAP	g488189	367	87	7.00E-22	29	51	RAS-like GTP-binding protein RYL2; (Z97204) hypothetical protein (L06970) ras-like protein [Yarrowia lipolytica]
18936	ENU02730	ANI61C4356:	23-42	632-651	NAP	g1020413	319	145	4.00E-34	34	41	[Schizosaccharomyces pombe] Cutinase precursor (L1); (D38311) Cutinase [Aspergillus oryzae] "NADH-ubiquinone oxidoreductase 21 KD subunit (complex I-21KD) (CI-21KD); NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) 20.9K chain -Neurospora crassa ; (X60829) NADH dehydrogenase, 21kDa subunit [Neurospora crassa]"
18937	ENU02731	ANI61C8178:	66-85	676-695	NAP	g1173334	401	157	9.00E-38	52	82	Cutinase [Aspergillus oryzae] Cutinase precursor (L1); (D38311) Cutinase [Aspergillus oryzae] "NADH-ubiquinone oxidoreductase 21 KD subunit (complex I-21KD) (CI-21KD); NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) 20.9K chain -Neurospora crassa ; (X60829) NADH dehydrogenase, 21kDa subunit [Neurospora crassa]"
18938	ENU02732	ANI61C9465:	22-52	631-651	NAP	g2226413	148	41	0.00002	43	65	YHR148W ; hypothetical protein YHR148w - yeast (Saccharomyces cerevisiae) ; (X69480) uORF1
18939	ENU02733	ANI61C1088	57-77	667-687	NAP	g1706202	656	152	1.00E-61	70	87	[Saccharomyces cerevisiae] ; (U10397) Yhr148wp [Saccharomyces cerevisiae] (AE00955) 2-nitropropane dioxygenase (ncd2) [Archaeoglobus fulgidus]
18940	ENU02734	ANI61C9472:	44-64	646-674	NAP	g464287	410	145	2.00E-34	56	82	
18941	ENU02735	ANI61C4807:	25-47	631-655	NAP	g418596	431	91	3.00E-19	56	93	
	3495..2823											
18942	ENU02736	ANI61C1125	22-53	632-652	NAP	g2648355	318	73	3.00E-17	34	72	
	73..3245											

Seq num	Seq id	Contig Source	Primer 3 pos	Primer Basis	Selection Database Hit	aat	Blast Score	Blast Prob	% id	% cvrg	Description	
18943	ENU02737	ANI61C5118:	71-91	NAP	g2492756	213	47	0.0001			putative sterigmatocystin biosynthesis ketoreductase STCE ; (U34740)	
			756..83								putative ketoreductase [Entericella nidulans]	
18944	ENU02738	ANI61C1354:	23-53	635-654	NAP	g729965	467	124	9.00E-39	66	44	"saccharopine dehydrogenase [NAD+, L-lysine forming] (lysine-2-oxoglutarate reductase) (SDH); saccharopine dehydrogenase (NAD+, L-lysine-forming) - yeast (Yarrowia lipolytica) (strain W29); (M34929) saccharopine dehydrogenase [Yarrowia lipolytica]" (Z97628) Similarity to Brugia peptidylprolyl isomerase (TR.G984562) [Caenorhabditis elegans]; (Z81080) Similarity to Brugia peptidylprolyl isomerase (TR.G984562) [Caenorhabditis elegans]
			82..755									
18945	ENU02739	ANI61C3530:	26-45	638-657	NAP	g3420982	502	112	2.00E-24	57	52	(AL034382) putative ras-related GTP-binding protein [Schizosaccharomyces pombe]
			5..678									
18946	ENU02740	ANI61C5321:	57-76	663-689	NAP	g3947880	533	120	4.00E-49	62	98	hypothetical protein YDR071c - yeast (Saccharomyces cerevisiae); (Z46796) unknown [Saccharomyces cerevisiae]; (Z74367) ORF YDR071c [Saccharomyces cerevisiae]
			303..977									
18947	ENU02741	ANI61C566:1	22-40	629-654	NAP	g1077519	163	85	4.00E-16	36	98	hypothetical protein YLR193c - yeast (Saccharomyces cerevisiae); (U14913) Ylr193cp [Saccharomyces cerevisiae] (Z69637) predicted using GeneFinder; Similarity to E.coli hypothetical protein YCAC (SW:YCAC_ECOLI)
			660..986									
18948	ENU02742	ANI61C7088:	22-57	636-655	NAP	g626443	140	68	5.00E-11	32	96	[Caenorhabditis elegans]
			2908..3583									
18949	ENU02743	ANI61C1134	54-73	668-687	NAP	g3876766	272	104	2.00E-23	45	86	(A1004810) cytochrome P450 monooxygenase [Zea mays] (AL034463) hypothetical protein [Schizosaccharomyces pombe] (K01609) gal1 [Saccharomyces carlsbergensis]
			4..2479..1804									
18950	ENU02744	ANI61C1253:	25-44	637-659	NAP	g2995384	706	242	2.00E-71	83	82	(A1004810) cytochrome P450 monooxygenase [Zea mays]
			7105..6501									
18951	ENU02745	ANI61C7538:	22-56	638-657	NAP	g4007800	323	61	3.00E-15	43	92	(AL034463) hypothetical protein [Schizosaccharomyces pombe] (K01609) gal1 [Saccharomyces carlsbergensis]
			242..920									
18952	ENU02746	ANI61C9073:	30-49	634-665	NAP	g171567	338	131	7.00E-34	35	42	
			3923..3246									

Seq num	Seq id	Contig Source	Primer 3 pos	Primer 3 pos	Selection Basis	Database Hit	aat	Blast Score	Blast Prob	% id	% cvrg	Description
18953	ENU02747	ANI61C7240:	70-92	686-705	NAP	g3006178	279	89	3.00E-17	32	32	(AL022304) putative mmra transport regulator [Schizosaccharomyces pombe]
18954	ENU02748	ANI61C3687:	61-80	670-697	NAP	g3169083	261	108	4.00E-23	36	66	(AL023705) hypothetical protein [Schizosaccharomyces pombe]
18955	ENU02749	ANI61C1049	31-51	648-667	NAP	g3041738	1512	81	2.00E-51	61	35	"T-complex protein 1,ETA subunit (TCP-1-ETA) (CCT-ETA) (HIV-1 NEF interacting protein); (AF026292) chaperonin containing t-complex polypeptide 1, eta subunit; CCT-eta [Homo sapiens]" transposase Tam3 - garden snapdragon transposon Tam3; (X55078) Tam3-transposase [Antirrhinum majus]; (AB013982) transposase [Antirrhinum majus]; (AB013983) transposase [Antirrhinum majus]; (AB013984) transposase [Antirrhinum majus]; (AB013986) transposase [Antirrhinum majus]; (AB013990) transposase [Antirrhinum majus]; (AB013991) transposase [Antirrhinum majus]; (AB013995) transposase [Antirrhinum majus]; (AB013997) transposase [Antirrhinum majus] (AL031740) putative rRNA biogenesis protein; rrp5 homolog; multiple S1 rna binding domain protein
18956	ENU02750	ANI61C5629:	40-59	643-676	NAP	g100489	133	72	3.00E-12			[Schizosaccharomyces pombe] "T-complex protein 1,ETA subunit (TCP-1-ETA) (CCT-ETA) (HIV-1 NEF interacting protein); (AF026292) chaperonin containing t-complex polypeptide 1, eta subunit; CCT-eta [Homo sapiens]" transposase Tam3 - garden snapdragon transposon Tam3; (X55078) Tam3-transposase [Antirrhinum majus]; (AB013982) transposase [Antirrhinum majus]; (AB013983) transposase [Antirrhinum majus]; (AB013984) transposase [Antirrhinum majus]; (AB013986) transposase [Antirrhinum majus]; (AB013990) transposase [Antirrhinum majus]; (AB013991) transposase [Antirrhinum majus]; (AB013995) transposase [Antirrhinum majus]; (AB013997) transposase [Antirrhinum majus] (AL031740) putative rRNA biogenesis protein; rrp5 homolog; multiple S1 rna binding domain protein [Schizosaccharomyces pombe] (Z99262) putative endosomal Vps protein complex subunit [Schizosaccharomyces pombe] possible apospory-associated protein C ; (U13148) possible apospory-associated protein [Pennisetum ciliare] (AJ13173) ubiquitin-conjugating enzyme E2 [Pseudotsuga menziesii]
18957	ENU02751	ANI61C7852:	57-88	664-693	NAP	g3650378	1057	154	5.00E-37	51	10	
18958	ENU02752	ANI61C5415:	49-70	668-687	NAP	g2414668	256	86	3.00E-16	39	85	[Schizosaccharomyces pombe] (Z99262) putative endosomal Vps protein complex subunit [Schizosaccharomyces pombe] possible apospory-associated protein C ; (U13148) possible apospory-associated protein [Pennisetum ciliare] (AJ13173) ubiquitin-conjugating enzyme E2 [Pseudotsuga menziesii]
18959	ENU02753	ANI61C7921:	69-88	678-708	NAP	g2501555	296	100	3.00E-24	38	62	
18960	ENU02754	ANI61C7147:	33-53	639-673	NAP	g4090259	218	83	2.00E-15	37	85	
			5245..5927									

Seq num	Seq id	Contig Source	Primer 3 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat	Blast Score	Blast Prob	% id	% cvrg	Description
18961	ENU02755	ANI61C7273:	22-47	642-662	NAP	g1723256	227	84	2.00E-19	34	93	"hypothetical 23.0 KD protein C3F10.12C in chromosome I; (Z69369) SPA.C3F10.12c, unknown, 201, similar to transcription factors and SW:CBFL_yeast P17106 centromere-binding protein 1 (39.8% identity in 113 aa) overlap), contains PS00038 Myc-type, 'helix-loop-helix' dimerization dom..."	
18962	ENU02756	ANI61C7786:	25-47	647-666	NAP	g1363314	213	53	2.00E-11	36	19	probable cell division control protein p55CDC - rat ; (U05341) p55CDC [Rattus norvegicus]	
18963	ENU02757	ANI61C1129	54-75	674-695	NAP	g549750	253	67	1.00E-10	39	71	hypothetical 29.4 KD protein in STE6-LOS1 intergenic region ; hypothetical protein YKL207w - yeast (Saccharomyces cerevisiae) ; (Z28207) ORF YKL207w [Saccharomyces cerevisiae]	
18964	ENU02758	ANI61C566:5	22-50	645-664	NAP	g1679882	1002	279	2.00E-74	61	31	(L35484) acetylglutamate synthase [Neurospora crassa]	
18965	ENU02759	ANI61C6119:	23-44	647-666	NAP	g3123033	365	90	3.00E-31	37	86	vacuolar protein sorting-associated protein VPS28 ; hypothetical protein YPL065w - yeast (Saccharomyces cerevisiae) ; (U39205) Lpe5p [Saccharomyces cerevisiae] ; (U50630) Vps28p [Saccharomyces cerevisiae]	
18966	ENU02760	ANI61C8915:	46-79	664-690	NAP	g1633466	111	56	0.000000	27	79	"Crystal Structure Of Bacteriorhodopsin In Purple Membrane ; Structure Of Bacteriorhodopsin At 3.0 Angstrom Determined By Electron Crystallography ; Chain A, X-Ray Structure Of The Bacteriorhodopsin Trimerlipid Complex ; Bacteriorhodopsinlipid complex " (AL031743) phosphatidylethanolamine methyltransferase.	
18967	ENU02761	ANI61C6486:	22-51	638-666	NAP	g3650386	1486	102	3.00E-21	38	20	[Schizosaccharomyces pombe] putative oxidoreductase precursor BLI-4 ; (X89499) bli-4 protein [Neurospora crassa]	
18968	ENU02762	ANI61C6019:	35-59	662-682	NAP	g3023397	320	160	8.00E-39	41	54		

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database	Hit gi	aat	Blast Score	Blast Prob	% id	% cvrg	Description
18969	ENU02763	ANI61C1042	32..51	660..679	NAP	ncbi	gi 7130832	258	111	6.00E-24	37	61	hypothetical 31.6 KD protein in SIN4-URE2 intergenic region ; hypothetical protein YNL232w - yeast
18971	ENU02765	ANI61C8095:	72..92	702..721	NAP	g731042	398	118	1.00E-32				(Saccharomyces cerevisiae) ; (Z69381) N1154 [Saccharomyces cerevisiae] ; (Z71508) ORF YNL232w [Saccharomyces cerevisiae] (AB010439) steroid monooxygenase [Rhodococcus rhodochrous]
18970	ENU02764	ANI61C191:1	22..52	647..670	NAP	g2804298	89	68	5.00E-11	26	40		ubiquitin carboxyl-terminal hydrolase 5 (ubiquitin thioesterase 5) (ubiquitin-specific processing protease 5) (DEubiquitinating enzyme 5) ; ubiquitin-specific proteinase UBP5 (EC 3.4.-.-) - yeast (Saccharomyces cerevisiae) ; (U10082) ubiquitin-specific protease [Saccharomyces cerevisiae] ; (U18917) Ubp5p: ubiquitin-specific protease [Saccharomyces cerevisiae] (AE000848) ribonuclease PH [Methanobacterium thermoautotrophicum] (Z99165) dehydrogenase [Schizosaccharomyces pombe] (Z99118) similar to opine catabolism [Bacillus subtilis] "Phenylalanyl-tRNA synthetase beta chain cytoplasmic (phenylalanine-tRNA ligase beta chain) ; phenylalanine-ttRNA ligase (EC 6.1.1.20) beta chain, cytosolic - yeast (Saccharomyces cerevisiae) ; (D50617) cytoplasmic phenylalanyl-tRNA synthetase beta chain [Saccharomyces cerevisiae]"
18972	ENU02766	ANI61C6486:	55..74	675..704	NAP	g2621768	73	40	0.0003	31	72		

Seq num	Seq id	Contig Source	Primer 3 pos	Primer Basis	Selection Database Hit	aat ncbi gi	Blast Score	Blast Prob	% id	% cvrg	Description
18976	ENU02770	ANI61C4361:	67-86	NAP	g586321	47	0.00002				hypothetical 25.3 KD protein in RIM2-MSI1 intergenic region ; hypothetical protein YBR193c - yeast
18977	ENU02771	ANI61C3960:	23-58	646-675	NAP	g130882	593	259	2.00E-68		(Saccharomyces cerevisiae) ; (Z21487) unknown product [Saccharomyces cerevisiae] ; (Z36062) ORF YBR193c [Saccharomyces cerevisiae]
			920..226								Potential proteasome component C5 (multicatalytic endopeptidase complex subunit C5); multicatalytic endopeptidase complex (EC 3.4.99.46) chain PRS3 - yeast (Saccharomyces cerevisiae) ; (M34777) proteasome subunit [Saccharomyces cerevisiae]; (D00845) proteasome subunit [Saccharomyces cerevisiae] ; (X78214) PRS3 [Saccharomyces cerevisiae]; (Z35802) ORF YBL041w [Saccharomyces cerevisiae] (Y15013) copalyl diphosphate synthase [Gibberella fujikuroi] (AB024617) isotrichodermin C-15 hydroxylase [Gibberella zeae] (Z8110) predicted using Genefinder; cDNA EST EMBL:D76086 comes from this gene; cDNA EST EMBL:T00045 comes from this gene; cDNA EST EMBL:T00046 comes from this gene; cDNA EST EMBL:D73101 comes from this gene; cDNA EST EMBL:C077... (AF063095) SEL1L [Mus musculus]
18978	ENU02772	ANI61C7782:	60-79	690-712	NAP	g3549899	1287	146	1.00E-34	32	23 [Gibberella fujikuroi]
18979	ENU02773	ANI61C548:7	69-88	698-721	NAP	g4589927	232	52	3.00E-13	32	39 [Ajellomyces capsulatus]
18980	ENU02774	ANI61C5279:	28-47	662-681	NAP	g3879255	261	117	7.00E-26	34	56 "hypothetical 21.1 KD protein in FUS1-AGP1 intergenic region ; hypothetical protein YCL026c-a - yeast (Saccharomyces cerevisiae) ; (X59720) YCL026c-a, len:192 [Saccharomyces cerevisiae]"
18981	ENU02775	ANI61C6626:	69-88	704-723	NAP	g4159995	577	93	2.00E-18		
18982	ENU02776	ANI61C4759:	46-65	680-700	NAP	g3135013	808	323	1.00E-87	66	25 (AJ005963) 100 kDa protein
18983	ENU02777	ANI61C322:5	52-71	688-707	NAP	g586554	160	56	0.000000	32	92 "hypothetical 21.1 KD protein in FUS1-AGP1 intergenic region ; hypothetical protein YCL026c-a - yeast (Saccharomyces cerevisiae) ; (X59720) YCL026c-a, len:192 [Saccharomyces cerevisiae]"

Seq num	Seq id	Contig Source	Primer 3 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat	Blast Score	Blast Score	% id	% cvrg	Description
18984	ENU02778	ANI61C8274:	72-93	708-727	NAP	g1171666	303	70	3.00E-16	51	87	NADH-ubiquinone oxidoreductase (CI-14.8KD); NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) - Neurospora crassa; (X76344) NADH dehydrogenase (ubiquinone)	
18985	ENU02779	ANI61C7893:	43-62	679-701	NAP	g1708501	245	73	8.00E-22	36	11	[Neurospora crassa] Integrin alpha chain-like protein (alpha-INT1); (U35070) integrin-like	
18986	ENU02780	ANI61C301:5	24-43	650-684	NAP	g1064798	256	83	6.00E-20	40	47	protein alpha Int1p [Candida albicans] (D78193) homologous to gp:PSEFD_1 (formaldehyde dehydrogenase) [Bacillus subtilis]; (Z99124) similar to formaldehyde dehydrogenase [Bacillus subtilis]	
18987	ENU02781	ANI61C1078	57-82	697-717	NAP	g3152652	365	155	4.00E-37	38	49	"(AF064870) endo-1,3(4)-beta-glucanase [Xanthophyllumycetes dendrophous]" hypothetical 27.6 KD protein in RPL26B-ACB1 intergenic region; probable membrane protein YGR036c-yeast (Saccharomyces cerevisiae); (Z72821) ORF YGR036c [Saccharomyces cerevisiae]	
18988	ENU02782	ANI61C3321:	57-77	698-717	NAP	g1723660	211	76	6.00E-20	33	89	(D78193) homologous to gp:PSEFD_1 (formaldehyde dehydrogenase) [Bacillus subtilis]; (Z99124) similar to formaldehyde dehydrogenase [Bacillus subtilis] (AL031825) putative membrane transport protein	
18989	ENU02783	ANI61C301:5	24-43	650-684	NAP	g1064798	256	83	6.00E-20	40	47	[Schizosaccharomyces pombe] probable membrane protein YOR206w - yeast (Saccharomyces cerevisiae); (Z75114) ORF YOR206w [Saccharomyces cerevisiae] [Schizosaccharomyces pombe] [Schizosaccharomyces pombe] (AL022304) 60s ribosomal protein 17- c. [Schizosaccharomyces pombe]	
18990	ENU02784	ANI61C3956:	42-74	677-703	NAP	g3702646	401	66	3.00E-10				
18991	ENU02785	ANI61C6073:	23-42	659-684	NAP	g2132916	448	136	2.00E-31	43	32		
18992	ENU02786	ANI61C2284:	70-90	707-731	NAP	g3766371	328	152	2.00E-36	40	90		
18993	ENU02787	ANI61C7986:	63-82	705-724	NAP	g3006189	646	81	4.00E-32	63	62		

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18994	ENU02788	ANI61C7899:	40-59	680-702	NAP	g417305	788	113	2.00E-30	42	35	"mannosyl-oligosaccharide alpha-1,2-mannosidase (MAN9)-alpha-mannosidase) ; alpha-mannosidase MNS1 (EC 3.2.1.-) - yeast (Saccharomyces cerevisiae) ; (M63598)	
18995	ENU02789	ANI61C6615:	72-96	715-734	NAP	g1363710	345	90	2.00E-17	27	54	[Saccharomyces cerevisiae] ; (Z49631) ORF YJR131w [Saccharomyces cerevisiae]" probable membrane protein YLR130c - yeast (Saccharomyces cerevisiae); (X91258) L3.120 [Saccharomyces cerevisiae]; (U53881) Ylr130cp [Saccharomyces cerevisiae]; (Z73302) ORF YLR130c [Saccharomyces cerevisiae]	
18996	ENU02790	ANI61C8963:	62-81	706-725	NAP	g1507666	100	38	0.073	(D84656) ORF N118 [Schizosaccharomyces pombe]			
18997	ENU02791	ANI61C7925:	3632..4337	59-82	699-723	NAP	g1703215	374	77	2.00E-16	31	37	alpha-glucosidase permease; alpha-glucoside transport protein - yeast (Saccharomyces cerevisiae); yeast (Saccharomyces cerevisiae); (Z73074) ORF YGR289c [Saccharomyces cerevisiae]
18998	ENU02792	ANI61C1046	1:848..1554	24-46	662-688	NAP	g4028590	625	144	3.00E-54	89	99	[AF104986] calmodulin [Magnaporthe grisea]
18999	ENU02793	ANI61C1518:	2666..1960	34-63	668-698	NAP	g117619	80	2.00E-17	choline transport protein - yeast (Saccharomyces cerevisiae); (J05603) choline transport protein [Saccharomyces cerevisiae]; (Z72599) ORF YGL077c [Saccharomyces cerevisiae]			
19000	ENU02794	ANI61C7112:	2765..3471	66-85	710-730	NAP	g1175951	328	114	1.00E-25	40	91	hypothetical 24.0 KD protein in EMP47-SEC53 intergenic region ; probable membrane protein YFL046w - yeast (Saccharomyces cerevisiae); (D50617) YFL046W [Saccharomyces cerevisiae]
19001	ENU02795	ANI61C9541:	60..767	61-92	700-726	NAP	g4160573	199	86	3.00E-16	33	24	(AL035226) guanine nucleotide binding protein beta subunit-like [Schizosaccharomyces pombe]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat	Blast Score	Blast Prob	% id	% cvrg	Description
19002	ENU02796	ANI61C7325:	2443	670-689	NAP	g3417433	411	117	9.00E-26	46	57	(AL031262) putative transcription factor [Schizosaccharomyces pombe]	
19003	ENU02797	ANI61C3136:	3090..2383	1862..1155	22-52	668-687	NAP	g3914054	783	256	1.00E-67	53	MUTS protein homolog 1 ; (Z98559) dna mismatch repair muts family
19004	ENU02798	ANI61C7529:	1958..1251	22-53	663-687	NAP	g4160343	482	102	8.00E-28	37	69	[Schizosaccharomyces pombe] (AL035216) similar to rat synaptic glycoprotein sc2
19005	ENU02799	ANI61C7521:	949..241	40-59	687-706	NAP	g117093	285	69	4.00E-13	50	86	[Schizosaccharomyces pombe] cytochrome C oxidase polypeptide VI precursor ; cytochrome-c oxidase (EC 1.9.3.1) chain VI precursor - yeast (Saccharomyces cerevisiae) ; (M10138) cytochrome c oxidase subunit VI [Saccharomyces cerevisiae] ; (U00062) Cox6p; cytochrome c oxidase subunit VI [Saccharomyces cerevisiae]
19006	ENU02800	ANI61C1008	8:14...556	34-53	680-700	NAP	g1764155	252	134	5.00E-31	42	39	(U16782) chlorophenol monooxygenase [Ralstonia eutropha] (U33115) high copy suppressor of polymerase alpha mutations
19007	ENU02801	ANI61C4037:	898..187	67-87	701-736	NAP	g992654	72	46	9.00E-10	45	8	[Saccharomyces cerevisiae] [Saccharomyces cerevisiae] lysozyme M1 precursor ([1,4-beta-N-acetylglucosaminidase M1]) ; lysozyme (EC 3.2.1.17) M1 precursor - Streptomyces globisporus ; (M30645) N-acetylglucosaminidase M1 precursor [Streptomyces globisporus] "
19008	ENU02802	ANI61C8195:	1171..1882	22-39	668-691	NAP	g126652	315	144	9.00E-35	38	71	(U85498) glutamate-cysteine ligase catalytic subunit [Mus musculus] hypothetical protein YOR252w - yeast (Saccharomyces cerevisiae) ; (Z75160) ORF YOR252w [Saccharomyces cerevisiae]
19009	ENU02803	ANI61C2626:	82..793	23-45	670-692	NAP	g1945070	727	223	9.00E-58	51	34	mitochondrial carrier protein PMT ; mitochondrial uncoupling protein homolog YKL120w - yeast (Saccharomyces cerevisiae) ; (L04948)
19010	ENU02804	ANI61C3329:	2735..2631	71-91	714-741	NAP	g2132100	75	4.00E-13	30	87	mitochondrial transporter protein [Saccharomyces cerevisiae] ; (Z28120) ORF YKL120w [Saccharomyces cerevisiae]	
19011	ENU02805	ANI61C8183:	108..820	34-53	684-704	NAP	g417500	568	127	6.00E-44	55	62	mitochondrial uncoupling protein homolog YKL120w - yeast (Saccharomyces cerevisiae) ; (L04948)

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Primer NAP	Database Hit	ncbi gi	aat	Blast Score	Blast Prob	% id	% cvrg	Description
19012	ENU02806	ANI61C1120	55-78	704-725	NAP		g2833337	103	73	2.00E-12	30	36	Dihydrofolate reductase / thymidylate synthase (DHFR-TS); (U20781)	
19013	ENU02807	ANI61C2275:	65-86	716-735	NAP		g4140255	2000	401	e-111	83	48	dihydrofolate reductase-thymidylate synthase [Trypanosoma brucei] (AJ009973) hexokinase [Aspergillus niger]	
19014	ENU02808	ANI61C559:8	22-49	664-693	NAP		g117619	37	0.17				choline transport protein ; choline transport protein - yeast (Saccharomyces cerevisiae); (I05603)	
19015	ENU02809	ANI61C7117:	27-46	676-698	NAP		g4249578	892	355	2.00E-97	75	97	choline transport protein [Saccharomyces cerevisiae]; (Z72599) ORF YGL077c [Saccharomyces cerevisiae]	
			1667..955										(AF022892) orotidine monophosphate pyrophosphorylase [Coccidioides immitis]	
19016	ENU02810	ANI61C414:1	26-51	675-698	NAP		g913016	332	124	3.00E-32	37	14	"(S76267) Sqn2 homolog=bfr1 [Schizosaccharomyces pombe=fission yeast, Peptide, 1530 aa]	
19017	ENU02811	ANI61C1124:	22-45	667-694	NAP		g1118129	524	88	4.00E-27	41	25	[Schizosaccharomyces pombe] " (U41625) coded for by C. elegans cDNA yk52e10.5; coded for by C. elegans cDNA yk52e10.3; coded for by C. elegans cDNA yk50f4.3; coded for by C. elegans cDNA yk50f4.5; Similar to acetyl-coenzyme A synthetase. [Caenorhabditis elegans] (AF036871) annexin XIV [Neurospora crassa]	
19018	ENU02812	ANI61C2113:	71-90	725-744	NAP		g3004934	490	144	6.00E-34	35	49	[Caenorhabditis elegans] (AF036871) annexin XIV [Neurospora crassa]	
19019	ENU02813	ANI61C8918:	54-74	697-727	NAP		g2132018	288	96	2.00E-25	36	94	hypothetical protein YOL135c - yeast (Saccharomyces cerevisiae); (Z74877)	
19020	ENU02814	ANI61C8241:	30-49	673-704	NAP		g2133287	421	189	2.00E-47	43	85	ORF YOL135c [Saccharomyces cerevisiae]; (X95465) ORF [Saccharomyces cerevisiae]	
			1541..2257										acid proteinase eapC precursor - chestnut blight fungus ; (X83997) acid proteinase [Cryphonectria parasitica]	

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Blast gi	aat Score	Blast Score	% id	% cvrg	Description
					Database Hit	gi 30582	173	92	4.00E-18	28	17
19021	ENU02815	ANI61C952:1	34-68	683-709	NAP						Retrovirus-related pol polyprotein from transposon TNT 1.94 [contains: protease; reverse transcriptase; endonuclease] ; hypothetical protein - common tobacco ; (X1377) ORF [Nicotiana tabacum]
19022	ENU02816	ANI61C9559:	23-58	678-698	NAP	g3913768	102	61	0.000000	28	98
		713..1430				009					[AE00735) phosphoglycolate phosphatase (PGP) ;
19023	ENU02817	ANI61C6527:	66-84	722-741	NAP	g3122361	271	116	2.00E-25	42	86
		2787..2619				g118126	59	0.000000	36	90	phosphatase [Aquifex aeolicus] putative lipoate-protein ligase B (lipoate biosynthesis protein B) ; (Z98980) hypothetical protein [Schizosaccharomyces pombe]
19024	ENU02818	ANI50C2369	22-43	672-698	NAP	g2499588	1079	248	e-100	98	62
		01_1:30..748				g2804298	372	85	4.00E-16	32	28
19025	ENU02819	ANI61C1250:	36-55	693-712	NAP	g2132880	284	83	8.00E-23	27	89
		3498..2780				[Rhodococcus rhodochrous] probable membrane protein YOR087w - yeast [Saccharomyces cerevisiae] ; (Z74995) ORF YOR087w [Saccharomyces cerevisiae]					
19026	ENU02820	ANI61C1099	44-65	689-720	NAP	[Saccharomyces cerevisiae]					
		9:1170..1888				[Saccharomyces cerevisiae] putative PRT1 protein ; probable PRT1 protein - yeast (Hansenula polymorpha) ; (X15111) put. PRT1 protein (AA 1-221) (1 is 1st base in codon) [Pichia angusta]					
19027	ENU02821	ANI61C1040	27-47	684-703	NAP	g131031	328	113	1.00E-29	41	96
		9:1373..655				putative dioxygenase YLL057C ; hypothetical protein YLL057c - yeast (Saccharomyces cerevisiae) ; (Z47973)					
19028	ENU02822	ANI61C5788:	22-49	678-698	NAP	ORF L0572 [Saccharomyces cerevisiae] ; (Z73162) ORF YLL057c [Saccharomyces cerevisiae]					
		5396..6114				GTP cyclohydrolase I (GTP-CH-I) ; (Z98849) gtp cyclohydrolase I [Schizosaccharomyces pombe]					
19030	ENU02824	ANI61C1211:	22-41	680-699	NAP	g3183014	706	150	3.00E-65	65	85
		821..102									

Seq num	Seq id	Contig Source	Primer 3 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat	Blast Score	Blast Prob	% id	% cvrg	Description
19031	ENU02825	ANI61C8770:	47-67	698-724	NAP	g2981719	776	91	1.00E-30	44	30	Crystal Structures Of The Copper-Containing Amine Oxidase From Arthrobacter Globiformis In The Holo- And Apo-Forms: Implications For The Biogenesis Of Topa Quinone ; Crystal Structures Of The Copper-Containing Amine Oxidase From Arthrobacter Globiformis In The Holo- And Apo-Forms: Implications For The Biogenesis Of Topa Quinone	
19032	ENU02826	ANI61C6467:	22-47	681-700	NAP	g461926	228	69	5.00E-22	33	95	Haloacetate dehalogenase H-2 ; haloacetate dehalogenase (EC 3.8.1.3) H-2 - Moraxella sp. plasmid pUO1 ; (D90423) haloacetate dehalogenase H-2 [Moraxella sp.]	
19033	ENU02827	ANI61C9085:	57-76	716-735	NAP	g2506921	158	45	0.0006	37	55	"probable taurine catabolism dioxygenase (sulfate starvation-induced protein 3) (SSI3) ; (D85613) dioxygenase [Escherichia coli] ; (UT3857) dioxygenase [Escherichia coli] ; (AE000143) taurine dioxygenase, 2-oxoglutarate-dependent [Escherichia coli]" hypothetical 25.6 KD protein in NTF2- SRP1 intergenic region ; hypothetical protein YER010c - yeast (Saccharomyces cerevisiae) ; (U18778) Yer010cp [Saccharomyces cerevisiae] (AF051914) C-4 methyl sterol oxidase [Candida albicans] (AL035521) hypothetical protein [Arabidopsis thaliana] (Z98056) putative glyoxylate pathway regulator [Schizosaccharomyces pombe] (Z98600) hypothetical atp-dependent transporter [Schizosaccharomyces pombe]	
19034	ENU02828	ANI61C3566:	44-65	697-723	NAP	g731439	132	54	0.00001	28	91		
19035	ENU02829	ANI61C353:2	27-56	688-706	NAP	g2970627	908	304	4.00E-82	60	71	(AF051914) C-4 methyl sterol oxidase [Candida albicans] (AL035521) hypothetical protein [Arabidopsis thaliana] (Z98056) putative glyoxylate pathway regulator [Schizosaccharomyces pombe] (Z98600) hypothetical atp-dependent transporter [Schizosaccharomyces pombe]	
19036	ENU02830	ANI61C8203:	23-44	682-702	NAP	g4455171	303	146	1.00E-34	33	27		
19037	ENU02831	ANI61C7700:	57-76	717-736	NAP	g2281979	362	131	5.00E-30	46	64		
19038	ENU02832	ANI61C9556:	26-45	687-706	NAP	g2330757	649	259	4.00E-68	61	86		

Seq num	Seq id	Contig Source	Primer 3 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat	Blast Score	Blast Prob	% id	% cvrg	Description
19039	ENU02833	ANI61C110	42-66	703-722	NAP	g585896	267	130	1.00E-29	38	94	"probable mitochondrial 60S ribosomal protein L16 precursor ; ribosomal protein L16 precursor, mitochondrial - yeast (Saccharomyces cerevisiae); (X78214) L16 ribosomal protein [Saccharomyces cerevisiae]; (Z35799) ORF YBL038w [Saccharomyces cerevisiae]"	
19040	ENU02834	ANI61C590:8	45-65	40..117	707-726	NAP	g549607	409	125	2.00E-36	38	35	hypothetical 74.7 KD TRP-ASP repeats containing protein in DAL80-GAP <sup>1</sup> intergenic region ; hypothetical protein YKR036c - yeast (Saccharomyces cerevisiae); (Z28261) ORF YKR036c [Saccharomyces cerevisiae] (Z99296) 60s ribosomal protein L32 [Schizosaccharomyces pombe] (AC005168) putative hydroxymethylglutaryl-CoA lyase precursor [Arabidopsis thaliana] hypothetical monooxygenase Y4FC; (AE00072) Y4fc [Rhizobium sp. NGR234] (AL031852) short-chain dehydrogenase [Schizosaccharomyces pombe] (AC000133) ORF [Emericella nidulans]
19041	ENU02835	ANI61C6543:	27-52	3639..2915	690-709	NAP	g2414650	346	93	2.00E-31	69	93	[Saccharomyces cerevisiae] (Z99296) 60s ribosomal protein L32 [Schizosaccharomyces pombe] (AC005168) putative hydroxymethylglutaryl-CoA lyase precursor [Arabidopsis thaliana] hypothetical monooxygenase Y4FC; (AE00072) Y4fc [Rhizobium sp. NGR234] (AL031852) short-chain dehydrogenase [Schizosaccharomyces pombe] (AC000133) ORF [Emericella nidulans]
19042	ENU02836	ANI61C7500:	22-51	2405..1681	684-704	NAP	g2426048	540	167	6.00E-52	51	50	[Saccharomyces cerevisiae] (Z99296) 60s ribosomal protein L32 [Schizosaccharomyces pombe] (AC005168) putative hydroxymethylglutaryl-CoA lyase precursor [Arabidopsis thaliana] hypothetical monooxygenase Y4FC; (AE00072) Y4fc [Rhizobium sp. NGR234] (AL031852) short-chain dehydrogenase [Schizosaccharomyces pombe] (AC000133) ORF [Emericella nidulans]
19043	ENU02837	ANI61C4138:	57-76	622..1346	719-739	NAP	g2496621	310	118	3.00E-26	50	64	[Saccharomyces cerevisiae] (Z99296) 60s ribosomal protein L32 [Schizosaccharomyces pombe] (AC000133) ORF [Emericella nidulans]
19044	ENU02838	ANI61C1289:	23-48	12..737	685-706	NAP	g3738145	147	90	1.00E-17	31	64	[Saccharomyces cerevisiae] (Z99296) 60s ribosomal protein L32 [Schizosaccharomyces pombe] (AC000133) ORF [Emericella nidulans]
19045	ENU02839	ANI61C5187:	60-80	2678..1953	721-743	NAP	g1870209	857	132	4.00E-34	38	42	[Saccharomyces cerevisiae] (Z99296) 60s ribosomal protein L32 [Schizosaccharomyces pombe] (AC000133) ORF [Emericella nidulans]
19046	ENU02840	ANI61C3158:	50-69	1742..2468	715-734	NAP	g1723421	318	87	1.00E-16	34	78	[Saccharomyces cerevisiae] (Z99296) 60s ribosomal protein L32 [Schizosaccharomyces pombe] (AC000133) ORF [Emericella nidulans]
19047	ENU02841	ANI61C6895:	23-43	1106..1832	688-707	NAP	g140519	120	74	9.00E-13	29	72	[Saccharomyces cerevisiae] (Z99296) 60s ribosomal protein L32 [Schizosaccharomyces pombe] (AC000133) ORF [Emericella nidulans]
19048	ENU02842	ANI61C5862:	25-49	104..830	684-709	NAP	g3183130	554	200	1.00E-50	52	52	[Saccharomyces cerevisiae] (Z99296) 60s ribosomal protein L32 [Schizosaccharomyces pombe] (AC000133) ORF [Emericella nidulans]

Seq num	Seq id	Contig Source	Primer 3 pos	Primer 3 pos	Selection Basis	Database Hit	nebi gi	aat	Blast Score	Blast Prob	% id	% cvrg	Description
19049	ENU02843	ANI61C3285:	33-52	700-718	NAP	g3850101	378	137	7.00E-32	47	93	(AL033388) putative ma-binding protein [Schizosaccharomyces pombe]	
19050	ENU02844	ANI61C459:	7	60-79	726-745	NAP	g3135988	652	69	3.00E-19	46	37	(AL023389) membrane transporter [Schizosaccharomyces pombe]
19051	ENU02845	ANI61C555:	56-77	723-742	NAP	g2501603	311	123	9.00E-28	38	31	hypothetical 77.0 KD protein in HES1-SEC63 intergenic region ; hypothetical protein YOR243c - yeast (Saccharomyces cerevisiae) ; (Z75151) ORF YOR243c [Saccharomyces cerevisiae]	
19052	ENU02846	ANI61C1617:	23-41	688-709	NAP	g1806234	63	1.00E-16					(Z84498) hypothetical protein Rv1928c
19053	ENU02847	ANI61C7616:	64-83	731-750	NAP	g2697132	287	87	3.00E-22	36	84	[Mycobacterium tuberculosis] (AF036580) necrosis and ethylene inducing peptide [Fusarium oxysporum f. sp. erythoxyli]	
19054	ENU02848	ANI61C990:	2 69-88	735-755	NAP	g1491795	486	201	6.00E-51	38	26	"(U39812) beta-1,4-mannanase [Caldicellulosiruptor saccharolyticus]" Pisatin demethylase (cytochrome P450 57A2) ; pisatin demethylase - fungus (Nectria haematococca) ; (X73145) pisatin demethylase [Nectria haematococca]	
19055	ENU02849	ANI61C3212:	34-53	699-720	NAP	g585695	232	120	1.00E-26	32	41	(AL022304) hypothetical protein [Schizosaccharomyces pombe]	
			197..925										hypothetical 36.3 KD protein C56F8.09 in chromosome I ; (Z69728) unknown [Schizosaccharomyces pombe]
													hypothetical 33.7 KD protein in ISC10 3'region ; hypothetical protein YER185w - yeast (Saccharomyces cerevisiae) ; (U18922) Yer185wp [Saccharomyces cerevisiae]
19059	ENU02853	ANI61C2954:	48-67	714-735	NAP	g2258125	164	64	0.000000	29	39	(Z83828) AmMst-1 [Amanita muscaria]	
19060	ENU02854	ANI61C8514:	67-87	722-755	NAP	g3287949	418	147	3.00E-39	41	30	hypothetical 79.5 KD protein C17A5.12 in chromosome I ; (Z98849) hypothetical protein [Schizosaccharomyces pombe]	

Seq num	Seq id	Contig Source	Primer 3 pos	Primer 3 pos Basis	Selection Database Hit	ncbi gi	Score	Blast Prob	% id	% cvrg	Description	
19061	ENU02855	ANI61C943:1	33-52	NAP	g140459	61	0.000000		01		"hypothetical 30.7 KD protein in RVS161-ADP1 intergenic region ; hypothetical protein YCR010c - yeast (Saccharomyces cerevisiae) ; (X59720) YCR010c, len:283 [Saccharomyces cerevisiae]"	
19062	ENU02856	ANI61C7480: 136..867	70-88	735-759	NAP	g3915154	245	102	3.00E-21	33	39	Trichodiene oxygenase (cytochrome P450 58) ; trichodiene oxygenase 4 - fungus (Fusarium sporotrichioides) ; (U22462) trichodiene oxygenase [Fusarium sporotrichioides]
19063	ENU02857	ANI61C6213: 4926..4195	69-100	740-758	NAP	g113449	552	152	2.00E-36	47	21	"probable ATP-dependent permease precursor ; ATP-dependent permease ADP1 precursor - yeast (Saccharomyces cerevisiae) ; (X59720) YCR011c, len:1049 [Saccharomyces cerevisiae]"
19064	ENU02858	ANI61C9775: 4974..4243	55-75	724-744	NAP	g371723	589	178	5.00E-44	46	68	hypothetical 34.9 KD protein in RPL44-DCD1 intergenic region ; hypothetical protein YHR142w - yeast (Saccharomyces cerevisiae) ; (U10397) Yhr142wp [Saccharomyces cerevisiae] (AB013443) cytochrome P450
19065	ENU02859	ANI61C1733: 1013..279	72-99	742-762	NAP	g3721844	296	73	5.00E-25	36	40	[Coprinus cinereus] (AL033503) putative mitochondrial carrier protein [Candida albicans] putative para-hydroxybenzoate—polyprenyltransferase precursor (PHB-polyprenyltransferase) ; (Z69728) unknown
19066	ENU02860	ANI61C7086: 1010..278	22-41	693-712	NAP	g3859687	527	150	8.00E-36	53	77	(AL033503) putative mitochondrial carrier protein [Candida albicans] putative para-hydroxybenzoate—polyprenyltransferase precursor (PHB-polyprenyltransferase) ; (Z69728) unknown
19067	ENU02861	ANI61C920:1 364..631	46-65	717-737	NAP	g1706003	76	3.00E-13				[Schizosaccharomyces pombe] Tryptophan synthase ; tryptophan synthase (EC 4.2.1.20) - Neurospora crassa ; (J04594) tryptophan synthetase [Neurospora crassa]
19068	ENU02862	ANI61C2401: 1006..273	40-59	711-731	NAP	g136372	2405	310	e-109	80	34	acetyl- <i>l</i> -hydrolase ; (M64783) acetyl-hydrolase [Streptomyces hygroscopicus] (AL049522) putative phosphatase component [Schizosaccharomyces pombe]
19069	ENU02863	ANI61C5992: 8770..8037	69-87	723-760	NAP	g1352065	69	2.00E-11				
19070	ENU02864	ANI61C933:1 777..1043	25-54	695-717	NAP	g4539598	322	76	9.00E-15	33	62	

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	Score	Score Prob	% id	% cvrg	Description
19071	ENU02865	ANI61C7676:	68..87	728..760	NAP	g3123232	643	152	1.00E-58	53	78	general stress protein 39 (GSP39); (AB001488) belongs to the insect-type alcohol dehydrogenase / ribitol dehydrogenase family [Bacillus subtilis]; (Z99106) similar to alcohol dehydrogenase [Bacillus subtilis]
19072	ENU02866	ANI61C8467:	23..48	694..716	NAP	g3114282	484	163	1.00E-39	47	93	"Chain N, Crystal Structure Of The 20s Proteasome From Yeast At 2.4 Angstroms Resolution ; Chain 2, Crystal Structure Of The 20s Proteasome From Yeast At 2.4 Angstroms Resolution "
19073	ENU02867	ANI61C9642:	40..59	706..735	NAP	g1175965	388	171	5.00E-42	41	99	hypothetical 25.2 KD protein in THI5 5'region and in THI12 5'region ; hypothetical protein YFL061w - yeast (Saccharomyces cerevisiae); (D50617) YFL061W [Saccharomyces cerevisiae]; (D44603) unknown [Saccharomyces cerevisiae]; (Z71611) ORF YNL335w [Saccharomyces cerevisiae] (Y11113) endoglucanase IV [Hypocrea jecorina]; (AL034583) hypothetical protein [Schizosaccharomyces pombe] (D85230) hypothetical protein [Plectonema boryanum]
19074	ENU02868	ANI61C6810:	22..41	692..717	NAP	g2315274	731	297	5.00E-80	56	70	hypothetical 69.8 KD protein in BDF1-SFP1 intergenic region ; hypothetical protein YLR401c - yeast (Saccharomyces cerevisiae); (U19729) Ylr401cp [Saccharomyces cerevisiae] (U61840) sodium transport ATPase FST [Fusarium solani f. sp. pisi] (Z99759) hypothetical protein [Schizosaccharomyces pombe]
19075	ENU02869	ANI61C7686:	54..73	730..749	NAP	g4056557	266	107	8.00E-23			glutamate synthase (NADH) precursor (NADH-GOGAT); glutamate synthase (NADH) (EC 1.4.1.14) - alfalfa; (L01660) NADH-glutamate synthase [Medicago sativa]
19076	ENU02870	ANI61C4371:	33..53	712..731	NAP	g1339949	174	73	2.00E-12	26	91	
19077	ENU02871	ANI61C1115	24..44	702..722	NAP	g2833203	515	189	1.00E-47	50	35	
19078	ENU02872	ANI61C1748:	64..86	739..762	NAP	g1438947	932	269	2.00E-94	68	46	(U61840) sodium transport ATPase FST [Fusarium solani f. sp. pisi] (Z99759) hypothetical protein [Schizosaccharomyces pombe]
19079	ENU02873	ANI61C1011	42..71	721..740	NAP	g2467272	867	356	9.00E-98	72	31	glutamate synthase (NADH) precursor (NADH-GOGAT); glutamate synthase (NADH) (EC 1.4.1.14) - alfalfa; (L01660) NADH-glutamate synthase [Medicago sativa]
19080	ENU02874	ANI61C1719:	40..60	720..739	NAP	g417073	754	302	1.00E-81	58	11	

Seq num	Seq id	Contig Source	Primer 3 pos	Primer 3 pos Basis	Selection Database Hit	ncbi gi	aat Score	Blast Prob	Blast % id	% cvrg	Description	
19081	ENU02875	ANI61C7336:	72-92	753-772	NAP	g2808725	57	0.000000	2	57	(AL021428) hypothetical protein Rv0068 [Mycobacterium tuberculosis]	
19082	ENU02876	ANI61C280:2	25-45	706-725	NAP	g113589	814	201	4.00E-51	48	65	Allantioicase ; allantoicase (EC 3.5.3.4) - Neurospora crassa ; (J02927)
19083	ENU02877	ANI61C5029:	33-53	709-734	NAP	g3183342	248	102	3.00E-21	36	57	allantioicase [Neurospora crassa] hypothetical protein C14C4.09 in chromosome I ; (Z98596)
19084	ENU02878	ANI61C5155:	43-62	717-744	NAP	g2132846	79	4.00E-14				[Schizosaccharomyces pombe] probable membrane protein YOL119c - yeast [Saccharomyces cerevisiae]; (Z74861) ORF YOL119c [Saccharomyces cerevisiae]; (X95258) unknown protein [Saccharomyces cerevisiae]
19085	ENU02879	ANI61C6256:	27-47	709-728	NAP	g731773	599	105	2.00E-44	59	69	hypothetical 31.9 KD protein in BET1-PAN1 intergenic region ; probable membrane protein YIL003w - yeast (Saccharomyces cerevisiae)
19086	ENU02880	ANI61C4645:	30-61	713-732	NAP	g2132214	233	98	7.00E-20			hypothetical protein YPL164c - yeast (Saccharomyces cerevisiae); (Z73520) ORF YPL164c [Saccharomyces cerevisiae]; (X96770) P2550 protein [Saccharomyces cerevisiae]
19087	ENU02881	ANI61C6841:	72-96	741-774	NAP	g1781102	552	185	4.00E-46	38	50	[Mycobacterium tuberculosis] "hypothetical 21.1 KD protein in FUS1-AGP1 intergenic region ; hypothetical protein YCL026c-a - yeast (Saccharomyces cerevisiae); (X59720) YCL026c-a, len:192 [Saccharomyces cerevisiae]"
19088	ENU02882	ANI61C1062	54-74	735-756	NAP	g586554	137	54	0.000001	29	92	(AL022071) fructosyl amine [Schizosaccharomyces pombe] (AL035655) 60s ribosomal protein l36 [Schizosaccharomyces pombe]
19089	ENU02883	ANI61C1146	54-73	737-756	NAP	g2950465	544	144	8.00E-34	37	52	
19090	ENU02884	ANI61C7987:	46-74	725-748	NAP	g4490679	180	82	6.00E-15	56	43	
			325..1069									

Seq num	Seq id	Contig Source	Primer 3 pos	Primer 5 pos	Selection Basis	Database Hit	nebi gi	aat	Blast Score	Blast Prob	% id	% cvrg	Description
19091	ENU02885	ANI61C1043	44-64	728-747	NAP	g231710	779	256	1.00E-67	86	89	cell division	control protein 42
			6.2415..3160										homolog (CDC42SP) ; cell division control protein 42
19092	ENU02886	ANI61C4663:	22-41	705-725	NAP	g3219969	156	70	2.00E-11	29	96		
			4535..5281										[Schizosaccharomyces pombe] ; (L25677) Cdc42p
19093	ENU02887	ANI61C7186:	30-52	715-734	NAP	g2621836	150	84	9.00E-16	32	92		
			317...1063										[Schizosaccharomyces pombe] hypothetical 22.4 KD protein
19094	ENU02888	ANI61C8897:	60-81	741-764	NAP	g113310	1070	193	6.00E-99	79	47		
			3183..2437										C6G10.10C in chromosome 1; (Z98603) hypothetical protein
19095	ENU02889	ANI61C6534:	22-45	707-726	NAP	g461540	883	336	9.00E-92				
			3269..2523										[Schizosaccharomyces pombe] [Saccharomyces pombe] (AE00853) conserved protein [Methanobacterium thermoadaptrophicum]
													acetyl-CoA hydrolase (acetyl-CoA deacylase) (acetyl-CoA acylase) (acetate utilization protein) ; acu-8 protein - Neurospora crassa ; (M31521) acetate permease (acu-8) [Neurospora crassa]
													"phospho-2-dehydro-3-deoxyheptonate aldolase, tyrosine-inhibited (phospho-2-keto-3-deoxyheptonate aldolase) (DAHP synthetase) (3-deoxy-D-arabino-heptulosonate 7-phosphate synthase) ; 2-dehydro-3-deoxyphosphohexonate aldolase (EC 4.1.2.15) ARO4 - yeast (Saccharomyces cerevisiae) ; (L20296) homology with DAHP-synthase (ARO4) gene [Saccharomyces cerevisiae] ; (X61107) phospho-2-dehydro-3-deoxyheptonate aldolase [Saccharomyces cerevisiae] ; (Z36118) ORF YBR249c [Saccharomyces cerevisiae]" (AL031853) putative zinc finger protein [Schizosaccharomyces pombe] (AB014595) KIAA0695 protein [Homo sapiens]
19096	ENU02890	ANI61C3210:	49-68	729-754	NAP	g3738206	215	46	0.0003				
			87..834										
19097	ENU02891	ANI61C4686:	30-49	715-737	NAP	g3327204	609	125	8.00E-44	44	31		
			89..838										

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat	Blast Score	Blast Prob	% id	% cvrg	Description
19098	ENU02892	ANI61C8599:	47-66	736-755	NAP	g465105	644	174	1.00E-61	54	31	[U04841] lanosterol synthase [Saccharomyces cerevisiae]	
19099	ENU02893	ANI61C4266:	206..1347	45-64	725-755	NAP	g731476	201	81	1.00E-14	42	55	hypothetical 14.4 KD protein in RNR1-ALD3 intergenic region ; hypothetical protein YER072w - yeast
19100	ENU02894	ANI61C1600:	43-67	732-753	NAP	g2293194	289	89	4.00E-23				(Saccharomyces cerevisiae) ; (U18813) Yer072wp [Saccharomyces cerevisiae] (AF008220) yteR [Bacillus subtilis]; (Z99119) similar to hypothetical proteins [Bacillus subtilis] (AF025475) Masc1 [Ascobolus immersus]
19101	ENU02895	ANI61C9279:	34-53	722-744	NAP	g2558956	343	124	5.00E-34	40	43	(AE001036) L-carnitine dehydratase (caIB-2) [Archaeoglobus fulgidus] (AL049558) putative	
19102	ENU02896	ANI61C9067:	62-86	746-773	NAP	g2649608	60	4.00E-17				[Schizosaccharomyces pombe] (AL035218) conserved hypothetical protein [Schizosaccharomyces pombe]	
19103	ENU02897	ANI61C8232:	62-82	752-774	NAP	g4581508	727	190	4.00E-69	63	11	ubiquitin-conjugating enzyme E2-18 KD (ubiquitin-protein ligase HUSS) (ubiquitin carrier protein HUSS5); HUSS protein - fission yeast	
19104	ENU02898	ANI61C8865:	33-52	726-745	NAP	g4160583	699	281	4.00E-75	53	80	(Schizosaccharomyces pombe); (Schizosaccharomyces pombe); (X81846) huss5 [Schizosaccharomyces pombe]; (Z67961) ubiquitin conjugating enzyme	
19105	ENU02899	ANI61C1147:	23-48	714-736	NAP	g731040	531	157	6.00E-38			[Schizosaccharomyces pombe]	
19106	ENU02900	ANI61C1073	60-80	754-773	NAP	g3024226	547	69	2.00E-23	35	53	ubiquitin-conjugating enzyme [Schizosaccharomyces pombe] NOT56-like protein ; (Y09022) Not56-like protein [Homo sapiens]	
19107	ENU02901	ANI61C352:7	26-46	719-739	NAP	g1730615	390	107	3.00E-36	48	90	ERV25 protein precursor; probable membrane protein YML012w - yeast (Saccharomyces cerevisiae); (Z49810) unknown [Saccharomyces cerevisiae] (Z97336) carnitine racemase homolog [Arabidopsis thaliana] (AL034565) putative abhydrolase	
19108	ENU02902	ANI61C7690:	65-84	751-780	NAP	g2244799	108	62	0.00000032	69		[Schizosaccharomyces pombe]	
19109	ENU02903	ANI61C1026:	793..36	22-49	709-737	NAP	g4049528	342	82	1.00E-25	39	70	
			1372..2129										

Seq num	Seq id	Contig	Source	5 pos	Primer 3 pos	Primer Basis	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Prob	% id	% cvrg	Description
19110	ENU02904	AN161C5273:	22-52	6842..6081	721-740	NAP	g731758	419	176	1.00E-43	44	37	hypothetical 67.8 KD protein in IKI1-ERG9 intergenic region ; hypothetical protein YHR188c [Saccharomyces cerevisiae] ; (U00030) Yhr188cp [Saccharomyces cerevisiae] (D85770) cysteine dioxygenase [Homo sapiens]	
19111	ENU02905	AN161C2115:	63-87	784..23	750-782	NAP	g1747324	200	68	3.00E-18	47	76	hypothetical zinc-type alcohol dehydrogenase-like protein in GDH3-CNE1 intergenic region ; FUN50 protein - yeast (Saccharomyces cerevisiae) ; (U12980) Yal061wp [Saccharomyces cerevisiae]	
19112	ENU02906	AN161C9458:	48-72	1566..804	740-767	NAP	g731294	532	108	3.00E-41	39	59	putative ATP-dependent RNA helicase T26G10.1 in chromosome III ; ATP-dependent RNA helicase homolog T26G10.1 - Caenorhabditis elegans ; (Z22915) similar to RNA helicases, deleted exon 1397-1495 which introduced stop codon at 3' splice; 5' splice looks v. good; ?possible alternate final exon; cDNA EST yk368a4.3 comes from this gene; cDNA EST yk368a4.5 comes fr..."	
19114	ENU02908	AN161C8348:	22-46	1359..596	723-743	NAP	g549012	512	216	2.00E-55	44	98	mating-type switching protein SWI10 ; SWI10 protein - fission yeast (Schizosaccharomyces pombe) ; (X61926) SWI10 [Schizosaccharomyces pombe] ; (AL031534) mating-type switching protein swi10. [Schizosaccharomyces pombe]	
19115	ENU02909	AN161C3366:	38-57	17..782	737-761	NAP	g2873363	346	95	8.00E-40	40	35	[U89492] arylsulfatase [Neurospora crassa]	
19116	ENU02910	AN161C3113:	68-99	1253..488	772-791	NAP	g2507070	429	39	0.027	32	39	N amino acid transport system protein (methyltryptophan resistance protein); neutral amino acid permease - Neurospora crassa ; (L34605) neutral amino acid permease [Neurospora crassa]	

Seq num	Seq id	Contig Source	Primer 3 pos	Primer 3 pos Basis	Selection Database Hit	nebi gi	Score	Blast Prob	% id	% cvrg	Description	
19117	ENU02911	ANI61C8607:	65-84	NAP	768-788	g549705	61	0.000000	007	36.1	KD protein in BUD2-MIF2 intergenic region; SEC14 protein homolog YKL091c - yeast (Saccharomyces cerevisiae); (Z228091)	
19118	ENU02912	ANI61C1114	53-72	754-777	NAP	g1175102	266	123	2.00E-27	32	85	ORF YKL091c [Saccharomyces cerevisiae]
			0:928..162									
19119	ENU02913	ANI61C1138	40-61	742-764	NAP	g2634109	235	107	8.00E-23	36	93	[Haemophilus influenzae] (Z99113) ymaE [Bacillus subtilis]
19120	ENU02914	ANI61C4135:	63-82	767-787	NAP	g1749446	399	153	1.00E-36	53	50	(D89119) unnamed protein product [Schizosaccharomyces pombe] (U04540) flavocytochrome b5 chimeric protein [synthetic construct]; (L227087) cytochrome b5 [Artificial gene]
19121	ENU02915	ANI61C1442:	62-81	769-788	NAP	g488428	181	75	6.00E-13	33	33	pseudouridylylate synthase 3 (pseudo尿嘧啶 synthase 3) (depressed growth-rate protein DEG1); depressed growth-rate protein DEG1 - yeast (Saccharomyces cerevisiae); (D50617) depressed growth-rate protein [Saccharomyces cerevisiae]; (D44600) depressed growth-rate protein DEG1 [Saccharomyces cerevisiae]
19122	ENU02916	ANI61C9241:	45-68	749-772	NAP	g399356	561	171	5.00E-42	49	44	(Saccharomyces cerevisiae); (D44600) depressed growth-rate protein DEG1 [Saccharomyces cerevisiae]; (U02618) RTM1 gene product [Saccharomyces cerevisiae]
19123	ENU02917	ANI61C4650:	72-91	774-799	NAP	g730689	120	50	0.00001	30	64	RTM1 protein; RTM1 protein - yeast (Saccharomyces cerevisiae); (U02618) RTM1 gene product [Saccharomyces cerevisiae]
19124	ENU02918	ANI61C3926:	55-74	759-783	NAP	g131761	220	112	3.00E-24	34	38	quinate permease (quinate transporter); quinate transport protein - Neurospora crassa; (X14603) quinate transporter [Neurospora crassa]
19125	ENU02919	ANI61C5774:	24-43	729-752	NAP	g3746897	178	96	3.00E-19	29	85	(AF088907) clock-controlled gene-8 protein [Neurospora crassa]
			818..48									

Seq num	Seq id	Contig Source	Primer 3 pos	Primer 3 pos	Selection Basis	Database Hit	nebi gi	aat	Blast Score	Blast Prob	% id	% cvrg	Description
19126	ENU02920	ANI61C3373:	27-60	736-755	NAP	g2133034	475	135	3.00E-31	39	37	probable membrane protein YPR156c - yeast [Saccharomyces cerevisiae]; (U28371) Similar to S. cerevisiae hypothetical protein Ybr008p (Swiss Prot, accession number P38124)	
19127	ENU02921	ANI61C6835:	42-61	751-770	NAP	g3130039	414	154	7.00E-37	40	95	[Saccharomyces cerevisiae] (AL023534) hypothetical protein	
			5945..6715									[Schizosaccharomyces pombe]	
19128	ENU02922	ANI61C1057	59-78	767-787	NAP	g1787246	178	64	9.00E-10	29	91	(AE00202) putative synthetase [Escherichia coli]	
19129	ENU02923	ANI61C5814:	49-68	752-778	NAP	g3130041	640	229	2.00E-59	53	64	(AL023534) hypothetical protein [Schizosaccharomyces pombe]; (AL031534) homology to longevity assurance protein.	
19130	ENU02924	ANI61C138:2	25-45	732-754	NAP	g1175373	237	80	3.00E-18	31	31	[Schizosaccharomyces pombe] hypothetical 72.5 KD protein C2F7.10 in chromosome I; hypothetical protein SPAC2F.7.10 - fission yeast (Schizosaccharomyces pombe); (Z50142) unknown	
			054...1283									[Schizosaccharomyces pombe] (U89985) serine/threonine protein phosphatase PPT1 [Neurospora crassa] (AB004537) hypothetical 47.4KD protein in SHP1-SEC17 intergenic region [Schizosaccharomyces pombe] (AL031798) 40s ribosomal protein s20.	
19131	ENU02925	ANI61C8631:	26-47	731-755	NAP	g2290382	1118	441	e-123	78	53	[Schizosaccharomyces pombe]	
19132	ENU02926	ANI61C2278:	44-63	755-774	NAP	g2257524	396	159	2.00E-38	41	92	(Z50142) unknown [Schizosaccharomyces pombe] (U89985) serine/threonine protein phosphatase PPT1 [Neurospora crassa] (AB004537) hypothetical 47.4KD protein in SHP1-SEC17 intergenic region [Schizosaccharomyces pombe] (AL031798) 40s ribosomal protein s20.	
19133	ENU02927	ANI61C8986:	43-62	752-773	NAP	g3687464	320	131	6.00E-30	62	65	[Schizosaccharomyces pombe]	
19134	ENU02928	ANI61C1011:	53-72	765-784	NAP	g2133323	588	163	1.00E-39	64	94	het-c4 protein - Podospora anserina; (L36210) het-c [Podospora anserina] putative mitochondrial carrier	
19135	ENU02929	ANI61C1071	62-92	773-793	NAP	g1723767	361	137	1.00E-31	40	62	YGR257C ; hypothetical protein YGR257c - yeast (Saccharomyces cerevisiae); (Z73042) ORF YGR257c [Saccharomyces cerevisiae]; (X99228) mitochondrial carrier protein [Saccharomyces cerevisiae]	
19136	ENU02930	ANI61C8371:	24-59	736-755	NAP	g1374920	227	86	2.00E-22	33	14	(L78243) alternative splice (exon 17) [Homo sapiens]	

Seq num	Seq id	Contig Source	Primer 3 pos	Primer 3 pos Basis	Selection Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19137	ENU02931	ANI61C9255:	23-51	735-755 NAP	g2764632	796	217	1.00E-67	71	99	(AJ001520) 19.3kD iron-sulfur subunit of mitochondrial complex I [Neurospora crassa]	
19138	ENU02932	ANI61C9182:	22-45	735-754 NAP	g2808634	860	192	2.00E-48	40	29	(AJ001909) transcriptional activator [Aspergillus niger]	
19139	ENU02933	ANI61C9243:	25-44	730-757 NAP	g2493049	303	59	5.00E-19	58	85	"ATP synthase delta chain, mitochondrial precursor; (Z82020) ATP-synthase delta-subunit [A garicus bisporus]" (AB025252) reverse transcriptase [Magnaporthe grisea]	
19140	ENU02934	ANI61C9220:	25-58	738-757 NAP	g4586458	113	85	7.00E-16	33	60	40S ribosomal protein S26E (CRP5) (13.6 KD ribosomal protein); ribosomal protein S26.e - Neurospora crassa; (X55637) ribosomal protein [Neurospora crassa] hypothetical 40.7 KD protein in SIN4-URE2 intergenic region ; hypothetical protein YNL231c - yeast (Saccharomyces cerevisiae); (Z69381) Similar to hypothetical yeast protein L3502 [Saccharomyces cerevisiae]; (Z71507) ORF YNL231c [Saccharomyces cerevisiae] (Z98056) hypothetical protein [Schizosaccharomyces pombe]	
19141	ENU02935	ANI61C1049	51-72	763-783 NAP	g133892	473	90	2.00E-22	80	82	putative sterigmatocystin biosynthesis protein STCT; (U34740) putative translation elongation factor 1 gamma [Emericella nidulans]	
19142	ENU02936	ANI61C1059	9-3190..2415	24-42	738-757 NAP	g1730831	543	214	5.00E-55	44	68	40S ribosomal protein S26E (CRP5) (13.6 KD ribosomal protein); ribosomal protein S26.e - Neurospora crassa; (X55637) ribosomal protein [Neurospora crassa] hypothetical 40.7 KD protein in SIN4-URE2 intergenic region ; hypothetical protein YNL231c - yeast (Saccharomyces cerevisiae); (Z69381) Similar to hypothetical yeast protein L3502 [Saccharomyces cerevisiae]; (Z71507) ORF YNL231c [Saccharomyces cerevisiae] (Z98056) hypothetical protein [Schizosaccharomyces pombe]
19143	ENU02937	ANI61C6671:	56-76	763-789 NAP	g2281983	809	252	3.00E-66	59	81	putative sterigmatocystin biosynthesis protein STCT; (U34740) putative translation elongation factor 1 gamma [Emericella nidulans]	
19144	ENU02938	ANI61C8852:	34-68	734-767 NAP	g2494268	252	64	1.00E-21	37	98	40S ribosomal protein S9 (S7); (X96613) cytoplasmic ribosomal protein S7 [Podospora anserina] hypothetical 31.2 KD protein in CYSP-AMIA intergenic region ; (AE000330) putative regulator [Escherichia coli] (AL022599) hypothetical protein [Schizosaccharomyces pombe] (AL021748) hypothetical protein [Schizosaccharomyces pombe]	
19145	ENU02939	ANI61C7170:	22-43	737-756 NAP	g1710780	744	225	1.00E-70	84	99		
19146	ENU02940	ANI61C6870:	24-43	737-758 NAP	g2494700	514	161	6.00E-39	51	77		
19147	ENU02941	ANI61C4612:	1542..2318	785-804 NAP	g3080524	1235	75	6.00E-13	38	34		
19148	ENU02942	ANI61C7417:	1762..986	66-86 NAP	g2842510	211	115	5.00E-25	36	26		
			2566..1791									

Seq num	Seq id	Contig Source	Primer 3 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19149	ENU02943	ANI61C17:10	61-80	777-796	NAP	g1723966	355	152	2.00E-36	43	77	hypothetical protein in GOG5-NIF3 intergenic region ; hypothetical protein YGL224c - yeast (Saccharomyces cerevisiae) ; (Z72746) ORF YGL224c [Saccharomyces cerevisiae]	
19150	ENU02944	ANI61C9622:	56-75	769-791	NAP	g2132860	366	107	2.00E-29	41	99	probable membrane protein YOL162w - yeast (Saccharomyces cerevisiae) ; (Z74904) ORF YOL162w	
19151	ENU02945	ANI61C8718:	22-44	737-757	NAP	g2654181	1289	195	1.00E-99	75	55	[Saccharomyces cerevisiae] (AF034963) calmodulin-dependent protein kinase; CgCMK [Glomerella cingulata]	
19152	ENU02946	ANI61C8415:	24-52	741-760	NAP	g2494268	342	123	2.00E-27	38	97	putative sterigmatocystin biosynthesis protein STCT ; (U34740) putative translation elongation factor 1 gamma [Emericella nidulans] (AJ009973) hexokinase [Aspergillus niger] (AB018382) Mok13; Mok13 is homologous to Mok1 which is an alpha-glucan synthase	
19153	ENU02947	ANI61C1835:	56-75	772-794	NAP	g4140255	1017	153	2.00E-36	43	43	[Schizosaccharomyces pombe] high-affinity glucose transporter ; (U22525) high affinity glucose transporter [Kluyveromyces lactis] (AL035065) putative nadh-dependent flavin oxidoreductase	
19154	ENU02948	ANI61C9772:	24-53	741-762	NAP	g4586977	2840	272	3.00E-72	47	10	[Schizosaccharomyces pombe] hypothetical 26.3 KD protein in OYE2-GND1 intergenic region ; hypothetical protein YHR181w - yeast (Saccharomyces cerevisiae) ; (U00028) Yhr181wp [Saccharomyces cerevisiae] (X83502) j0916 [Saccharomyces cerevisiae]	
19155	ENU02949	ANI61C1091	42-65	762-781	NAP	g1346290	1048	216	5.00E-63	49	47	(AL035065) putative nadh-dependent flavin oxidoreductase	
19156	ENU02950	ANI61C3316:	70-89	790-809	NAP	g4106687	480	178	4.00E-44	39	64	[Schizosaccharomyces pombe] hypothetical 26.3 KD protein in OYE2-GND1 intergenic region ; hypothetical protein YHR181w - yeast (Saccharomyces cerevisiae) ; (U00028) Yhr181wp [Saccharomyces cerevisiae] (X83502) j0916 [Saccharomyces cerevisiae]	
19157	ENU02951	ANI61C6374:	22-55	741-762	NAP	g731752	432	178	3.00E-44	46	94	(AL031740) 60s ribosomal protein 110a. [Schizosaccharomyces pombe]	
19158	ENU02952	ANI61C1159:	61-81	776-801	NAP	g929862	648	141	7.00E-33	35	51		
19159	ENU02953	ANI61C5218:	47-66	768-787	NAP	g3650379	811	250	1.00E-65	77	95		

Seq num	Seq id	Contig Source	Primer 3 pos	Primer 3 pos Basis	Selection Database Hit	aat ncbi gi	blast Score	blast Prob	% id	% cvrg	Description
19160	ENU02954	ANI61C9551:	22-42	NAP	738-762	g730589	347	153	1.00E-36	41	99 "mitochondrial 60S ribosomal protein L6 precursor (YML6) ; ribosomal protein L6 precursor, mitochondrial - yeast ( <i>Saccharomyces cerevisiae</i> ) ; (U10397) MRPL6p: Mitochondrial ribosomal protein L6 [ <i>Saccharomyces cerevisiae</i> ] "
19161	ENU02955	ANI61C1209:	25-46	740-766	NAP	g1168402	689	273	7.00E-73	69	99 minor allergen ALT A 7 (ALT A VII); minor allergen - <i>Alternaria alternata</i> (X78225) minor allergen [ <i>Alternaria alternata</i> ]
19162	ENU02956	ANI61C1656:	42-61	764-783	NAP	g3929362	202	53	3.00E-20	34	35 pisatin demethylase (cytochrome P450 57A1) ; pisatin demethylase - fungus ( <i>Nectria haematoxocca</i> ) ; (L20976) pisatin demethylase [ <i>Nectria haematoxocca mpVI</i> ]
19163	ENU02957	ANI61C1095:	61-80	781-803	NAP	g2828147	486	86	4.00E-34	54	88 (AF042384) BC-2 protein [Homo sapiens]
19164	ENU02958	ANI50C6268	55-76	762-797	NAP	_1:785..6	g5886551	76	3.00E-13	27	73 hypothetical 33.5 KD protein in MRP59-YSW1 intergenic region ; probable membrane protein YBR147w - yeast ( <i>Saccharomyces cerevisiae</i> ) ; (Z36016) ORF YBR147w [ <i>Saccharomyces cerevisiae</i> ] (X99215) leucine zipper [ <i>Aspergillus niger</i> ]
19165	ENU02959	ANI61C1064	22-51	745-765	NAP	g1429204	568	208	3.00E-53	56	98 beta-glucosidase precursor (gentiobiase) (cellobiase) (beta-D-glucoside glucohydrolase) ; beta-glucosidase (EC 3.2.1.21) precursor - yeast ( <i>Kluyveromyces marxianus</i> var. <i>marxianus</i> ) ; (X05918) beta-glucosidase (AA 1 - 845) [ <i>Kluyveromyces marxianus</i> ]
19167	ENU02961	ANI50C1_19	26-46	751-770	NAP	01:889..103	g1706333	343	7.00E-94	61	45 pyruvate decarboxylase ; (U00967) pyruvate decarboxylase [ <i>Aspergillus parasiticus</i> ]

Seq num	Seq id	Contig Source	Primer 3 pos	Primer Basis	Selection Database Hit	aat ncbi gi	blast Score	blast Prob	% id	% cvrg	Description	
19168	ENU02962	ANI61C7922:	72-91	796-816	NAP	g1176153	290	131	6.00E-30	35	86	"hypothetical 27.4 KD protein in RNPB-SOHA intergenic region (ORF 1); (U18997) ORF_T256 [Escherichia coli]; (AE000394) orf, hypothetical protein [Escherichia coli]" regulatory subunit [Schizosaccharomyces pombe] (Z81035) predicted using Genefinder; Similarity to dehydrogenases; cDNA EST EMBL:D65800 comes from this gene; cDNA EST EMBL:D76184 comes from this gene; cDNA EST EMBL:D69322 comes from this gene; cDNA EST EMBL:C08158 comes from... (AC005106) T25N20.15 [Arabidopsis thaliana]
19170	ENU02964	ANI61C9746:	72-91	799-818	NAP	g3874345	51	0.00001				
			1406..2194									
19171	ENU02965	ANI61C7857:	25-44	753-772	NAP	g3935151	377	133	9.00E-44	43	94	
			2128..2917									
19172	ENU02966	ANI61C8794:	62-81	791-810	NAP	g1705884	725	98	1.00E-57	58	50	"probable citrate synthase, mitochondrial precursor" (Z98943) hypothetical protein Rv1533
19173	ENU02967	ANI61C6439:	54-73	783-802	NAP	g2370322	173	55	2.00E-11	32	40	[Mycobacterium tuberculosis] 26S proteasome regulatory subunit MTS3; (X92682) 26S protease regulatory subunit
19174	ENU02968	ANI61C1076	63-82	792-813	NAP	g1709170	263	112	3.00E-24	35	82	[Schizosaccharomyces pombe]; 26S protease subunit [Schizosaccharomyces pombe]
			5..866..1658									
19175	ENU02969	ANI61C4271:	32-55	762-782	NAP	g2132860	453	124	7.00E-30	46	93	probable membrane protein YOL162w - yeast (Saccharomyces cerevisiae); (Z74904) ORF YOL162w [Saccharomyces cerevisiae] (US6245) kymurenine 3-monoxygenase [Drosophila melanogaster]
19176	ENU02970	ANI61C9024:	34-54	756-784	NAP	g1336011	548	180	1.00E-44	42	47	
			4502..5294									

નુક્લોડિક એસેસ્ટર ડાયુનિટ " નુક્લોડિક એસેસ્ટર ડાયુનિટ "

Seq num	Seq id	Contig Source	Primer 3 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat	Blast Score	Blast Prob	% id	% cvrg	Description
19177	ENU02971	ANI61C8832:	25.44	745-776	NAP	g731651	1143	205	2.00E-52	41	38	hypothetical aldehyde-dehydrogenase like protein in PJT2-SRB2 intergenic region ; hypothetical protein YHR039c - yeast (Saccharomyces cerevisiae); (U0062) Yhr039cp [Saccharomyces cerevisiae]	
19178	ENU02972	ANI61C9335:	23.44	756-776	NAP	1039..1834	g465506	334	162	3.00E-39	43	97	HTP reductase ; RIB7 protein - yeast (Saccharomyces cerevisiae); (X71329) YBR12.03 [Saccharomyces cerevisiae]; (Z36022) ORF YBR153w [Saccharomyces cerevisiae]; (Z21622) HTP reductase [Saccharomyces cerevisiae]
19179	ENU02973	ANI61C8182:	47.67	774-800	NAP	109..904	g417454	823	309	1.00E-83	63	94	proliferating cell nuclear antigen (PCNA) ; proliferating cell nuclear antigen - fission yeast (Schizosaccharomyces pombe); (X54857) proliferating cell nuclear antigen [Schizosaccharomyces pombe] ; (AL035637) proliferating cell nuclear antigen [Schizosaccharomyces pombe] (AL034463) Xeropus 14s cohesin smc1 subunit homolog [Schizosaccharomyces pombe] "40S ribosomal protein S6 : ribosomal protein S6.e, cytosolic - fission yeast (Schizosaccharomyces pombe); (M36382) ribosomal protein S6 (rps6) precursor [Schizosaccharomyces pombe]; (Z54308) 40S ribosomal protein [Schizosaccharomyces pombe]"
19180	ENU02974	ANI61C3990:	72.91	802-825	NAP	797..2	g4007792	716	287	6.00E-77	60	20	(AJ012752) maltose permease [Saccharomyces cerevisiae] (Z83828) AmMst-1 [Amanita muscaria]
19181	ENU02975	ANI61C2420:	44.63	778-797	NAP	876..81	g133980	591	136	2.00E-31	75	64	

Seq num	Seq id	Contig Source	Primer 3 pos	Primer 3 pos Basis	Selection Database Hit	aat	Blast Score	Blast Prob	% id	% cvrg	Description
19184	ENU02978	ANI61C4093:	56-75	792-811	NAP	g3929361	758	167	2.00E-67	75	NADH-ubiquinone oxidoreductase 23 KD subunit precursor (complex I-23KD) (Cl-23KD) ; (X95547)
19185	ENU02979	ANI61C7409:	55-75	793-812	NAP	g1679597	37	0.15			ferredoxin-like iron-sulfur subunit of mitochondrial complex I [Neurospora crassa] (Z50095) mannosidase [Agaricus bisporus]
19186	ENU02980	ANI61C3696:	54-73	793-812	NAP	g2996620	207	83	2.00E-15	32	91 lactone hydrolase [Acinetobacter sp. ADP1]; beta-ketoadipate enol-lactone hydrolase [Acinetobacter calcoaceticus]
19187	ENU02981	ANI61C8073:	22-46	761-780	NAP	g2435400	162	71	9.00E-12	34	55 (U80663) lipase LipA [Streptomyces cinnamoneus]
19188	ENU02982	ANI50C8867	50-69	787-808	NAP	g3334403	69	3.00E-11	53	99 vacuolar ATP synthase 16 KD proteolipid subunit (V-ATPase C-subunit); (AF008924) V-ATPase C-subunit [Aedes aegypti]	
19189	ENU02983	ANI61C8446:	47-68	783-806	NAP	g1654074	217	52	0.000005	35	53 (Y09021) fructosyl amino acid oxidase [Penicillium janthinellum]
19190	ENU02984	ANI61C4168:	53-76	793-812	NAP	g2134574	200	35	0.74	37	95 mucin - rhesus macaque (fragment); (U00483) mucin [Macaca mulatta]
19191	ENU02985	ANI61C1026	56-79	795-816	NAP	g1169871	956	211	2.00E-81	65	33 GCN20 protein ; GCN20 protein - yeast (Saccharomyces cerevisiae); (U19971) Gen20p [Saccharomyces cerevisiae]; (D50617) YFR009W [Saccharomyces cerevisiae]
19192	ENU02986	ANI61C7203:	38-57	779-798	NAP	g3193292	520	116	1.00E-25	42	66 (AF069298) similar to ATPases associated with various cellular activities (Pfam: A.A.A_hmm; score: 230.91) [Arabidopsis thaliana]" "cytochrome P450 52L9 (CYPL1A9) (alkane-inducible P450-ALK5-A); cytochrome P450 ALK5-A, alkane-inducible - yeast (Candida maltosa); (D12717) n-alkane inducible cytochrome P-450 [Candida maltosa]" (A010475) RNA helicase [Arabidopsis thaliana]
19194	ENU02988	ANI61C6305:	23-42	765-784	NAP	g3776027	624	107	6.00E-38	45	31
			82..885								

Seq num	Seq id	Contig Source	Primer 3 pos	Primer Basis	Selection Database Hit	aat	Blast Score	Blast Prob	% id	% cvrg	Description	
19195	ENU02989	ANi61C8325:	23.45	NAP	g4455301	337	88	7.00E-22	45	87	(AL035528) putative protein [Arabidopsis thaliana]	
19196	ENU02990	ANi61C2426:	22.41	NAP	g1723231	229	114	7.00E-25	36	92	hypothetical 27.1 KD protein C1D4.09C in chromosome I; (Z69239)	
			1175..371								unknown [Schizosaccharomyces pombe] (U81790) PiG8 [Uromyces fabae]	
19197	ENU02991	ANi61C1087:	52-71	790-814	NAP	g1764133	346	115	4.00E-25	36	94	
19198	ENU02992	ANi61C3686:	64-83	807-827	NAP	g126066	230	83	3.00E-15	35	52	L-lactate dehydrogenase (LDH); L-lactate dehydrogenase (EC 1.1.1.27) chain Ldh1 - maize ; (Z11754) lactate dehydrogenase [Zea mays]
19199	ENU02993	ANi61C9004:	56-75	798-820	NAP	g2507431	967	266	2.00E-70	48	55	"phenylalanyl-tRNA synthetase mitochondrial precursor (phenylalanine--tRNA ligase) (PHERS) ; phenylalanine--tRNA ligase (EC 6.1.1.20) alpha chain precursor, mitochondrial - yeast (Saccharomyces cerevisiae) ; (Z49219) Msf1p [Saccharomyces cerevisiae]; (Z71255) Msf1p [Saccharomyces cerevisiae]" "(AF050353) alpha 1,2-mannosidase [Spodoptera frugiperda]" (AL022117) hypothetical protein [Schizosaccharomyces pombe] (AC006069) similar to yeast ccc1 protein [Arabidopsis thaliana]
19200	ENU02994	ANi61C9827:	37-57	766-801	NAP	g2245570	205	84	5.00E-16	36	23	putative dioxygenase YLL057C; hypothetical protein YLL057c - yeast (Saccharomyces cerevisiae); (Z47973) ORF L0572 [Saccharomyces cerevisiae]; (Z73162) ORF YLL057c [Saccharomyces cerevisiae]
19201	ENU02995	ANi61C1114:	63-87	808-828	NAP	g2959376	980	203	1.00E-51	56	68	
19202	ENU02996	ANi61C8366:	35-54	782-801	NAP	g4220472	301	73	2.00E-23	34	98	
19203	ENU02997	ANi61C1234:	49-68	786-815	NAP	g2497056	586	123	1.00E-27	41	56	
			3091..2283								homolog [Kaposi's sarcoma-associated herpesvirus] ; (U75698) ORF 73; extensive acidic domains, potential leucine zipper; immediate early protein homolog [Kaposi's sarcoma-associated herpesvirus]"	
19204	ENU02998	ANi61C5032:	37-58	778-804	NAP	g1633572	115	47	0.0002			
			1371..2180									

Seq num	Seq id	Contig Source	5 pos	Primer 3 pos	Primer Basis	Selection Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19205	ENU02999	ANI61C8256:	41-60	790-809	NAP	g2497179	145	57	2	0.000000	28	18	hypothetical 113-2 KD protein in SSO2-HSC82 intergenic region ; hypothetical protein YMR185w - yeast (Saccharomyces cerevisiae) ; (Z49808) unknown [Saccharomyces cerevisiae]
19206	ENU03000	ANI61C45:26	33-53	782-801	NAP	g125886	657	181	5.00E-45	41	67	lactate 2-monoxygenase (lactate oxidase) ; lactate 2-monoxygenase (EC 1.13.12.4) - Mycobacterium smegmatis ; (J05402) L-lactate 2-monoxygenase [Mycobacterium smegmatis]	
19207	ENU03001	ANI61C6754:	22-52	769-790	NAP	g1723578	652	266	2.00E-70	49	83	probable oxidoreductase C26F1.07 in chromosome 1 ; (Z73100) unknown [Schizosaccharomyces pombe] (AE001600) Hypothetical Protein [Chlamydia pneumoniae]	
19208	ENU03002	ANI61C6415:	58-77	809-828	NAP	g4376408	384	96	1.00E-30	36	64	"(AE000952) 2-hydroxyhepta-2,4-diene-1,7-dioate isomerase (hpcE-2) [Archaeoglobus fulgidus]"	
19209	ENU03003	ANI61C1054	29-50	780-799	NAP	g2648302	290	108	4.00E-32	46	79	succinyl-CoA transferase precursor; COA:3-ketoacid-coenzyme A transferase precursor (succinyl COA:3-oxoacid COA-transferase) (OXCT); (U62961) succinyl CoA:3-oxoacid CoA transferase precursor [Homo sapiens]	
19210	ENU03004	ANI61C6496:	24-57	776-795	NAP	g4557817	1234	250	7.00E-66	54	48	(Z98974) hypothetical protein [Schizosaccharomyces pombe] AFG1 protein ; AFG1 protein - yeast (Saccharomyces cerevisiae) ; (U18779) Afg1p [Saccharomyces cerevisiae] (AF003835) isopentenyl diphosphate:dimethylallyl diphosphate isomerase [Rattus norvegicus]	
19211	ENU03005	ANI61C4798:	41-62	793-812	NAP	g2388907	606	50	0.00002			alpha-glucoside transport protein - yeast [Saccharomyces cerevisiae] (AL049498) rho1 gdp-gtp exchange protein 1 [Schizosaccharomyces pombe]	
19212	ENU03006	ANI61C9801:	59-78	812-831	NAP	g416589	445	207	7.00E-53	42	49		
19213	ENU03007	ANI61C9149:	42-65	794-814	NAP	g2253701	524	90	1.00E-45	53	89		
19214	ENU03008	ANI61C7738:	65-91	810-837	NAP	g2146821	107	48	0.000000	29	32		
19215	ENU03009	ANI61C2364:	23-50	772-796	NAP	g4539279	867	259	1.00E-75	55	18		
		513..1328											

Seq num	Seq id	Contig Source	Primer 3 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat	Blast Score	Blast Score	% id	% cvrg	Description
19216	ENU03010	ANI61C1752:	55-74	809-828	NAP	g1723371	1081	406	e-113	63	51	hypothetical protein in CRTE 3'region (ORF2); (M87280) ORF2 [Erwinia herbicola]	
19217	ENU03011	ANI61C3291:	25-55	778-799	NAP	g1514667	331	104	1.00E-26	36	63	"(AF068712) similar to cytochrome P450 (Pfam: p450.hmm, score: 265.98) (X92509) crg1 [Ustilago maydis]	
19218	ENU03012	ANI61C6315:	46-75	801-820	NAP	g3168924	64	9.00E-10				[Caenorhabditis elegans] "	
19219	ENU03013	ANI61C7472:	55-72	813-832	NAP	g1709012	253	59	0.000000	34	55	microfibrillar-associated protein 1 ; microfibrillar protein MFAP1 - human ; (U04209) associated microfibrillar protein [Homo sapiens]	
19220	ENU03014	ANI61C9978:	40-59	794-818	NAP	g2645229	488	199	3.00E-50	40	55	(U78597) kinesin light chain [Plectonema boryanum]	
19221	ENU03015	ANI61C3973:	51-70	810-829	NAP	g544370	439	82	1.00E-30			GAR1 protein ; GAR1 protein - fission yeast (Schizosaccharomyces pombe) ; (Z19576) snoRNP protein GAR1 [Schizosaccharomyces pombe] ; (AB000537) snoRNP protein GAR 1 [Schizosaccharomyces pombe] ; (Z95397) Gar1p [Schizosaccharomyces pombe] ; (AL021747) gar1 protein; small nucleolar rnp required for pre-mma for pre-mma processing [Schizosaccharomyces pombe] "5-formyltetrahydrofolate cyclo-ligase (5,10-methenyl-tetrahydrofolate synthetase) (methenyl-THF synthetase) (MTHFS) ; indoleacetate-lysine synthetase (EC 6.3.2.20) - human ; (L38928) 5,10-methyltetrahydrofolate synthetase [Homo sapiens]" hypothetical 39.6 KD protein in MTDI-NUP133 intergenic region ; hypothetical protein YKR081c - yeast (Saccharomyces cerevisiae) ; (Z27116) ORF YKR401 [Saccharomyces cerevisiae] ; (Z28306) ORF YKR081c [Saccharomyces cerevisiae]	
19222	ENU03016	ANI61C1000	22-41	777-800	NAP	g1706921	173	81	1.00E-14	36	99		
19223	ENU03017	ANI61C406:9	39-58	798-818	NAP	g549638	500	171	4.00E-42	38	77		
		57..136											

ફોર્મ ફોર્મ વાર્ષિક ફોર્મ નું કોર્પોરેશન ફોર્મ નું

Seq num	Seq id	Contig Source	Primer 3 pos	Primer 3 pos	Selection Basis	Database Hit	nebi gi	aat	Blast Score	Blast Prob	% id	% cvrg	Description
19224	ENU03018	ANI61C8156:	67-86	826-846	NAP	g452120			64	2.00E-15			(L28112) complete cds [Rattus norvegicus]
19225	ENU03019	ANI61C6265:	25-46	785-805	NAP	g2326188	622	182	4.00E-49	43	79		(U81606) mixed-linked glucanase precursor [Cochliobolus carbonum]
19226	ENU03020	ANI61C8257:	40-59	799-820	NAP	g1175386	245	77	2.00E-13	30	78		hypothetical 37.7 KD protein C18B11.06 in chromosome I; hypothetical protein SPAC18B11.06 - fission yeast (Schizosaccharomyces pombe); (Z50728) hypothetical protein [Schizosaccharomyces pombe] (D64004) hypothetical protein
19227	ENU03021	ANI61C8772:	43-62	796-823	NAP	g1208451	347	129	2.00E-29	32	67		[Synechoctysis sp.]
19228	ENU03022	ANI61C7523:	22-41	784-803	NAP	g1078634	1309	281	e-130	98	36		sepB protein - Emericella nidulans ; sepB protein - [Emericella nidulans ; (X86399) sepB [Emericella nidulans ; probable membrane protein YPR011c - yeast [Saccharomyces cerevisiae]; (Z49919) unknown [Saccharomyces cerevisiae]; (U31900) Lpz1lp [Saccharomyces cerevisiae]; (Z71255) unknown [Saccharomyces cerevisiae] (AB016066) mitochondrial phosphate transporter [Arabidopsis thaliana] (X78712) glycerol kinase [Homo sapiens] (AF020040) xylose reductase [Pichia guilliermondii] (Z93941) YuxA [Bacillus subtilis]; (Z99120) alternate gene name: yvxA; similar to retinol dehydrogenase [Bacillus subtilis]]
19229	ENU03023	ANI61C5260:	22-50	770-804	NAP	g1362406	531	131	8.00E-30	46	65		(Z49919) unknown [Saccharomyces cerevisiae]; (U31900) Lpz1lp [Saccharomyces cerevisiae]; (Z71255) unknown [Saccharomyces cerevisiae] (AB016066) mitochondrial phosphate transporter [Arabidopsis thaliana] (X78712) glycerol kinase [Homo sapiens] (AF020040) xylose reductase [Pichia guilliermondii] (Z93941) YuxA [Bacillus subtilis]; (Z99120) alternate gene name: yvxA; similar to retinol dehydrogenase [Bacillus subtilis]]
19230	ENU03024	ANI61C1027	22-50	786-805	NAP	g3318617	537	140	3.00E-52	64	71		(AB016066) mitochondrial phosphate transporter [Arabidopsis thaliana] (X78712) glycerol kinase [Homo sapiens] (AF020040) xylose reductase [Pichia guilliermondii] (Z93941) YuxA [Bacillus subtilis]; (Z99120) alternate gene name: yvxA; similar to retinol dehydrogenase [Bacillus subtilis]]
19231	ENU03025	ANI61C1491:	40-61	806-825	NAP	g516124	1027	109	2.00E-32	43	43		(Z93941) YuxA [Bacillus subtilis]; (Z99120) alternate gene name: yvxA; similar to retinol dehydrogenase [Bacillus subtilis]]
19232	ENU03026	ANI61C7207:	62-81	828-847	NAP	g4103055	827	146	1.00E-73	59	80		(PPE) (RPE); POS18 protein - yeast (Saccharomyces cerevisiae); (X83571) Ribulose-5-Phosphate-Epimerase [Saccharomyces cerevisiae]; (Z49396) ORF YJL121c [Saccharomyces cerevisiae]
19233	ENU03027	ANI61C1024	31-52	798-817	NAP	g2624002	213	101	7.00E-21	31	85		(AC004218) unknown protein [Arabidopsis thaliana]
19234	ENU03028	ANI61C9660:	67-86	834-853	NAP	g1173139	546	105	1.00E-50	55	86		ribulose-phosphate 3-epimerase (pentose-5-phosphate 3-epimerase) (PPE) (RPE); POS18 protein - yeast (Saccharomyces cerevisiae); (X83571) Ribulose-5-Phosphate-Epimerase [Saccharomyces cerevisiae]; (Z49396) ORF YJL121c [Saccharomyces cerevisiae]
19235	ENU03029	ANI61C2864	70-89	836-856	NAP	g3355474	359	148	3.00E-35	32	65		(AC004218) unknown protein [Arabidopsis thaliana]

Seq num	Seq id	Contig Source	Primer 3 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat	Blast Score	Blast Prob	% id	% cvrg	Description
19236	ENU03030	ANI61C1875:	54-74	822-841	NAP	g4539944	218	76	1.00E-20	38	61	(AFI33841) aldose reductase	
			33..862									[ALDRXV4 [Xerophyta viscosa]	
19237	ENU03031	ANI61C819:2	23-53	790-810	NAP	g1477466	612	128	2.00E-57	50	44	(U35246) vacuolar protein sorting homolog h-vps45 [Homo sapiens]	
19238	ENU03032	ANI61C1128	22-51	792-811	NAP	g2047309	71	1.00E-11				(U44750) NAD-dependent 15-hydroxyprostaglandin dehydrogenase [Rattus norvegicus]	
19239	ENU03033	ANI61C3329:	27-55	786-816	NAP	g3184115	646	111	5.00E-24	29	52	(AL023780) DNA binding protein [Schizosaccharomyces pombe]	
19240	ENU03034	ANI61C3763:	43-62	811-833	NAP	g1351714	297	71	1.00E-11	31	50	(Z68166) unknown putative transporter C11D3.18C;	
19241	ENU03035	ANI61C3280:	22-41	786-813	NAP	g603587	1340	404	e-112	70	58	[Schizosaccharomyces pombe] (X83512) Ynlp [Saccharomyces cerevisiae]	
19242	ENU03036	ANI61C7044:	64-83	835-855	NAP	g731638	1109	380	e-105	65	50	"asparaginyl-tRNA synthetase, cytoplasmic (asparagine--tRNA ligase) (ASNRS); hypothetical protein YHR019c - yeast (Saccharomyces cerevisiae); (U10399) Dct81p: Asparaginyl-tRNA synthetase [Saccharomyces cerevisiae]" (AB000704) ribosomal protein S11 homolog [Schizosaccharomyces pombe]	
19243	ENU03037	ANI61C1058	46-66	818-838	NAP	g1813337	491	159	2.00E-38	82	71	pisatin demethylase (cytochrome P450 57A1); pisatin demethylase - fungus (Nectria haematococca); (L20976) pisatin demethylase [Nectria haematococca mpV1]	
			9.6360..7537									(U59215) cyclin-dependent protein kinase PHO4(M1) [Emericella nidulans]	
19244	ENU03038	ANI61C7997:	22-53	792-815	NAP	g3929362	292	114	7.00E-25	40	36	pisatin demethylase (cytochrome P450 57A1); pisatin demethylase - fungus (Nectria haematococca); (L20976) pisatin demethylase [Nectria haematococca mpV1]	
19245	ENU03039	ANI61C1048	35-56	808-829	NAP	g3643644	1098	194	9.00E-82	70	59	(U59215) cyclin-dependent protein kinase PHO4(M1) [Emericella nidulans]	
19246	ENU03040	ANI61C566:1	50-69	823-844	NAP	g731801	269	66	4.00E-25	32	80	36.7 KD protein in CBR5-NOT3 intergenic region ; hypothetical protein YIL041w - yeast (Saccharomyces cerevisiae); (Z40861) unknown [Saccharomyces cerevisiae]	
19247	ENU03041	ANI61C6225:	30-49	802-825	NAP	g4539334	36	0.27				(AL035539) putative protein [Arabidopsis thaliana]	
19248	ENU03042	ANI61C2571:	45-64	821-840	NAP	g2880049	251	126	2.00E-28	35	54	(AC002240) hypothetical protein [Arabidopsis thaliana]	
			858..21										

Seq num	Seq id	Contig Source	Primer 3 pos	Primer 3 pos	Selection Basis	Database Hit	nebi gi	aat	Blast Score	Blast Prob	% id	% cvrg	Description
19249	ENU03043	ANI50C346_	65-87	835-860	NAP	g731285		66	4.00E-10	35	81		hypothetical 27.1 KD protein in ACS1-GCV3 intergenic region ; hypothetical protein YAL049c - yeast (Saccharomyces cerevisiae) ; (U12980) Yal049cp [Saccharomyces cerevisiae] probable membrane protein YOR378w - yeast (Saccharomyces cerevisiae) ; (Z75286) ORF YOR378w [Saccharomyces cerevisiae]
19250	ENU03044	ANI61C3044:	40-60	816-835	NAP	g2132957	310	66	4.00E-10	29	47		(AL035216) probable involvement in ergosterol biosynthesis
19251	ENU03045	ANI61C8498:	43-62	806-839	NAP	g4160344	682	264	5.00E-70	48	54		[Schizosaccharomyces pombe] DNA-binding protein arndA - Emericella nidulans ; (L28810) regulatory protein [Emericella nidulans]
19252	ENU03046	ANI61C7244:	62-81	830-858	NAP	g2133268	575	112	4.00E-49	41	31		hypothetical 35.9 KD protein C56F8.03 in chromosome I ; (Z69728) unknown [Schizosaccharomyces pombe] (Z98943) hypothetical protein Rv1533 [Mycobacterium tuberculosis] hypothetical oxidoreductase in PTA-ROCC intergenic region ; hypothetical protein - Bacillus subtilis ; (X73124) ipa-82d [Bacillus subtilis] ; (Z99123) alternate gene name: ipa-82d; similar to glucose 1-dehydrogenase [Bacillus subtilis]
19253	ENU03047	ANI61C1118	23-58	801-820	NAP	g1723440	608	204	8.00E-52	50	74		(D63916) protein phosphotase 2A 65kD regulatory subunit (A subunit) [Schizosaccharomyces pombe] (AL031534) Major facilitator superfamily protein
19254	ENU03048	ANI61C4142:	22-56	788-819	NAP	g2370322	220	87	1.00E-16	32	70		[Schizosaccharomyces pombe] (Z98943) hypothetical protein Rv1533 [Mycobacterium tuberculosis]
19255	ENU03049	ANI61C9321:	33-52	811-830	NAP	g732372	202	97	1.00E-19	33	66		hypothetical oxidoreductase in PTA-ROCC intergenic region ; hypothetical protein - Bacillus subtilis ; (X73124) ipa-82d [Bacillus subtilis] ; (Z99123) alternate gene name: ipa-82d; similar to glucose 1-dehydrogenase [Bacillus subtilis]
19256	ENU03050	ANI61C1077	48-72	826-845	NAP	g1235752	1535	215	2.00E-69	65	38		(D63916) protein phosphotase 2A 65kD regulatory subunit (A subunit) [Schizosaccharomyces pombe] (AL031534) Major facilitator superfamily protein
19257	ENU03051	ANI61C4209:	64-83	842-862	NAP	g3560142	454	160	1.00E-38	32	45		[Schizosaccharomyces pombe] putative cytochrome C1 heme lyase (CCHL) ; (Z98601) cytochrome c1 heme lyase [Schizosaccharomyces pombe]
19258	ENU03052	ANI61C2329:	42-61	814-840	NAP	g3183375	284	161	8.00E-39	47	95		
			3142..2302										

Seq num	Seq id	Contig Source	Primer 3 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat	Blast Score	Blast Prob	% id	% cvrg	Description
19259	ENU03053	ANI50C1079	32-51	811-830	NAP	g134966		I53	1.00E-36	37	27	"STE6 protein ; ste6 protein - fission yeast (Schizosaccharomyces pombe) ; (X53254) ste6 [Schizosaccharomyces pombe] ; (AL049559) guanine-nucleotide releasing factor, Ste6p [Schizosaccharomyces pombe] ; ste6 gene [Schizosaccharomyces pombe]"	
19260	ENU03054	ANI61C7943:	28-47	799-827	NAP	g632081		I03	1.00E-21				hypothetical protein 4 - Xanthobacter sp ; (X79863) orf4 [Xanthobacter sp. Py2]
19261	ENU03055	ANI61C8446:	47-68	823-846	NAP	g1654074	217	S2	0.000005	34	55	[Penicillium janthinellum]	putative dioxygenase YLL057C; hypothetical protein YLL057c - yeast (Saccharomyces cerevisiae); (Z47973) ORF L0572 [Saccharomyces cerevisiae]; (Z7362) ORF YLL057c
19262	ENU03056	ANI61C4954:	39-59	820-839	NAP	g2497056	327	I05	8.00E-24	31	60		
19263	ENU03057	ANI61C2666:	45-64	826-845	NAP	g130971	531	I93	1.00E-48	47	93	[Saccharomyces cerevisiae] pyrroline-5-carboxylate reductase (PSCR) (PSC_reductase) ; pyrroline-5-carboxylate reductase (EC 1.5.1.2) precursor - Pseudomonas aeruginosa (strain PAO) ; (M33557) delta-1-pyrroline-5-carboxylate reductase (EC 1.5.1.2) [Pseudomonas aeruginosa] (D30688) cytochrome P-450 17 alpha-hydroxylase/C17,20-lyase [Equus caballus]	(Y09021) fructosyl amino acid oxidase [Penicillium janthinellum] " (Z99113) endo-1,4-beta-xylanase (xylanase D) [Bacillus subtilis]" lactate 2-monoxygenase (lactate oxidase) ; lactate 2-monoxygenase (EC 1.13.12.4) - Mycobacterium smegmatis ; (I05402) L-lactate 2-monoxygenase [Mycobacterium smegmatis] (AL023634) cyclin
19268	ENU03062	ANI61C3172:	33-54	818-837	NAP	g3150260	169	S7	1.00E-10	28	71	[Schizosaccharomyces pombe]	
			1727..881										

Seq num	Seq id	Contig Source	Primer 3 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	Score	Score Prob	% id	% cvrg	Description
19269	ENU03063	ANI61C2645:	22-49	805-826	NAP	g2132011	501	208	5.00E-53	42	94	hypothetical protein YOL080c - yeast (Saccharomyces cerevisiae); (Z74822) ORF YOL080c [Saccharomyces cerevisiae]
19270	ENU03064	ANI61C1036	58-80	838-864	NAP	g3334212	1108	235	5.00E-97	65	82	delta-aminolevulinic acid dehydratase (porphobilinogen synthase) (ALADH); (AF038566) porphobilinogen synthase [Candida glabrata] (AL032639) predicted using Genefinder; similar to iron-containing alcohol dehydrogenases; cDNA EST yk372c11.5 comes from this gene; cDNA EST yk304d8.3 comes from this gene; cDNA EST yk304d8.5 comes from this gene; cDNA EST yk26... UTR2 protein - yeast (Saccharomyces cerevisiae); (U18779) Utr2p [Saccharomyces cerevisiae]
19271	ENU03065	ANI61C6401:	22-54	809-829	NAP	g3880867	728	217	1.00E-55	56	56	hypothetical protein YOL080c - yeast (AF038566) porphobilinogen synthase [Candida glabrata]
19272	ENU03066	ANI61C5735:	22-46	807-829	NAP	g320712	418	159	2.00E-38	31	60	hypothetical protein 42.4 KD protein in CDC12-ORC6 intergenic region; hypothetical protein YHR112c - yeast (Saccharomyces cerevisiae); (U00059) Yhr112cp [Saccharomyces cerevisiae] "mitogen-activated protein kinase HOG1 (MAP kinase HOG1)" (osmosensing protein HOG1); protein kinase HOG1 (EC 2.7.1.-), mitogen-activated - yeast (Saccharomyces cerevisiae); (X89514) mitogen-activated protein kinase [Saccharomyces cerevisiae]; (Z73285) ORF YLR113w [Saccharomyces cerevisiae]" hypothetical 36.7 KD protein C2F7.14C in chromosome I; hypothetical protein SPAC2F7.14c - fission yeast (Schizosaccharomyces pombe); (Z50142) unknown [Schizosaccharomyces pombe]
19273	ENU03067	ANI61C8613:	27-47	800-834	NAP	g731700	817	252	3.00E-66	47	71	
19274	ENU03068	ANI61C8213:	23-54	805-830	NAP	g2507192	584	158	5.00E-38	63	47	
19275	ENU03069	ANI61C8076:	36-55	817-845	NAP	g1175376	475	184	6.00E-46	54	67	
852..1												

Seq num	Seq id	Contig Source	Primer 3 pos	Primer Basis	Selection	Blast at	Blast at	% id	% cvrg	Description		
					Database Hit	ncbi gi	Score	Prob				
19276	ENU03070	ANI61C1075	59..78	NAP	g285211	366	128	4.00E-29	40	"[3-methyl-2-oxobutanoate dehydrogenase (lipoamide)] kinase (EC 2.7.1.115) - rat ; branched-chain alpha-ketoacid dehydrogenase kinase 44 kda isoform [rat, lung, heart, Peptide Mitochondrial, 412 aa] ; (M93271) branched-chain alpha-ketoacid dehydrogenase kinase [Rattus norvegicus]"		
19277	ENU03071	ANI61C1018	52..71	842..864	NAP	g4007783	320	85	7.00E-26	37	"(X72850) hydroxyquinol 1,2-dioxygenase [Sphingomonas sp.]"	
19278	ENU03072	ANI61C5164:	40..59	834..853	NAP	g1169885	966	314	7.00E-85	65	"putative glycine dehydrogenase (decarboxylating) precursor (glycine decarboxylase) (glycine cleavage system P-protein) ; hypothetical protein SPAC13G6.06c - fission yeast (Schizosaccharomyces pombe) ; (Z54308) putative glycine dehydrogenase (decarboxylase) [Schizosaccharomyces pombe] (Z64354) unknown [Schizosaccharomyces pombe] (Y13633) Vip1 protein [Schizosaccharomyces pombe] ; (AL009197) hypothetical protein [Schizosaccharomyces pombe] hypothetical protein 4 - Xanthobacter sp ; (X79863) orf4 [Xanthobacter sp. Py2] (Z92954) product highly similar to metabolite transport proteins [Bacillus subtilis] ; (Z99122) similar to metabolite transport protein [Bacillus subtilis]"	
19279	ENU03073	ANI61C8668:	58..77	849..871	NAP	g4160354	274	119	3.00E-26	31	"(Z64354) unknown [Schizosaccharomyces pombe] (Y13633) Vip1 protein [Schizosaccharomyces pombe] ; (AL009197) hypothetical protein [Schizosaccharomyces pombe] hypothetical protein 4 - Xanthobacter sp ; (X79863) orf4 [Xanthobacter sp. Py2] (Z92954) product highly similar to metabolite transport proteins [Bacillus subtilis] ; (Z99122) similar to metabolite transport protein [Bacillus subtilis]"	
19280	ENU03074	ANI61C1132:	24..43	819..838	NAP	g2190516	224	99	3.00E-20	34	"(Y13633) Vip1 protein [Schizosaccharomyces pombe] ; (AL009197) hypothetical protein [Schizosaccharomyces pombe] hypothetical protein 4 - Xanthobacter sp ; (X79863) orf4 [Xanthobacter sp. Py2] (Z92954) product highly similar to metabolite transport proteins [Bacillus subtilis] ; (Z99122) similar to metabolite transport protein [Bacillus subtilis]"	
19281	ENU03075	ANI61C1081	6..1297..2153	37..56	832..851	NAP	g632081	285	87	2.00E-23	41	"(Y13633) Vip1 protein [Schizosaccharomyces pombe] ; (AL009197) hypothetical protein [Schizosaccharomyces pombe] hypothetical protein 4 - Xanthobacter sp ; (X79863) orf4 [Xanthobacter sp. Py2] (Z92954) product highly similar to metabolite transport proteins [Bacillus subtilis] ; (Z99122) similar to metabolite transport protein [Bacillus subtilis]"
19282	ENU03076	ANI61C3713:	943..87	53..72	846..867	NAP	g1894771	362	135	3.00E-31	31	"hypothetical 23.2 KD protein C5D6.06C in chromosome I ; (Z98056) putative osmotolerance protein [Schizosaccharomyces pombe]"
19283	ENU03077	ANI61C539:2	464..2568	28..47	823..842	NAP	g3183310	235	112	3.00E-24	46	"hypothetical 23.2 KD protein C5D6.06C in chromosome I ; (Z98056) putative osmotolerance protein [Schizosaccharomyces pombe]"

Seq num	Seq id	Contig Source	Primer 3 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19284	ENU03078	ANI61C1029:	51-70	838-866	NAP	g1175915	189	64	7.00E-14	44	44	44	hypothetical 28.8 KD protein in SMC1-SEC4 intergenic region ; probable membrane protein YFL006W - yeast (Saccharomyces cerevisiae) ; (D50617) YFL006W [Saccharomyces cerevisiae] ; (D44604) unknown [Saccharomyces cerevisiae]
19285	ENU03079	ANI61C3377:	22-49	816-837	NAP	g3192044	226	86	3.00E-16	36	80	80	(AL023796) hypothetical protein [Schizosaccharomyces pombe]
19286	ENU03080	ANI61C683:1	22-51	814-837	NAP	g134777	248	128	6.00E-29	29	84	84	stage V sporulation protein K ; spoVJ [Bacillus subtilis] (Y13623) multifunctional protein2
19287	ENU03081	ANI61C1140	43-63	840-859	NAP	g3005897	338	175	4.00E-43	34	38	38	[Cavia porcellus] (Y09021) fructosyl amino acid oxidase [Penicillium janthinellum]
19288	ENU03082	ANI61C7321:	61-80	858-878	NAP	g1654074	240	118	5.00E-26	29	57	57	ubiquinol-cytochrome C reductase iron-sulfur subunit precursor (Rieske iron-sulfur protein) (RISP) ; ubiquinol-cytochrome-c reductase (EC 1.10.2.2) iron-sulfur protein - Neurospora crassa ; (X02472) cytochrome c reductase iron-sulfur protein [Neurospora crassa]
19289	ENU03083	ANI61C9902:	70-89	869-888	NAP	g136704	666	162	1.00E-47	66	85	85	branched-chain amino acid aminotransferase (BCAT) ; (AE000647) branched- $\alpha$ -chain-amino-acid aminotransferase (ilvE) [Helicobacter pylori 26695] (AF133841) aldose reductase ALDRXV4 [Xerophyta viscosa] probable adenosine deaminase (adenosine aminohydrolase) ; adenosine deaminase homolog YNL141w - yeast (Saccharomyces cerevisiae) ; (Z46843) adenosine deaminase (putative) [Saccharomyces cerevisiae] ; (Z71417) ORF YNL141w [Saccharomyces cerevisiae]
19290	ENU03084	ANI61C7849:	33-54	819-852	NAP	g3024012	404	184	6.00E-46	36	82	82	
19291	ENU03085	ANI61C1875:	54-74	854-873	NAP	g4539944	218	76	1.00E-20	37	65	65	
19292	ENU03086	ANI61C8984:	23-42	821-843	NAP	g1703166	704	218	4.00E-56	45	80	80	
			1974..1112										

Seq num	Seq id	Contig Source	Primer 3 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat	Blast Score	Blast Score	% id	% cvrg	Description
19293	ENU03087	ANI61C229:3	59-83	857-880	NAP	g549723	738	282	2.00E-75	54	39		
			436..2573										
19294	ENU03088	ANI61C6709:	58-76	853-879	NAP	g2104455	456	98	8.00E-38	48	77	(Z95397) unknown	
			3506..2643									[Schizosaccharomyces pombe]	
19295	ENU03089	ANI61C9444:	22-49	825-844	NAP	g1542843	397	162	4.00E-39	34	94	(D87681) acetyltransferase [Aspergillus awamori]	
			1599..735									[Plectonema boryanum]	
19296	ENU03090	ANI61C2926:	67-86	867-890	NAP	g2645229	457	129	3.00E-43	37	58	bimD protein - <i>Emericella nidulans</i> ; (L03200) bimD [Emericella nidulans]; (Z98979) putative phosphatidylserine decarboxylase proenzyme	
			4377..3210									[Schizosaccharomyces pombe]	
19297	ENU03091	ANI61C5745:	50-72	854-873	NAP	g1078626	1501	413	e-114	99	19	-yeast (Saccharomyces cerevisiae); (U20865) Yir241 wp [Saccharomyces cerevisiae]	
			29..894										
19298	ENU03092	ANI61C9795:	24-55	829-848	NAP	g2388966	1410	294	4.00E-79	52	27	probable membrane protein YLR241 w	
			3152..2286									-yeast (Saccharomyces cerevisiae); (U20865) Yir241 wp [Saccharomyces cerevisiae]	
19299	ENU03093	ANI61C3270:	22-43	828-847	NAP	g1363743	1110	168	6.00E-41	42	35	mannitol-1-phosphate 5-dehydrogenase ; (U18943) mannitol-1-phosphate dehydrogenase [Bacillus stearothermophilus]	
			1954..2821									(AE00105) acyl-CoA dehydrogenase (acd-9) [Archaeoglobus fulgidus]	
19300	ENU03094	ANI61C7067:	55-74	861-880	NAP	g2494101	628	237	9.00E-62	41	74	(U68040) polyketide synthase [Cochliobolus heterostrophus]	
			928..61									N amino acid transport system protein (methytryptophan resistance protein); neutral amino acid permease -	
19301	ENU03095	ANI61C3705:	53-72	852-878	NAP	g2649289	103	2.00E-21				Neurospora crassa; (L34605) neutral amino acid permease [Neurospora crassa]	
			2000..1133									(AL04950) T5C23.70 [Arabidopsis thaliana]	
19302	ENU03096	ANI61C1705:	27-52	825-852	NAP	g1546072	1002	112	4.00E-24	31	10		
			3803..4670										
19303	ENU03097	ANI61C322:1	26-45	834-853	NAP	g2507070	1257	299	2.00E-80	62	57		
			1819..12688										
19304	ENU03098	ANI61C1188:	24-48	832-852	NAP	g4539455	365	154	6.00E-37	40	69		
			9136..8271										

Seq num	Seq id	Contig Source	Primer 3 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat	Blast Score	Blast Score	% id	% cvrg	Description
19305	ENU03099	ANI61C9049:	22-52	827-850	NAP	g2500006	708	287	5.00E-77	52	99		formyltetrahydrofolate DEformylase (formyl-FH(4) hydrolyase); formyltetrahydrofolate deformylase (EC 3.5.1.10) - <i>Corynebacterium</i> sp ; (U23955) 10-formyltetrahydrofolate hydrolase [Corynebacterium sp.] (AL023777) coenzyme a synthetase [Schizosaccharomyces pombe] (AL022197) putative protein
19306	ENU03100	ANI61C2649:	64-86	869-892	NAP	g3184098	307	142	4.00E-33	33	53		[Arabidopsis thaliana] (AF034260) protein kinase NRC-2 [Neurospora crassa]
19307	ENU03101	ANI61C1190:	25-44	825-853	NAP	g2980795	379	90	3.00E-40	45	97		"ribosomal protein L31 e.B, cytosolic - yeast (Saccharomyces cerevisiae); (U19729) Ylr406cp; member of L31E ribosomal protein family [Saccharomyces cerevisiae]" (AL022304) eukaryotic translation initiation factor 3 rna-binding subunit [Schizosaccharomyces pombe]
19308	ENU03102	ANI61C3127:	40-72	849-869	NAP	g2654106	1056	228	e-111	79	41		yeast (Saccharomyces cerevisiae); (U19729) Ylr406cp; member of L31E ribosomal protein family [Saccharomyces cerevisiae]" (AL022304) eukaryotic translation initiation factor 3 rna-binding subunit [Schizosaccharomyces pombe]
19309	ENU03103	ANI61C1713:	31-49	840-860	NAP	g1084846	321	96	2.00E-19	68	40		vacuolar protein sorting-associated protein VPS16 ; vacuolar protein sorting-associated protein VPS16 - yeast (Saccharomyces cerevisiae); (U44030) Vsp16p; Vacuolar sorting protein [Saccharomyces cerevisiae] (AE000715) chorismate mutase/prephenate dehydratase [Aequifex aeolicus]
19310	ENU03104	ANI61C2402:	68-90	870-898	NAP	g3006180	545	121	8.00E-41	45	90		hypothetical 36.4 KD protein in SMP1-MBA1 intergenic region ; probable membrane protein YBR183w - yeast (Saccharomyces cerevisiae); (Z36052) ORF YBR183w [Saccharomyces cerevisiae] ; (U02073) unknown [Saccharomyces cerevisiae] (AL022072) arginine n-methyltransferase
19311	ENU03105	ANI61C5793:	33-57	843-863	NAP	g2507153	123	57	2.00E-10	24	33		[Schizosaccharomyces pombe]
19312	ENU03106	ANI61C212:2	22-53	833-852	NAP	g2983461	139	2.00E-32					[Schizosaccharomyces pombe]
19313	ENU03107	ANI61C1730:	39-59	851-870	NAP	g586314	199	47	3.00E-12	30	66		membrane protein YBR183w - yeast (Saccharomyces cerevisiae); (Z36052) ORF YBR183w [Saccharomyces cerevisiae] ; (U02073) unknown [Saccharomyces cerevisiae] (AL022072) arginine n-methyltransferase
19314	ENU03108	ANI61C8793:	24-51	836-855	NAP	g4008547	745	145	3.00E-47	42	55		[Schizosaccharomyces pombe] (AF052586) beta-ketoacyl reductase [Pseudomonas aeruginosa]
19315	ENU03109	ANI61C6738:	22-49	832-854	NAP	g2970667	293	101	6.00E-21	35	73		

નુક્સાન કરી શકતી હોય એવી વિધાની પ્રદૂષણીય વિધાની પ્રદૂષણીય

Seq num	Seq id	Contig Source	Primer 3 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat	Blast Score	Blast Prob	% id	% cvrg	Description
19316	ENU03110	ANI61C6877:	22-46	827-854	NAP	g3724291	64	8.00E-16					(AB011417) phosphate permease [Gibberella zae]
1.875													
19317	ENU03111	ANI61C9103:	23-46	836-855	NAP	g2951785	248	66	3.00E-11	41	95		(AB011822) clathrin light chain [Schizosaccharomyces pombe]
120..995													
19318	ENU03112	ANI61C1065	24-46	837-856	NAP	g3881189	413	103	1.00E-21	52	98		(Z99281) similar to ADP-ribosylation factor; cDNA EST EMBL:C08179 comes from this gene; cDNA EST EMBL:C08337 comes from this gene; cDNA EST EMBL:C09829 comes from this gene; cDNA EST yk291b4.5 comes from this gene; cDNA EST yk4...
2.2656..1781													
19319	ENU03113	ANI61C4534:	59-78	865-892	NAP	g4164400	574	93	2.00E-18	36	41		(AL035248) putative cell surface protein by similarity
2584..3459													
19320	ENU03114	ANI61C9963:	22-46	834-855	NAP	g585956	397	108	5.00E-28	34	95		[Schizosaccharomyces pombe] "probable mitochondrial 40S ribosomal protein S9 precursor ; mitochondrial protein S9 precursor ; ribosomal yeast (Saccharomyces cerevisiae); (Z36015) ORF YBR146w [Saccharomyces cerevisiae]"
1350..2225													
19321	ENU03115	ANI61C2000:	43-70	841-876	NAP	g585695	70	2.00E-11					pisatin demethylase (cytochrome P450 57A2); pisatin demethylase - fungus ( <i>Nectria haematococca</i> ); (X73145) pisatin demethylase [ <i>Nectria haematococca</i> ]
422..1297													

Seq num	Seq id	Contig Source	Primer 3 pos	Primer 3 pos	Selection Basis	Database Hit	aat	Blast Score	Blast Score	% id	% cvrg	Description
19322	ENU03116	ANI50C5234	28-50	843-862	NAP	g1170012	334	6.00E-91				UDP-N-acetylglucosamine-dolichyl-phosphate N-
			_1:1735..859									acetylglucosamineprophosphotransferase (GPT) (G1PT) (N-acetylglucosamine-1-phosphate transferase) (GLCNAC-1-P transferase); UDP-N-acetylglucosamine-dolichyl-phosphate N-
												acetylglucosamineprophosphotransferase (EC 2.7.8.15) - fission yeast (Schizosaccharomyces pombe); (U09454) UDP-N-acetylglucosamine:dolichyl phosphate N-acetylglucosamine-1-phosphate transferase [Schizosaccharomyces pombe]; (AL031349) N-acetylglucosamine-1-phosphate transferase [Schizosaccharomyces pombe]
19323	ENU03117	ANI61C9036:	22-50	837-856	NAP	g2132491	210	78	2.00E-24	33	81	probable membrane protein YDR284c - yeast (Saccharomyces cerevisiae); (U51031) Ydr284cp [Saccharomyces cerevisiae]
19324	ENU03118	ANI61C1093	22-51	835-856	NAP	g286165	498	217	6.00E-56	41	96	"D14846" endo alpha-1,4 polygalactosaminidase precursor [Pseudomonas sp.] "
19325	ENU03119	ANI61C2150:	70-89	881-904	NAP	g1723784	264	75	7.00E-13	38	88	hypothetical 31.3 KD protein in TAF145-YOR1 intergenic region; hypothetical protein YGR280c - yeast (Saccharomyces cerevisiae); (Z73065) ORF YGR280c [Saccharomyces cerevisiae]
19326	ENU03120	ANI61C8019:	66-85	874-903	NAP	g4154817	955	300	4.00E-87	61	86	(AE001466) putative [Helicobacter pylori]_199
19327	ENU03121	ANI61C5895:	23-46	841-860	NAP	g4490676	643	121	6.00E-63	68	98	(AL025655) ras-related protein [Schizosaccharomyces pombe]

Seq num	Seq id	Contig Source	Primer 3 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat	Blast Score	Blast Prob	% id	% cvrg	Description
19328	ENU03122	ANI61C538:3	45-65	864-883	NAP	g2132846	476	175	5.00E-43	32	55	probable membrane protein YOL119c - yeast (Saccharomyces cerevisiae); (Z74861) ORF YOL119c	
19329	ENU03123	ANI61C1077	22-47	837-860	NAP	g482365	426	175	4.00E-43	51	97	[Saccharomyces cerevisiae]; unknown protein [Saccharomyces cerevisiae]	
19330	ENU03124	ANI61C8:219	56-78	876-895	NAP	g130858	650	201	2.00E-59	-	-	protein-L-isoaspartate(D-aspartate) O-methyltransferase (EC 2.1.1.77) form II - bovine	
19331	ENU03125	ANI61C1097	72-91	887-911	NAP	g1086919	84	1.00E-15	-	-	-	proteasome component C7-alpha (macropain subunit C7-alpha) (proteinase YSC-E subunit 7) (multicatalytic endopeptidase complex C7) (component Y8) (SCL1 suppressor protein); multicatalytic endopeptidase complex (EC 3.4.99.46) chain YC7-alpha - yeast (Saccharomyces cerevisiae); (M63641) proteasome Y8 [Saccharomyces cerevisiae]; (M55440) yeast proteasome subunit YC7-alpha [Saccharomyces cerevisiae]; (X56732) proteasome Y8 subunit [Saccharomyces cerevisiae]; (Z72533) ORF YGL011c [Saccharomyces cerevisiae]; (S58126) Unknown [Saccharomyces cerevisiae]; proteasome PRS2 [Saccharomyces cerevisiae] (U41279) similar to E. coli acyl-CoA thioesterase II (SP:P23911) [Caenorhabditis elegans]	
19332	ENU03126	ANI61C8922:	63-82	881-904	NAP	g2499790	1425	388	e-107	98	94	antigen 1 precursor (ASPND1); (Z50175) Aspergillus nidulans antigen 1 [Emericella nidulans] (X98252) HA Vcr-1 protein [Chlorocebus aethiops]	
19333	ENU03127	ANI50C6641	40-59	862-881	NAP	g1526574	46	0.0002	-	-	-	-	

Seq num	Seq id	Contig	Source	Primer 3 pos	Primer 3 pos	Selection Basis	Database	Hit	ncbi gi	aat	Blast Score	Blast Prob	% id	% cvrg	Description
19334	ENU03128	ANI61C8587:	22-47	841-863	NAP			g731865	313	96	4.00E-19	26	50		KGD1-SIM1 intergenic region ; probable membrane protein YIL121w - yeast (Saccharomyces cerevisiae); (Z46833) unknown [Saccharomyces cerevisiae]
19335	ENU03129	ANI61C905:	22-50	843-864	NAP			g4336889	961	189	2.00E-78	97	92		(AF107254) cyclophilin B; CYPB [Emericella nidulans]
19336	ENU03130	ANI61C6956:	53-76	865-895	NAP			g1710852	786	189	2.00E-55	93	94		GTP-binding protein SARA ; (Z67742) sarA [Aspergillus niger] (AL032684) ER lumen protein retaining receptor protein [Schizosaccharomyces pombe] (AL031825) putative membrane transport protein
19337	ENU03131	ANI61C8618:	43-62	860-885	NAP			g4038630	523	122	1.00E-47	58	99		
19338	ENU03132	ANI61C1162:	71-90	882-913	NAP			g3702646	625	105	5.00E-25	34	47		[Schizosaccharomyces pombe] activator 1 41 KD subunit (replication factor C 41 KD subunit); replication factor C chain RFC2 - yeast (Saccharomyces cerevisiae); (D28499) Rfc2 protein [Saccharomyces cerevisiae]; (U26028) Rfc2p [Saccharomyces cerevisiae]; (Z49568) ORF YJR068w [Saccharomyces cerevisiae]; (L47993) ORF YJR068w [Saccharomyces cerevisiae]
19339	ENU03133	ANI61C9958:	47-66	871-890	NAP			g730502	721	277	1.00E-73				
			948..63												
19340	ENU03134	ANI61C7904:	22-46	846-865	NAP			g585304	596	188	5.00E-47				eIF-5 - yeast (Saccharomyces cerevisiae); (Z68111) Tif5p [Saccharomyces cerevisiae]; (Z71255) Tif5p [Saccharomyces cerevisiae]; (Z73616) eukaryotic translation initiation factor 5 [Saccharomyces cerevisiae]
			526..1411												

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19341	ENU03135	ANI61C873.2	2645	843-870	NAP	g1350594	699	136	5.00E-70	79	95	RHO1 protein ; Rho1 protein - fission yeast (Schizosaccharomyces pombe) ; hypothetical protein SPA.C1F7.04 - fission yeast (Schizosaccharomyces pombe) ; (D38180) Rho1 [Schizosaccharomyces pombe] ; (Z67998) unknown	
19342	ENU03136	ANI61C9705:	45-64	870-889	NAP	g642577	1691	592	e-169	99	94	(U19882) FlbD [Emericella nidulans] ; Myb-like DNA binding protein [Emericella nidulans]	
19343	ENU03137	ANI61C4397:	50-71	876-895	NAP	g4056553	514	145	3.00E-34	42	43	[AL014583] putative exonuclease "putative D-3-phosphoglycerate dehydrogenase YIL074W (pGDH) ; hypothetical protein YIL074c - yeast (Saccharomyces cerevisiae) ; (Z37997) orf; len: 469, CAL: 0.23, similar to SERA_ ECOLI P08328 D-3-	
19344	ENU03138	ANI61C7016:	38-61	858-884	NAP	g731830	1371	277	1.00E-81	66	51	phosphoglycerate dehydrogenase [Saccharomyces cerevisiae]" (D87444) Similar to S.cerevisiae EMP70 protein precursor (S25110) [Homo sapiens]	
19345	ENU03139	ANI61C7328:	43-63	870-889	NAP	g1665777	884	166	1.00E-48	44	41	haloacetate dehalogenase H-1 ; haloacetate dehalogenase (EC 3.8.1.3) H-1 - Moraxella sp. plasmid pUO1 ; (D90422) haloacetate dehalogenase H-1 [Moraxella sp.]	
19346	ENU03140	ANI61C8058:	72-91	888-918	NAP	g461925	408	188	4.00E-47	38	95	ribonucleoside-Diphosphate reductase M2 chain (ribonucleotide reductase) ; ribonucleoside-diphosphate reductase (EC 1.17.4.1) chain M2 - mouse ; Protein R2 Of Ribonucleotide Reductase From Mouse ; (X15666) M2 ribonucleotide reductase [Mus musculus] ; (M14223) ribonucleotide reductase subunit M2 [Mus musculus]	
19347	ENU03141	ANI61C8183:	25-50	853-872	NAP	g132626	877	182	2.00E-70				
			2180..3069										

Seq num	Seq id	Contig	Source	5 pos	Primer 3 pos	Primer Basis	Selection	aat	Blast Score	Blast Prob	% id	% cvrg	Description
							Database Hit	ncbi gi					
19348	ENU03142	ANI61C6083:	63-83	1014..124	892-911	NAP	g131771	473	179	4.00E-45	36	53	"probable metabolite transport protein GT1; probable membrane protein YCR098c - yeast (Saccharomyces cerevisiae); (X59720) YCR098c, len:518 [Saccharomyces cerevisiae]" putative transporter C11D3.18C; (Z68166) unknown
19349	ENU03143	ANI61C6144:	43-70	24..915	870-892	NAP	g1351714	134	8.00E-31				
19350	ENU03144	ANI61C7133:	35-54	2531..3422	865-884	NAP	g4104775	177	95	6.00E-19	28	70	[Schizosaccharomyces pombe] (AF039534) salicylate hydroxylase [Pseudomonas stutzeri]
19351	ENU03145	ANI61C5627:	53-80	952..61	882-902	NAP	g2493389	313	48	5.00E-13	30	45	probable sterigmatocystin biosynthesis P450 monooxygenase STCF (cytochrome P450 60A2); (U34740) putative p450 monooxygenase [Emericella nidulans]
19352	ENU03146	ANI61C1479:	53-75	1081..189	879-903	NAP	g134427	269	87	1.00E-16			
19353	ENU03147	ANI61C7638:	64-84	647..1540	886-915	NAP	g3336839	365	108	8.00E-23	28	44	tRNA-splicing endonuclease subunit SEN2 (tRNA-intron endonuclease); tRNA-splicing endonuclease beta chain - yeast (Saccharomyces cerevisiae); (M32356) tRNA splicing endonuclease beta-subunit [Saccharomyces cerevisiae]; (U53876) Sen2p: tRNA-splicing endonuclease beta-subunit [Saccharomyces cerevisiae]; (Z73277) ORF YLR105c [Saccharomyces cerevisiae] (Y16834) hexose transporter [Candida albicans]
19354	ENU03148	ANI61C5168:	26-45	2742..1848	857-878	NAP	g3820984	239	103	2.00E-21	36	91	"(AL031228) dJ1033B10.9 (Short-chain alcohol dehydrogenase family member (HKE6, RING2)) [Homo sapiens]"
19355	ENU03149	ANI61C7755:	63-87	123..1018	895-916	NAP	g173384	1021	185	3.00E-94	66	25	(L07734) DNA polymerase delta [Schizosaccharomyces pombe] (AL021839) topoisomerase ii associated protein [Schizosaccharomyces pombe] (U78319) chitinase [Entamoeba histolytica]
19356	ENU03150	ANI61C363..3	32-51	154..4049	864-885	NAP	g2894266	759	159	4.00E-41	35	35	
19357	ENU03151	ANI61C9942:	50-70	55..950	880-903	NAP	g1685362	459	179	3.00E-44	32	57	

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat	Blast Score	Blast Prob	% id	% cvrg	Description
19358	ENU03152	ANI61C7955:	57-76	893-912	NAP	g544276	1444	291	e-110	76	70	glutathione-dependent FORMaldehyde dehydrogenase (FDH) (FALDH); FDH1 protein - yeast (Candida maltosa); (M58332) encoding formaldehyde resistance [Candida maltosa]	
19359	ENU03153	ANI61C9825:	64-83	900-919	NAP	g3023753	328	138	7.00E-32	35	94	potential formate transporter; (U52681) FdhC [Methanobacterium thermoformicum]	
19360	ENU03154	ANI61C1073	43-62	879-898	NAP	g416643	770	153	1.00E-70	63	69	"aristolochene synthase (sesquiterpene cyclase) (AS); sesquiterpene cyclase, AS- aristolochene synthase, AS- Penicillium roqueforti; (L05193) aristolochene synthase [Penicillium roqueforti]" hypothetical 65.3 KD protein in SUN4-MA55 intergenic region ; probable membrane protein YNL065w- yeast (Saccharomyces cerevisiae); (U12141) membrane protein [Saccharomyces cerevisiae]; (Z71341) ORF YNL065w [Saccharomyces cerevisiae] (AF029913) beta glucosidase homolog [Cochliobolus heterostrophus] probable membrane protein YOL137w -yeast (Saccharomyces cerevisiae); (Z74879) ORF YOL137w [Saccharomyces cerevisiae]; (X95465) ORF [Saccharomyces cerevisiae] cytochrome B5 ; cytochrome b5 - yeast (Saccharomyces cerevisiae); (Z69382) Cytochrome B5 [Saccharomyces cerevisiae]; (Z71387) ORF YNL11c [Saccharomyces cerevisiae] (AB004538) probable membrane protein YOL130w	
19361	ENU03155	ANI61C5905:	61-85	890-916	NAP	g1730741	392	60	0.000000	25	47	[Schizosaccharomyces pombe]; (AL021766) hypothetical protein [Schizosaccharomyces pombe]	
19362	ENU03156	ANI61C1640:	49-68	883-904	NAP	g2583218	594	212	2.00E-54	51	21	[Schizosaccharomyces pombe]; (AF029913) beta glucosidase homolog [Cochliobolus heterostrophus] probable membrane protein YOL137w -yeast (Saccharomyces cerevisiae); (Z74879) ORF YOL137w [Saccharomyces cerevisiae]; (X95465) ORF [Saccharomyces cerevisiae] cytochrome B5 ; cytochrome b5 - yeast (Saccharomyces cerevisiae); (Z69382) Cytochrome B5 [Saccharomyces cerevisiae]; (Z71387) ORF YNL11c [Saccharomyces cerevisiae] (AB004538) probable membrane protein YOL130w	
19364	ENU03158	ANI61C9393:	22-45	861-880	NAP	g1706221	106	55	0.000000	25	66	[Schizosaccharomyces pombe]; (AL021766) hypothetical protein [Schizosaccharomyces pombe]	
19365	ENU03159	ANI61C6658:	22-50	847-880	NAP	g2257554	806	210	3.00E-81	57	34		
		1..901											

Seq num	Seq id	Contig Source	Primer 3 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat	Blast Score	Blast Prob	% id	% cvrg	Description
19366	ENU03160	ANI61C7097:	69-88	909-928	NAP	g1363775	295	136	2.00E-31	40	90	hypothetical protein YDR041w - yeast (Saccharomyces cerevisiae); (Z54075) unknown [Saccharomyces cerevisiae] (AL022554) 40s ribosomal protein s3.	
19367	ENU03161	ANI61C5156:	53-72	894-913	NAP	g3133108	648	182	4.00E-45	64	93	[Schizosaccharomyces pombe]	
19368	ENU03162	ANI61C7054:	22-49	864-883	NAP	g1749716	1313	367	e-101	60	58	"(D89254) similar to <i>Saccharomyces cerevisiae</i> dihydroxy-acid dehydratase precursor, SWISS-PROT Accession Number P39522 [Schizosaccharomyces pombe]" (AB016896) Pcu1	
19369	ENU03163	ANI61C7052:	47-68	883-911	NAP	g4587302	1541	226	2.00E-73	54	35	[Schizosaccharomyces pombe]	
19370	ENU03164	ANI61C1092	46-69	876-911	NAP	g131768	178	62	3.00E-14	28	33	quinate permease (quinate transporter); midulans; (X13525) quinate permease [Emericella nidulans] (AB004537) hypothetical 47.4KD protein in SHPI-SEC17 intergenic region [Schizosaccharomyces pombe]	
19371	ENU03165	ANI61C2278:	22-43	868-887	NAP	g2257524	396	161	5.00E-39	40	95	chromosome segregation protein SMC2 (DA-BOX protein SMC2); chromosome segregation protein SMC2 -yeast ( <i>Saccharomyces cerevisiae</i> ); (U05820) Smc2p [ <i>Saccharomyces cerevisiae</i> ]; (D50617) chromosome segregation protein SMC2p [ <i>Saccharomyces cerevisiae</i> ]; (D44602) DA-box protein Smc2p [ <i>Saccharomyces cerevisiae</i> ] (Z98979) hypothetical protein [Schizosaccharomyces pombe]	
19373	ENU03167	ANI61C1000	22-45	865-888	NAP	g2388953	350	113	3.00E-37	42	96		
			4:4856..5763										

Seq num	Seq id	Contig Source	Primer 3 pos	Primer Basis	Selection	aat	Blast Score	Blast Prob	% id	% cvrg	Description
			5 pos	Database	ncbi gi	Score	Score	e-140			
19374	ENU03168	ANI61C6610:	24-59	NAP	g464862	503	498				26S protease regulatory subunit 7 homolog (CIM5 protein) (TAT-binding homolog 3); tat-binding protein homolog YTA3 - yeast (Saccharomyces cerevisiae); (X73571) 26S proteasome subunit Rpt1 [Saccharomyces cerevisiae]; (Z22817) putative ATPase [Saccharomyces cerevisiae]; (Z28145) ORF YKL145w [Saccharomyces cerevisiae]; 26S protease [Saccharomyces cerevisiae] (AL033502) uroporphyrinogen-III synthase [Candida albicans]
19375	ENU03169	ANI61C9449:	53-72	NAP	g3859663	70	5.00E-16				hydroxymethylglutaryl-CoA synthase [Schizosaccharomyces pombe]; (U32187) 3-hydroxy-3-methylglutaryl coenzyme A synthase; hydroxymethylglutaryl-CoA synthase - fission yeast (Schizosaccharomyces pombe); (U32187) 3-hydroxy-3-methylglutaryl coenzyme A synthase [Schizosaccharomyces pombe]; (Z98530) itr1; myo-inositol transporter [Schizosaccharomyces pombe] cytochrome B2 precursor (L-lactate dehydrogenase (cytochrome)) (L-lactate ferricytochrome C oxidoreductase) (L-LCR); L-lactate dehydrogenase (cytochrome) (EC 1.1.2.3) precursor - yeast (Pichia anomala); (X16051) L-lactate:cytochrome c oxidoreductase preprotein [Pichia anomala]
19376	ENU03170	ANI61C1038	22-56	NAP	g1708240	1190	379	e-104			(AL031525) mitochondrial carrier protein [Schizosaccharomyces pombe] hypothetical 81.2 KD protein in MES1-FOL2 intergenic region ; probable membrane protein YGR266w - yeast (Saccharomyces cerevisiae); (Z73051) ORF YGR266w [Saccharomyces cerevisiae]; (Y07893) ORF YGR266w [Saccharomyces cerevisiae]
19377	ENU03171	ANI61C7185:	36-56	NAP	g117803	635	169	2.00E-41	38	47	
19378	ENU03172	ANI61C7334:	22-49	NAP	g3560163	925	201	8.00E-96	67	89	
		1694..784									
19379	ENU03173	ANI61C5271:	22-56	NAP	g1723773	128	59	0.000000	23	28	
		67..978									

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19380	ENU03174	ANI61C4304:	25-44	875-894	NAP	g3169083	282	116	2.00E-25	34	79	(AL023705) hypothetical protein [Schizosaccharomyces pombe]	
19381	ENU03175	ANI61C8225:	1882..971	22-52	NAP	g4587575	220	77	1.00E-20	28	96	"(AC006550) Belongs to PFF01121 Uncharacterized protein family UPF0038 containing ATP/GTP binding domain. ESTs gba AA585719, gba AA728503 and gba T22272 come from this gene. [Arabidopsis thaliana]"	
19382	ENU03176	ANI61C1734:	3869..2956	22-50	864-893	NAP	g1351729	388	87	1.00E-17	43	73	MAL3 protein ; (Z68198) putative chromosome segregation protein [Schizosaccharomyces pombe] ; (Y09518) MAL3 protein [AE000705) hypothetical protein [Aquitex aeolicus]
19383	ENU03177	ANI61C1699:	950..35	24-55	878-897	NAP	g2983324	578	201	4.00E-51	43	89	(X91837) G1315 [Saccharomyces cerevisiae]
19384	ENU03178	ANI61C3794	647..5731	23-42	878-897	NAP	g1177632	187	91	9.00E-18	32	79	hypothetical oxidoreductase in MRP14-MTF1 intergenic region ; hypothetical protein YMIR226c - yeast (Saccharomyces cerevisiae) ; (Z49939) unknown [Saccharomyces cerevisiae] cytochrome P450 51 (CYPL1) (P450-L1A1) (sterol 14-alpha demethylase) (eburicol 14-alpha-demethylase) (P450-14DM) ; lanosterol 14alpha-demethylase (EC 1.14.14.-)
19385	ENU03179	ANI61C4995	008..5925	40-59	894-914	NAP	g2492763	572	112	1.00E-44	54	94	cytochrome P450 51 - Penicillium italicum ; (Z49750) cytochrome P-450 [Penicillium italicum]
19386	ENU03180	ANI61C9494:	1079..872	59-78	915-934	NAP	g2493386	1608	337	7.00E-92	58	57	Phosphatidylinositol-Specific Phospholipase C In Complex With Myo-inositol ; Phosphatidylinositol-Specific Phospholipase C ; Phosphatidylinositol-Specific Phospholipase C In Complex With Glucosamine-(Alpha-1-6)-Myo-Inositol
19387	ENU03181	ANI61C8220:	1681..764	44-64	898-919	NAP	g1633139	95	82	6.00E-15	29	91	

Seq num	Seq id	Contig Source	Primer 3 pos	Primer 3 pos	Selection Basis	Database Hit	nebi gi Score	aat Score	Blast Prob	% id	% cvrg	Description
19388	ENU03182	ANI61C674.9	31..54	887-906	NAP	g1723510	446	108	2.00E-43	37	76	hypothetical 42.4 KD protein C1F12.05 in chromosome I ; hypothetical protein - fission yeast (Schizosaccharomyces pombe) ; (Z69944) unknown [Schizosaccharomyces pombe] (AL031787) putative heavy metal transport protein
19389	ENU03183	ANI61C776.1	67..86	911-943	NAP	g3687489	432	69	4.00E-30	49	93	[Schizosaccharomyces pombe] "40S ribosomal protein RP10; ribosomal protein S0.e.B, cytosolic - yeast (Candida albicans) ; (X82017) ribosomal protein 10 [Candida albicans]"
19390	ENU03184	ANI61C3974.	42..62	892-919	NAP	g730655	923	280	8.00E-89	76	97	hypothetical 50.4 KD protein C1F8.04C in chromosome I ; (Z81312) unknown [Schizosaccharomyces pombe]
19391	ENU03185	ANI61C8192.	34..53	893-912	NAP	g2842689	733	258	4.00E-68	53	59	(AL033391) hypothetical membrane protein [Candida albicans] (AB015511) Avicelase III [Aspergillus aculeatus]
19392	ENU03186	ANI61C3842.	38..57	890-917	NAP	g3850125	399	161	5.00E-39	32	60	(AL049495) conserved phosducin-like hypothetical protein [Schizosaccharomyces pombe] (Z99753) rho protein [Schizosaccharomyces pombe]
19393	ENU03187	ANI61C2363.	48..67	900-927	NAP	g3242655	2990	316	1.00E-85	58	35	[Schizosaccharomyces pombe] (YER185w - yeast (Saccharomyces cerevisiae) ; (U18922) Yer185wp [Saccharomyces cerevisiae] (AL032288) hypothetical protein [Schizosaccharomyces pombe]
19394	ENU03188	ANI61C1084.	68..87	923-947	NAP	g4539262	321	73	5.00E-22	38	92	hypothetical protein
19395	ENU03189	ANI61C6527.	62..81	923-942	NAP	g2465150	419	86	4.00E-38	61	88	glycerate dehydrogenase (NADH-dependent hydroxypyruvate reductase) (HPR) (GDH) (hydroxypyruvate dehydrogenase) (glyoxylate reductase) (HPR-A)
19396	ENU03190	ANI61C1037	22..51	883-905	NAP	g2494084	335	134	9.00E-31	37	87	hypothetical 33.7 KD protein in ISC10 3'region ; hypothetical protein YER185w - yeast (Saccharomyces cerevisiae) ; (U18922) Yer185wp [Saccharomyces cerevisiae] (AL032288) hypothetical protein [Schizosaccharomyces pombe]
19397	ENU03191	ANI61C1103	24..47	883-908	NAP	g731385	329	73	2.00E-12	39	79	hypothetical 33.7 KD protein in ISC10 3'region ; hypothetical protein YER185w - yeast (Saccharomyces cerevisiae) ; (U18922) Yer185wp [Saccharomyces cerevisiae] (AL032288) hypothetical protein [Schizosaccharomyces pombe]
19398	ENU03192	ANI61C9880.	60..80	920-944	NAP	g3116131	60	48	0.00007	27	32	

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19399	ENU03193	AN161C1141 1.1275..348	65..84	929..949	NAP	g515503	634	192	7.00E-50	43	55	(U12013) 4-coumarate-CoA ligase	
19400	ENU03194	AN161C6468: 620..1547	48..67	914..933	NAP	g2258125	892	171	6.00E-42	47	46	(U39404) 4-enzyme [[Pinus taeda]]; (U39405) 4-coumarate:CoA ligase	
19401	ENU03195	AN161C7752: 979..50	33..52	902..920	NAP	g2132923	747	210	1.00E-62	48	76	[Pinus taeda] (Z83828) AmMst-1 [Amanita muscaria]	
19402	ENU03196	AN161C9305: 40..969	61..80	928..948	NAP	g2414604	1119	146	4.00E-46	43	49	(AL031852) conserved hypothetical protein [Schizosaccharomyces pombe]; probable membrane protein cerevisiae; - yeast (Saccharomyces pombe) (Z75147) ORF YOR240w	
19403	ENU03197	AN161C4048: 1855..2784	41..63	909..928	NAP	g1709062	147	221	2.00E-84	55	71	[Saccharomyces cerevisiae] kinase (AB010078) dihydroxyacetone kinase isoenzyme 1 [Schizosaccharomyces pombe] pombe] galactosyltransferase MNN10 (BUD1 emergenece delay protein 1); BED1 protein - yeast (Saccharomyces cerevisiae); (Z49701) unknown cerevisiae); (L42540) [Saccharomyces cerevisiae] cerevisiae] Mn10p [Saccharomyces cerevisiae] (AF072709) putative oxidoreductase (AF072709) putative oxidoreductase [Streptomyces lividans] DNA repair protein RAD18; (X80929) DNA repair protein RAD18 [Schizosaccharomyces pombe] rad18 [Schizosaccharomyces pombe] (AL033406) dna repair protein rad18 [Schizosaccharomyces pombe] hypothetical 33..3 KD protein in PERR-RAD18 [Schizosaccharomyces pombe] RGF intergenic region; (AE000134) putative [Escherichia coli] putative [Escherichia coli] esterase [Amycolatopsis colicola] (AF040570) esterase [Amycolatopsis colicola] (AF040570) esterase [Amycolatopsis colicola] (AF07317) benzyl alcohol dehydrogenase [Sphingomonas mediterranea]	
19404	ENU03198	AN161C460..1 255..324	23..53	893..912	NAP	g3293547	249	85	1.00E-18	30	95	(AF072709) putative oxidoreductase [Streptomyces lividans] DNA repair protein RAD18 [Streptomyces lividans] DNA repair protein rad18 [Schizosaccharomyces pombe] rad18 [Schizosaccharomyces pombe] (AL033406) dna repair protein rad18 [Schizosaccharomyces pombe] hypothetical 33..3 KD protein in PERR-RAD18 [Schizosaccharomyces pombe] RGF intergenic region; (AE000134) putative [Escherichia coli] putative [Escherichia coli] esterase [Amycolatopsis colicola] (AF040570) esterase [Amycolatopsis colicola] (AF040570) esterase [Amycolatopsis colicola] (AF07317) benzyl alcohol dehydrogenase [Sphingomonas mediterranea]	
19405	ENU03199	AN161C1122 5..2657..1725	25..44	895..914	NAP	g1709997	214	61	2.00E-17	40	18	(AF072709) putative oxidoreductase [Streptomyces lividans] DNA repair protein RAD18 [Streptomyces lividans] DNA repair protein rad18 [Schizosaccharomyces pombe] rad18 [Schizosaccharomyces pombe] (AL033406) dna repair protein rad18 [Schizosaccharomyces pombe] hypothetical 33..3 KD protein in PERR-RAD18 [Schizosaccharomyces pombe] RGF intergenic region; (AE000134) putative [Escherichia coli] putative [Escherichia coli] esterase [Amycolatopsis colicola] (AF040570) esterase [Amycolatopsis colicola] (AF040570) esterase [Amycolatopsis colicola] (AF07317) benzyl alcohol dehydrogenase [Sphingomonas mediterranea]	
19406	ENU03200	AN161C620..8 8..1022	29..50	894..921	NAP	g2494090	90	3.00E-17					
19407	ENU03201	AN161C1094: 1494..2429	39..58	913..932	NAP	g2792328	370	152	3.00E-36	35	96	(AF072709) putative oxidoreductase [Streptomyces lividans] DNA repair protein RAD18 [Streptomyces lividans] DNA repair protein rad18 [Schizosaccharomyces pombe] rad18 [Schizosaccharomyces pombe] (AL033406) dna repair protein rad18 [Schizosaccharomyces pombe] hypothetical 33..3 KD protein in PERR-RAD18 [Schizosaccharomyces pombe] RGF intergenic region; (AE000134) putative [Escherichia coli] putative [Escherichia coli] esterase [Amycolatopsis colicola] (AF040570) esterase [Amycolatopsis colicola] (AF040570) esterase [Amycolatopsis colicola] (AF07317) benzyl alcohol dehydrogenase [Sphingomonas mediterranea]	
19408	ENU03202	AN161C2632: 1105..2041	27..46	900..921	NAP	g23378273	613	113	5.00E-50	43	79	(AF072709) putative oxidoreductase [Streptomyces lividans] DNA repair protein RAD18 [Streptomyces lividans] DNA repair protein rad18 [Schizosaccharomyces pombe] rad18 [Schizosaccharomyces pombe] (AL033406) dna repair protein rad18 [Schizosaccharomyces pombe] hypothetical 33..3 KD protein in PERR-RAD18 [Schizosaccharomyces pombe] RGF intergenic region; (AE000134) putative [Escherichia coli] putative [Escherichia coli] esterase [Amycolatopsis colicola] (AF040570) esterase [Amycolatopsis colicola] (AF040570) esterase [Amycolatopsis colicola] (AF07317) benzyl alcohol dehydrogenase [Sphingomonas mediterranea]	
19409	ENU03203	AN161C8017: 4869..5806	36..55	911..930	NAP								



Seq num	Seq id	Contig Source	Primer 3 pos	Primer Selection Basis	Database Hit	ncbi gi	Score	Score Prob	% id	% cvrg	Description
19421	ENU03215	ANI61C7354:	59-78	NAP	g2769696	318	143	2.00E-33	33	80	(AC003982) unknown function; 60% similar to Z50177 (PID:g927403) (PID:g927402) [Homo sapiens]
19422	ENU03216	ANI61C1019	63-82	NAP	g2501598	411	120	2.00E-26	40	89	hypothetical 28.3 KD protein in PPR1-SNF7 intergenic region ; hypothetical protein YLR022c - yeast (Saccharomyces cerevisiae); (Z73194) ORF YLR022c [Saccharomyces cerevisiae]
19423	ENU03217	ANI61C5194:	37-56	NAP	g133961	801	128	2.00E-56	74	90	40S ribosomal protein S4 (omnipotent suppressor protein SUP44) (RPL12) (S2E); ribosomal protein S2.e - yeast (Saccharomyces cerevisiae); (MS9375) ribosomal protein S4 [Saccharomyces cerevisiae]; (Z72645) ORF YGL123w [Saccharomyces cerevisiae]; (X94106) SUP44 [Saccharomyces cerevisiae] (AL033503) transcription regulatory protein [Candida albicans] (L39639) kievitone hydratase [Fusarium solani] esterase D; (AFI12219) esterase D [Homo sapiens] (Z97204) hypothetical protein [Schizosaccharomyces pombe] serine/threonine protein phosphatase PPE1 (phosphatase ESP1); cell shape control protein phosphatase ppe1 - fission yeast (Schizosaccharomyces pombe); (Z18925) type2A-like protein phosphatase [Schizosaccharomyces pombe]; (D13712) protein phosphatase [Schizosaccharomyces pombe]; (AL031540) serine-threonine protein phosphatase [Schizosaccharomyces pombe]
			1513..567								

Seq num	Seq id	Contig Source	Primer 3 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat	Blast Score	Blast Prob	% id	% cvrg	Description
19429	ENU03223	ANI61C7183:	25-56	912-933	NAP	g2498438	58	48	0.00007	18	48		transcriptional coactivator HFI1/ADA1 ; HFI1 protein - yeast (Saccharomyces cerevisiae) ; (Z67751) putative protein [Saccharomyces cerevisiae] ; (Z73610) ORF YPL254w [Saccharomyces cerevisiae] ; (U75735) putative transcriptional coactivator [Saccharomyces cerevisiae] (AF063095) SEL1L [Mus musculus]
19430	ENU03224	ANI61C6626:	72-92	963-982	NAP	g4159995	577	130	2.00E-29	36	29		
19431	ENU03225	ANI61C1070	6.6101..5146	916-935	NAP	g3219924	276	52	0.000005	29	34		hypothetical 57.6 KD protein C30D10.15 in chromosome II ; (Z97992) conserved hypothetical protein [Schizosaccharomyces pombe] hypothetical 44.9 KD protein in URA10-NRC1 intergenic region ; probable membrane protein YMR272c - yeast (Saccharomyces cerevisiae) ; (Z49260) unknown [Saccharomyces cerevisiae]
19432	ENU03226	ANI61C6762:	70-91	956-984	NAP	g2493967	854	151	2.00E-75	53	72		
19433	ENU03227	ANI61C8592:	40-59	934-954	NAP	g4099311	604	165	5.00E-40	44	62		(U85909) hydroxylase [Aureobasidium pullulans]
19434	ENU03228	ANI61C2749:	24-46	921-940	NAP	g1546072	373	173	2.00E-42	35	12		(U68040) polyketide synthase [Cochliobolus heterostrophus]
19435	ENU03229	ANI61C4206:	50-70	944-966	NAP	g508233	1246	191	e-106	67	35		(U09358) RecA [Saccharomyces cerevisiae]
19436	ENU03230	ANI61C4920:	51-77	949-969	NAP	g1911741	1223	326	e-121	82	82		"(S83228) beta-isopropylmalate dehydrogenase [Aspergillus niger, strain A733, Peptide, 363 aa] [Aspergillus niger]" ; (U51130) beta-isopropylmalate dehydrogenase [Aspergillus niger]"
19437	ENU03231	ANI61C9581:	24-46	925-944	NAP	g2492754	354	111	4.00E-33	38	87		sorbitol utilization protein SOU1 ; (AF002134) Soul1p [Candida albicans] (AL033385) transketolase [Schizosaccharomyces pombe] (AC004450) putative carboxyphosphoenolpyruvate mutase [Arabidopsis thaliana]

Seq num	Seq id	Contig Source	Primer 3 pos	Primer Basis	Selection Database Hit	atn	Blast Score	Blast Prob	% id	% cvrg	Description	
19440	ENU03234	ANI61C8700:	32-49	NAP	927-955	g1703215	399	175	6.00E-43	31	51	general alpha-glucoside permease ; alpha-glucoside transport protein - yeast (Saccharomyces cerevisiae); (Z73074) ORF YGR289c
19441	ENU03235	ANI61C8700:	32-49	927-955	NAP	17..982						[Saccharomyces cerevisiae]
19442	ENU03236	ANI61C8861:	50-69	959-978	NAP	169..1139						general alpha-glucoside permease ; alpha-glucoside transport protein - yeast (Saccharomyces cerevisiae); (Z73074) ORF YGR289c
19443	ENU03237	ANI61C4087:	40-59	949-968	NAP	2719..1749						[Saccharomyces cerevisiae]
19444	ENU03238	ANI61C9249:	22-52	932-952	NAP	7183..8155						hypothetical protein YLL029w - yeast (Saccharomyces cerevisiae); (Z73134) ORF YLL029w [Saccharomyces cerevisiae]
19445	ENU03239	ANI61C1997:	23-44	933-954	NAP	1399..426						acid phosphatase precursor ; acid phosphatase (EC 3.1.3.2) - Aspergillus ficuum ; (L20566) acid phosphatase [Aspergillus niger] (Z83867) fadB4 [Mycobacterium tuberculosis]
19446	ENU03240	ANI61C1025	25-46	921-956	NAP	5:1065..92						hypothetical 103.4 KD TRP-ASP repeats containing protein C3D6.12 in chromosome II ; (Z95620) ttp asp repeat protein [Schizosaccharomyces pombe]
19447	ENU03241	ANI61C6477:	41-60	951-972	NAP	7088..6115						endonuclease III homolog (DNA-(apurinic or apyrimidinic site) lyase) ; endonuclease III (EC 3.1.-.-) - fission yeast (Schizosaccharomyces pombe) ; hypothetical protein SPA.C30D11.07 - fission yeast (Schizosaccharomyces pombe) ; (Z67961) endonuclease III homolog [Schizosaccharomyces pombe] (AL023702) hypothetical protein SC1C3.24 [Streptomyces coelicolor]

Seq num	Seq id	Contig Source	Primer 3 pos	Primer Basis	Selection	Blast Score	Blast Prob	% id	% cvrg	Description	
		5 pos	5 pos	NAP	Database Hit	ncbi gi	Score				
9526..8552		9526..8552	961-983	NAP	g2497056	183	52	6.00E-12		putative dioxygenase YLL057C ; hypothetical protein YLL057c - yeast (Saccharomyces cerevisiae) ; (Z47973) ORF L0572 [Saccharomyces cerevisiae] ; (Z73_62) ORF YLL057c [Saccharomyces cerevisiae]	
19449	ENU03243	ANI61C8589:	24-44	926-956	NAP	g3183360	411	155	4.00E-37	27	57 hypothetical protein C17H9_20 in chromosome I ; (Z98597) hypothetical protein [Schizosaccharomyces pombe] awamori]
19450	ENU03244	ANI61C8537:	22-51	934-954	NAP	g1542843	1046	206	e-105	66	94 (D87681) acetyltransferase [Aspergillus
11961..10987						g585064	296	146	2.00E-34	28	"DNA polymerase beta ; Dna Polymerase Beta (Beta Polymerase) (E.C.2.7.7.7) (Apo, Full Protein) ; Rattus norvegicus ; Rattus norvegicus ; Rattus norvegicus "
19451	ENU03245	ANI61C266:1	41-60	955-974	NAP	g1401216	471	145	6.00E-34	41	95 (U59376) N-carbamoyl-D-amino acid amidohydrolase [Agrobacterium radiobacter]
2401..1424						g2506663	339	162	3.00E-39	38	99 "hypothetical 29.7 KD protein in HRP_A-LDA intergenic region ; (D90780) ORF_ID:o270#; similar to [SwissProt Accession Number P34209] [Escherichia coli]; (D90781) ORF_ID:o270#1; similar to [SwissProt Accession Number P34209] [Escherichia coli]; (AE000239) orf, hypothetical protein [Escherichia coli]"
19452	ENU03246	ANI61C9849:	47-67	950-982	NAP	g1401216	471	145	6.00E-34	41	(AB017112) mCAC [Mus musculus]
2401..1424						g4239974	68	1.00E-10			
19453	ENU03247	ANI61C4859:	22-46	931-960	NAP	g1730685	1466	270	8.00E-72	67	44 hypothetical GTP-binding protein in POP2-HOL1 intergenic region ; hypothetical protein YNR053c - yeast (Saccharomyces cerevisiae) ; (Z71668) ORF YNR053c [Saccharomyces cerevisiae]
849..1829											
19454	ENU03248	ANI61C1038	32-58	942-971	NAP						
3..2442..3423											
19455	ENU03249	ANI61C7390:	22-39	942-961	NAP						
2129..2247											

Seq num	Seq id	Contig Source	Primer 3 pos	Primer Basis	Selection	Blast gi	aat	Blast Score	Prob	% id	% cvrg	Description
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19456	ENU03250	ANI61C7332:	2948	NAP	g3122261	843	164	2.00E-84	74	99		eukaryotic translation initiation factor 6 (EIF-6); hypothetical protein YPR016c - yeast [Saccharomyces cerevisiae]; (Z49919) unknown [Saccharomyces cerevisiae]; (U31900) Lpz15p
19457	ENU03251	ANI61C8252:	58-77	977-997	NAP	g3850125	624	199	3.00E-50	35	63	[Saccharomyces cerevisiae]; (Z71255) unknown [Saccharomyces cerevisiae] (AL033391) hypothetical membrane protein [Candida albicans]
19458	ENU03252	ANI61C1118	31-53	946-971	NAP	g2370496	354	173	1.00E-42	33	35	(Z98944) hypothetical protein [Schizosaccharomyces pombe] (AB010465) lactonohydrolase
19459	ENU03253	ANI61C9343:	60-79	973-1001	NAP	g3810873	478	150	1.00E-35	41	76	[Fusarium oxysporum] "hypothetical 67.7 KD protein C23C11.03 in chromosome I; (Z98559) SPAC23C11.03; len:598aa, similar eg. to YJR002W, YJX2, yeast, P47083, hypothetical 67.0 kd protein, (593aa), fasta scores, opt:855, E():0, (33.0% identity in 610 aa overlap)
19461	ENU03255	ANI61C3731:	32-51	954-973	NAP	g135407	1617	590	e-168	97	67	[Schizosaccharomyces pombe]" tubulin alpha-2 chain; tubulin alpha-2 chain [Emericella nidulans] (AL035570) putative nitrilase homolog [Schizosaccharomyces pombe] (AF002660) aflatoxin [Aspergillus parasiticus]
19462	ENU03256	ANI61C1106	31-50	942-977	NAP	g4467274	575	206	2.00E-52	48	97	[Aspergillus parasiticus] probable membrane protein YOR262w - yeast (Saccharomyces cerevisiae); (Z75170) ORF YOR262w
19463	ENU03257	ANI61C6325:	45-65	970-991	NAP	g2738309	408	73	1.00E-27	31	70	[Saccharomyces cerevisiae]
19464	ENU03258	ANI61C4666:	51-73	980-998	NAP	g2132930	814	222	3.00E-57	47	83	"2,4-dihydroxyhept-2-ene-1,7-dioic acid aldolase - Escherichia coli ; (Z47799) 2,4-dihydroxyhept-2-ene-1,7-dioic acid aldolase [Escherichia coli] ; (Z37980) hypothetical 2,4-dihydroxyhepta-2-ene-1,7-dioate aldolase [Escherichia coli] " (AJ223327) rAsp f9 [Aspergillus fumigatus]
19465	ENU03259	ANI61C4278:	42-61	955-990	NAP	g1073302	269	126	3.00E-28	30	100	
600..1590												
19466	ENU03260	ANI61C1072	29-50	955-977	NAP	g2879890	503	220	1.00E-56	37	99	
3:1241..2230												

Seq num	Seq id	Contig Source	Primer 3 pos	Primer Basis	Selection	Blast gi	aat	Blast Score	Prob	% id	% cvrg	Description
			5 pos	NAP	Database Hit	ncbi gi	Score	Score	Prob	55	93	
19467	ENU03261	ANI61C9659:	72-98	1002-1021	g1723239	784	314	6.00E-85	55	93		hypothetical 35.7 KD protein C26A3.11 in chromosome I; (Z69240) putative amidohydrolase
19468	ENU03262	ANI61C7455:	65-84	995-1014 NAP	6773..7764	g417090	878	138	2.00E-84			[Schizosaccharomyces pombe] GTP-binding nuclear protein GSP1/CNR1 ; GTP-binding protein GSP1 - yeast [Saccharomyces cerevisiae] ; (L08690) GTP-binding protein [Saccharomyces cerevisiae]; (X71945) CNR2 [Saccharomyces cerevisiae] ; (U17243) GTP-binding nuclear protein. Highly similar to GSP2_yeast. Belongs to the Ran family of Ras proteins [Saccharomyces cerevisiae] (AL031825) putative membrane transport protein
19469	ENU03263	ANI61C5172:	33-52	964-983 NAP	3310..2318	g3702646	298	78	3.00E-26	31	54	[Schizosaccharomyces pombe] (AL031644) possible zinc-finger protein [Schizosaccharomyces pombe] hypothetical 33.5 KD protein C1D4.02C in chromosome I; (Z69239) unknown [Schizosaccharomyces pombe]
19470	ENU03264	ANI61C7232:	22-52	949-972 NAP	5559..4567	g3647335	145	67	2.00E-10	25	74	cytochrome C PRoxidase precursor (CCP) ; cytochrome-c peroxidase (EC 1.11.1.5) precursor - yeast [Saccharomyces cerevisiae]; (X62422) Cytochrome c peroxidase [Saccharomyces cerevisiae]; (Z228291) ORF YKR066c [Saccharomyces cerevisiae]
19471	ENU03265	ANI61C3420:	22-46	940-972 NAP	1758..2750	g1723224	302	96	5.00E-19	32	99	hypothetical 32.6 KD protein in DAL5-TH11 intergenic region ; aryl-alcohol dehydrogenase homolog YJR155w - yeast [Saccharomyces cerevisiae]; (Z49655) ORF YJR155w [Saccharomyces cerevisiae]
19472	ENU03266	ANI61C9030:	66-85	997-1016 NAP	2449..3441	g543969	478	217	7.00E-56	44	74	
19473	ENU03267	ANI61C2045:	58-78	989-1008 NAP	3325..2331	g1352946	411	73	2.00E-21	42	94	

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19474	ENU03268	ANI61C1109	22-57	953-973	NAP	g1293655	783	249	3.00E-65	44	49	(U51327) versicolorin B synthase [Aspergillus parasiticus] ; (J51328) versicolorin B synthase [Aspergillus parasiticus]	
19475	ENU03269	ANI61C9633:	38-57	970-989	NAP	g3668160	203	59	0.000000	23	47	(AL031764) hexose transporter. [Schizosaccharomyces pombe]; (AF098076) ghtfp	
19476	ENU03270	ANI61C7613:	22-45	950-974	NAP	g1353673	151	62	2.00E-17	30	75	[Schizosaccharomyces pombe] (U42349) 39 kDa encoded by N33 [Homo sapiens]	
19477	ENU03271	ANI61C1373:	24-43	949-977	NAP	g3122964	432	129	3.00E-50	41	94	putative thiosulfate sulfurttransferase; hypothetical protein YOR251c - yeast (Saccharomyces cerevisiae); (Z75159) ORF YOR251c [Saccharomyces cerevisiae]	
19478	ENU03272	ANI61C7897:	43-62	976-996	NAP	g2131132	1110	444	e-124	66	22	UDPglucose--glycoprotein glucosidophototransferase (EC 2.7.8.19) - fission yeast (Schizosaccharomyces pombe); (U38417) UDP-Glc:Glycoprotein Glucosyltransferase [Schizosaccharomyces pombe]	
19479	ENU03273	ANI61C1083	22-46	957-976	NAP	g1708467	333	148	4.00E-35	35	82	branched-chain amino acid aminotransferase (transaminase B) (BCAT); branched-chain-amino-acid transaminase homolog - Haemophilus influenzae (strain Rd KW20); (U32798) branched-chain-amino-acid transaminase (liver) [Haemophilus influenzae Rd]	
19480	ENU03274	ANI61C5227:	46-65	973-1000	NAP	g125935	578	76	2.00E-35	36	46	lactose permease ; lactose permease - yeast (Kluyveromyces marxianus var. lactis); (X06997) lactose permease (AA 1-587) [Kluyveromyces lactis] (AL023780) DNA binding protein [Schizosaccharomyces pombe] (AB010442) PMR1 [Penicillium digitatum] (AF010494) sorbitol dehydrogenase [Callithrix sp.]	
19481	ENU03275	ANI61C9068:	26-48	951-981	NAP	g3184115	377	166	3.00E-40	30	63		
19482	ENU03276	ANI61C4858:	54-74	981-1009	NAP	g3288709	1234	458	e-128	68	22		
19483	ENU03277	ANI61C1942:	45-65	975-1001	NAP	g2352843	715	104	5.00E-36	42	80		
		3132..2133											

Seq num	Seq id	Contig Source	Primer 3 pos	Primer Basis	Selection Database Hit	nebi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19484	ENU03278	ANI61C9666:	33..53	965..990	NAP	g2132925	517	263	2.00E-69	41	77	probable membrane protein YOR245c - yeast [Saccharomyces cerevisiae]; (Z75153) ORF YOR245c
19485	ENU03279	ANI61C4960:	53..72	988..1010	NAP	g729534	739	146	1.00E-75	51	58	[Saccharomyces cerevisiae] UTR1 protein (unknown transcript 1 protein); UTR1 protein - yeast (Saccharomyces cerevisiae); (L26347) orf gtE530 [Saccharomyces cerevisiae]; (Z49549) ORF YJR049c [Saccharomyces cerevisiae]; (L36344) ORF; putative [Saccharomyces cerevisiae]
19486	ENU03280	ANI61C6471:	42..61	973..1000	NAP	g547648	949	280	2.00E-92			histidinol-phosphate aminotransferase (imidazole acetol-phosphate transaminase); his3 protein - fission yeast [Schizosaccharomyces pombe]; (L19523) imidazoleglycerol-phosphate dehydratase [Schizosaccharomyces pombe]; (L19524) imidazoleglycerol-phosphate dehydratase [Schizosaccharomyces pombe]; (AB004534) histidinol-phosphate aminotransferase [Schizosaccharomyces pombe] (Z99107) similar to hypothetical proteins [Bacillus subtilis]
19487	ENU03281	ANI61C7553:	40..59	979..998	NAP	g2633013	351	145	1.00E-38	30	93	phosphate-repressible phosphate permease ; phosphate-repressible phosphate permease - Neurospora crassa ; (M31364) phosphate permease [Neurospora crassa] (AF032688) putative transmembrane transporter Lz1p
19488	ENU03282	ANI61C1037	49..72	989..1008	NAP	g130117	869	214	7.00E-55	35	56	[Schizosaccharomyces pombe]; (AL023706) transmembrane transporter Lz1p
19489	ENU03283	ANI61C1131:	34..53	964..994	NAP	g2981103	107	2.00E-22	39	21		[Schizosaccharomyces pombe] (AL023706) apoptosis specific protein homologue [Schizosaccharomyces pombe]
19490	ENU03284	ANI61C7525:	23..47	964..983	NAP	g3169097	190	74	1.00E-12	28	85	

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Primer	Blast ncbi gi	aat	Blast Prob	% id	% cvrg	Description
19491	ENU03285	ANI50C202	23-42	950-983	NAP	g2239196	257	6.00E-68	45	98	(Z97209) hypothetical protein	
19492	ENU03286	ANI61C8836:	3:1765..2767	38-60	966-999	NAP	g135407	823	341	5.00E-93	60	[Schizosaccharomyces pombe] tubulin alpha-2 chain ; tubulin alpha-2 chain - <i>Emericella nidulans</i>
19493	ENU03287	ANI50C721	1..3356..2353	25-50	967-986	NAP	g116929	272	3.00E-75	49	63	hexaprenyl pyrophosphate synthetase precursor (HPS) ; trans-pentaprenyltransferase (EC 2.5.1.33) precursor - yeast
19494	ENU03288	ANI61C1055	34-53	976-995	NAP	g549725	332	126	8.00E-31			(Saccharomyces cerevisiae); (J05547) hexaprenyl pyrophosphate synthetase (COQ1) [Saccharomyces cerevisiae]; (Z35872) ORF YBR003w
19495	ENU03289	ANI61C562:1	22-48	964-984	NAP	g1346485	889	182	3.00E-54	41	53	[Saccharomyces cerevisiae]; "NADH-cytochrome B5 reductase precursor (P34/P32) ; cytochrome-b5 reductase (EC 1.6.2.2), mitochondrial outer membrane form - yeast (Saccharomyces cerevisiae); (Z26877) unknown [Saccharomyces cerevisiae]; (Z28150) ORF YKL150w [Saccharomyces cerevisiae]; (X81474) NADH-cytochrome b5 reductase [Saccharomyces cerevisiae]; ORF [Saccharomyces cerevisiae]" malate oxidoreductase (malic enzyme) (NADP-dependent malic enzyme) (NADP-ME); (X56233) malic enzyme [Populus balsamifera subsp. trichocarpa] (M96667) proteosome-related protein [Saccharomyces cerevisiae]
19496	ENU03290	ANI61C30:36	23-52	967-986	NAP	g172260	721	111	6.00E-38	67	52	hypothetical 55.1 KD protein in FAB1-PES4 intergenic region ; probable membrane protein YFR021w - yeast (Saccharomyces cerevisiae); (D50617) YFR021W [Saccharomyces cerevisiae] (Z99126) hypothetical oxidoreductase [Schizosaccharomyces pombe]
19499	ENU03293	ANI61C1649:	36-55	976-1002	NAP	g3183055	461	216	2.00E-55	41	47	probable serine/threonine-protein kinase C29A4.16; (Z97210) protein kinase [Schizosaccharomyces pombe]

Seq num	Seq id	Contig Source	Primer 3 pos	Primer Basis	Selection	aat	Blast Score	Blast Prob	% id	% cvrg	Description
			5 pos	NAP	Database Hit	ncbi gi	Score	Prob	39	88	"ZRT1 protein ; zinc transport protein, high affinity - yeast (Saccharomyces cerevisiae) ; (X67787) ORF <sup>1</sup>
19500	ENU03294	ANI61C1183:	2847	976-995	g418391	589	236	1.00E-61	39	88	[Saccharomyces cerevisiae]; (X94357) ORF NRC376; EMBL:SCFZFI; X67787; PIR:DEBY4,S07614 [Saccharomyces cerevisiae]; (Z72777) ORF YGL255w [Saccharomyces cerevisiae]"
19501	ENU03295	ANI61C6843:	46-65	994-1013	NAP	g2330719	105	73	2.00E-12	32	93 (Z98597) hypothetical nadh- cytochrome reductase
19502	ENU03296	ANI61C9202:	22-48	968-990	NAP	g730684	2522	226	e-113	73	35 [Schizosaccharomyces pombe] ubiquitin--protein ligase RSp5; hypothetical protein YER125w - yeast (Saccharomyces cerevisiae); (U18916) Rsp5p [Saccharomyces cerevisiae] (AB016895) Pop3
19503	ENU03297	ANI61C6531:	22-55	971-990	NAP	g3434986	778	255	1.00E-85	62	81 [Schizosaccharomyces pombe] glycerol-3-phosphate dehydrogenase (NAD <sup>+</sup> ) 1 ; glycerol-3-phosphate dehydrogenase (NAD <sup>+</sup> ) (EC 1.1.1.8) precursor yeast (Saccharomyces cerevisiae); (Z24454) glycerol 3-phosphate dehydrogenase [Saccharomyces cerevisiae]; (U04621) dihydroxyacetone phosphate reductase [Saccharomyces cerevisiae]; (X76859) glycerol-3-phosphate dehydrogenase (NAD <sup>+</sup> ) [Saccharomyces cerevisiae]; (Z48432) glycerol-3-phosphate dehydrogenase (NAD <sup>+</sup> ) (X76859) [Saccharomyces cerevisiae]; (Z74071) ORF YDL022w [Saccharomyces cerevisiae] (AF002576) translation initiation factor eIF3 p40 subunit; eIF3p40 [Homo sapiens]
19504	ENU03298	ANI61C1100	25-45	973-993	NAP	g462197	726	223	6.00E-59		(AB000703) phosphomannomutase [Schizosaccharomyces pombe] (AL02353) hypothetical protein [Schizosaccharomyces pombe]
9.844..1854											

Seq num	Seq id	Contig Source	Primer 3 pos	Primer Basis	Selection Database Hit	ncbi gi	aat	Blast Score	Blast Prob	% id	% cvrg	Description
19508	ENU03302	ANI50C66_1:	22-51	NAP	966-993	g2879890	245	e-101	70	91	(AJ22327) rAsp f 9 [Aspergillus fumigatus]	
19509	ENU03303	ANI61C9775:	33-61	NAP	7754..8767	g2873958	194	103	2.00E-21	26	95	(Z81458) similar to transposable element [Caenorhabditis elegans] (M77661) putative gag protein [Magnaporthe grisea]
19510	ENU03304	ANI61C8634:	22-51	NAP	7809..6794	g538066	181	62	0.000000	25	96	(AC005168) unknown protein [Arabidopsis thaliana]
19511	ENU03305	ANI61C8943:	55-80	NAP	1264..250	g3426039	273	127	9.00E-29	49	25	[Arabidopsis thaliana] hypothetical 55.4 KD protein in STE3-GIN10 intergenic region ; hypothetical protein YKL175W - yeast (Saccharomyces cerevisiae); (Z26878) unknown [Saccharomyces cerevisiae]; (Z28175) ORF YKL175w [Saccharomyces cerevisiae]; ORF [Saccharomyces cerevisiae]
19513	ENU03307	ANI61C9973:	38-57	NAP	1393..379	g2318125	316	82	4.00E-18	38	75	(AF014404) HIV-Nef associated acyl CoA thioesterase [Homo sapiens]; (AL008726) dj337O18.3.1 (Thioesterase II) (isoform 1) [Homo sapiens]
19514	ENU03308	ANI61C1292:	59-78	NAP	1044..26	g2271503	64	7.00E-17				(AF009672) unknown [Acinetobacter sp. ADP1]
19515	ENU03309	ANI61C1011	22-56	NAP	0.7268..6251	g2924499	331	124	8.00E-28	35	91	(AL022019) putative 3 beta-hydroxysteroid dehydrogenase(delta 5->4-isomerase(3beta-hsd) [Schizosaccharomyces pombe] (AL031786) putative delta-1-pyroline-5-carboxylate dehydrogenase [Schizosaccharomyces pombe] (AF009418) trichothecene biosynthesis transcription factor [Myrothecium roridum]
19516	ENU03310	ANI61C1143	68-91	NAP	4..1206..190	g3687478	1534	414	e-115	60	61	(AL021815) hypothetical protein [Schizosaccharomyces pombe]; (AL05675) adducin N terminal domain protein [Schizosaccharomyces pombe] (U68714) isocitrate lyase 1 [Botryotinia fuckeliana]
19517	ENU03311	ANI61C541:2	23-49	NAP	380..1362	g2267603	246	121	9.00E-27	35	54	
19518	ENU03312	ANI61C7921:	24-58	NAP	4205..3186	g2879861	148	84	1.00E-17	25	97	
19519	ENU03313	ANI61C8093:	33-52	NAP	1073..52	g3282211	1131	211	e-117	70	69	

Seq num	Seq id	Contig Source	Primer 3 pos	Primer 5 pos	Selection Basis	Database Hit	nebi gi	aat	Blast Score	Blast Prob	% id	% cvrg	Description
19520	ENU03314	ANI61C1147	36-55	1000-	NAP	g3318897	337	161	8.00E-39	30	48	"Chain A, Phenol Hydroxylase From Trichosporon Cutaneum ; Chain B, Phenol Hydroxylase From Trichosporon Cutaneum ; Chain C, Phenol Hydroxylase From Trichosporon Cutaneum ; Chain D, Phenol Hydroxylase From Trichosporon Cutaneum "	
19521	ENU03315	ANI61C1118:	58-78	1020-	NAP	g3150262	713	178	4.00E-44	42	85	(AL023634) hypothetical protein [Schizosaccharomyces pombe]	
19522	ENU03316	ANI61C7162:	24-44	1040	984-1006	NAP	g2492816	74	3.00E-24			[Schizosaccharomyces pombe] uracil permease ; (X98696) uracil permease [Schizosaccharomyces pombe]	
19523	ENU03317	ANI61C4572:	38-71	1002-	NAP	g1174417	970	129	5.00E-42	71	65	spermidine synthase (putrescine aminopropyltransferase) (SPDSY); (Z54140) putrescine aminopropyltransferase	
19524	ENU03318	ANI61C6048:	49-71	1013-	1034	NAP	g1723920	355	134	1.00E-31	40	77	[Schizosaccharomyces pombe] hypothetical 37.4 KD protein in SEC27-SSM1B intergenic region ; hypothetical protein YGLJ36c - yeast (Saccharomyces cerevisiae) ; (X92670) G2830 [Saccharomyces cerevisiae]; (Z72658) ORF YGLI36c
19525	ENU03319	ANI61C1082	6-211..1083	27-46	993-1012	NAP	g1351122	1143	324	e-122	74	98	[Saccharomyces cerevisiae] thiazole biosynthetic enzyme (stress-inducible protein STI35) ; stress-inducible protein sti35 - fungus (Fusarium oxysporum) ; (M33643) STI35 protein [Fusarium oxysporum] hypothetical 33.9 KD protein C14C4.12C in chromosome 1; (Z98596) hypothetical protein [Schizosaccharomyces pombe] plasma membrane Ca2+-ATPase isoform 4 - rat ; (U15408) plasma membrane Ca2+-ATPase isoform 4 [Rattus norvegicus] Pectin Lyase A
19526	ENU03320	ANI61C1026	55-79	1012-	NAP	g3183345	259	127	1.00E-28	36	61		
19527	ENU03321	ANI61C7819:	25-44	993-1012	NAP	g1083757	781	156	4.00E-55	44	25		
19528	ENU03322	ANI61C1019	3:1386..356	22-47	991-1010	NAP	g2624697	1322	155	e-101	73	75	

Seq num	Seq id	Contig Source	Primer 3 pos	Primer Basis	Selection	aat	Blast Score	Blast Prob	% id	% cvrg	Description	
					Database Hit	ncbi gi	Score	Prob				
19529	ENU03323	ANI61C7349:	62-80	NAP	g1657510	628	175	8.00E-62	39	70	(U73857) betaine-aldehyde dehydrogenase [Escherichia coli]	
19530	ENU03324	ANI61C1834:	54-73	1024-	NAP	g2500755	486	173	2.00E-47	57	31	response regulator MCS4 (mitotic catastrophe suppressor 4); (Y11927)
			4387..3555	1044							Mcs4 protein [Schizosaccharomyces pombe]; (AF004694) Mcs4 [Schizosaccharomyces pombe]; (AL033388) response regulator mcs4 [Schizosaccharomyces pombe] (AL021837) hypothetical protein [Schizosaccharomyces pombe] (D90916) hypothetical protein [Synechocystis sp.] (AL031854) hypothetical zinc-finger protein [Schizosaccharomyces pombe] C-8 sterol isomerase (delta-8--delta-7 sterol isomerase); C-8 sterol isomerase - rice blast fungus ; C-8 sterol isomerase - rice blast fungus ; (Z22775) C-8 sterol isomerase [Magaporthe grisea]	
19531	ENU03325	ANI61C9207:	53-75	1021-	NAP	g2894293	822	284	9.00E-76	43	65	[Schizosaccharomyces pombe] (AL021837) hypothetical protein [Schizosaccharomyces pombe] (D90916) hypothetical protein [Synechocystis sp.] (AL031854) hypothetical zinc-finger protein [Schizosaccharomyces pombe] C-8 sterol isomerase (delta-8--delta-7 sterol isomerase); C-8 sterol isomerase - rice blast fungus ; C-8 sterol isomerase - rice blast fungus ; (Z22775) C-8 sterol isomerase [Magaporthe grisea]
19532	ENU03326	ANI61C3172:	38-58	1004-	NAP	g1653791	159	104	1.00E-23	32	97	[Schizosaccharomyces pombe] (D90916) hypothetical protein [Synechocystis sp.] (AL031854) hypothetical zinc-finger protein [Schizosaccharomyces pombe] C-8 sterol isomerase (delta-8--delta-7 sterol isomerase); C-8 sterol isomerase - rice blast fungus ; C-8 sterol isomerase - rice blast fungus ; (Z22775) C-8 sterol isomerase [Magaporthe grisea]
19533	ENU03327	ANI61C1086	70-93	1033-	NAP	g3738189	314	131	6.00E-30	27	69	[Schizosaccharomyces pombe] (D90916) hypothetical protein [Synechocystis sp.] (AL031854) hypothetical zinc-finger protein [Schizosaccharomyces pombe] C-8 sterol isomerase (delta-8--delta-7 sterol isomerase); C-8 sterol isomerase - rice blast fungus ; C-8 sterol isomerase - rice blast fungus ; (Z22775) C-8 sterol isomerase [Magaporthe grisea]
19534	ENU03328	ANI61C8189:	71-101	1043-	NAP	g462023	715	129	4.00E-29	65	62	[Schizosaccharomyces pombe] (D90916) hypothetical protein [Synechocystis sp.] (AL031854) hypothetical zinc-finger protein [Schizosaccharomyces pombe] C-8 sterol isomerase (delta-8--delta-7 sterol isomerase); C-8 sterol isomerase - rice blast fungus ; C-8 sterol isomerase - rice blast fungus ; (Z22775) C-8 sterol isomerase [Magaporthe grisea]
19535	ENU03329	ANI61C9130:	51-71	1022-	NAP	g399766	100	78	7.00E-14	29	59	[Schizosaccharomyces pombe] (D90916) hypothetical protein [Synechocystis sp.] (AL031854) hypothetical zinc-finger protein [Schizosaccharomyces pombe] C-8 sterol isomerase (delta-8--delta-7 sterol isomerase); C-8 sterol isomerase - rice blast fungus ; C-8 sterol isomerase - rice blast fungus ; (Z22775) C-8 sterol isomerase [Magaporthe grisea]
			1173..139	1043								
19536	ENU03330	ANI61C9354:	24-49	987-1016	NAP	g1770301	196	71	7.00E-14	36	94	[Zymomonas mobilis] (X95074) Translin [Gallus gallus]
19537	ENU03331	ANI61C139:1	40-62	1011-	NAP	g731893	1070	128	9.00E-56	47	54	putative transporter YIL166C; probable membrane protein YIL166c - yeast (Saccharomyces cerevisiae); (Z46921) unknown [Saccharomyces cerevisiae]
19538	ENU03332	ANI61C1034	72-91	1030-	NAP	g2370487	1901	444	e-124	65	48	(Z98849) glutamyl-tma synthetase [Schizosaccharomyces pombe]
			0:1354..319	1065								

Seq num	Seq id	Contig Source	Primer 3 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat	Blast Score	Blast Score	% id	% cvrg	Description
19539	ENU03333	ANI61C4602:	49-75	1023-	NAP	g1723769	269	55	3.00E-11				probable membrane protein YGR260W;
		902..1937		1042									-yeast ( <i>Saccharomyces cerevisiae</i> ); (Z73044) ORF YGR260w
													[ <i>Saccharomyces cerevisiae</i> ]; (Y07777) YGR260w ORF [ <i>Saccharomyces cerevisiae</i> ] (AL04352) putative phosphodiesterase-nucleotide pyrophosphatase precursor [ <i>Schizosaccharomyces pombe</i> ] (AB000281) krev-1 [ <i>Neurospora crassa</i> ]
19540	ENU03334	ANI61C7359:	28-47	1002-1489..454	NAP	g3925755	533	246	2.00E-64	39	65		(AL04352) putative phosphodiesterase-nucleotide pyrophosphatase precursor [ <i>Schizosaccharomyces pombe</i> ] (AB000281) krev-1 [ <i>Neurospora crassa</i> ]
		1489..454		1021									(AB016807) flavohemoglobin [ <i>Fusarium oxysporum</i> ]
19541	ENU03335	ANI61C1897:	24-51	999-1018	NAP	g3434937	503	158	5.00E-38	61	94		Pepsinogen II-2/3 precursor (pepsinogen A); (M59235) pepsinogen [ <i>Oryctolagus cuniculus</i> ] (AL034491) conserved hypothetical protein [ <i>Schizosaccharomyces pombe</i> ] (AB011836) alkyl hydroperoxide reductase large subunit [ <i>Bacillus halodurans</i> ] (AJ223327) rAsp f 9 [ <i>Aspergillus fumigatus</i> ]
		2896..1859											(AJ223327) rAsp f 9 [ <i>Aspergillus fumigatus</i> ]
19542	ENU03336	ANI61C8156:	69-89	1043-2505..3542	NAP	g3551511	910	320	9.00E-87	47	83		Isotrichodermin C-15 hydroxylase (cytochrome P450 65A1); (AF011355) isotrichodermin C-15 hydroxylase [ <i>Fusarium sporotrichioides</i> ] (AF008220) yteR [ <i>Bacillus subtilis</i> ]; (Z99119) similar to hypothetical proteins [ <i>Bacillus subtilis</i> ]
		69-89		1064									
19543	ENU03337	ANI61C6276:	31-56	1007-133..1170	NAP	g129781	355	175	4.00E-43	32	87		
		31-56		1026									
19544	ENU03338	ANI61C7530:	22-48	993-1018	NAP	g4008577	348	111	8.00E-24	32	98		
		4427..3389											
19545	ENU03339	ANI61C5932:	59-78	1033-6356..5318	NAP	g4512354	224	83	5.00E-20				
		59-78		1055									
19546	ENU03340	ANI61C8268:	32-67	1010-4374..5413	NAP	g2879890	782	185	4.00E-77	52	98		
		32-67		1029									
19547	ENU03341	ANI61C1048	27-47	1005-5..5667..6705	NAP	g3915140	678	89	2.00E-46	36	63		
		27-47		1024									
19548	ENU03342	ANI61C8858:	22-41	996-1020	NAP	g2293194	303	152	3.00E-36	28	89		
		22-41		1041..1									

Seq num	Seq id	Contig Source	Primer 3 pos	Primer Basis	Selection	Blast at	Blast Blast	% id	% cvrg	Description	
			5 pos	NAP	Database Hit	ncbi gi	Score	Score	Prob		
19549	ENU03343	ANI61C2233:	24-46	1003-1022	g585542	541	223	1.00E-57		putative NADH-cytochrome B5 reductase (P35); cytochrome-b5 reductase (EC 1.6.2.2) - yeast (Saccharomyces cerevisiae); (Z28365)	
			3..1043							cytochrome b5 reductase [Saccharomyces cerevisiae]; (Z46861)	
19550	ENU03344	ANI61C3401:	22-52	998-1021	NAP	g2131525	108	39	0.01	25	94
			493..1534							[Saccharomyces cerevisiae] hypothetical protein YDR489w - yeast (Saccharomyces cerevisiae); (U33050) Ydr489wp; CAI: 0.16 [Saccharomyces cerevisiae]	
19551	ENU03345	ANI61C9825:	47-66	1028-1047	NAP	g3850084	230	63	5.00E-17	29	90
			5460..4418							(AL033389) alcohol dehydrogenase [Schizosaccharomyces pombe] (AL022071) hypothetical protein	
19552	ENU03346	ANI61C1042	51-77	1032-1051	NAP	g2950464	1087	312	e-102	67	58
			7..30..1072							[Schizosaccharomyces pombe] Heat shock protein HSP1 (65 KD IGE-binding protein); (U92465) heat shock protein [Aspergillus fumigatus]	
19553	ENU03347	ANI61C5619:	65-84	1046-1065	NAP	g2851483	1706	493	e-138	93	78
			2226..1184							glucosamine-6-phosphate isomerase (glucosamine-6-phosphate deaminase); glucosamine-6-phosphate isomerase (nagB) homolog - Haemophilus influenzae (strain Rd KW20); (U32700) glucosamine-6-phosphate isomerase (nagB) [Haemophilus influenzae Rd] protein transport protein SEC13; SEC13 protein - yeast (Saccharomyces cerevisiae); (L05929) Sec13p [Saccharomyces cerevisiae]; (U14913) Sec13p [Saccharomyces cerevisiae] (AL034583) related to yeast zds family proteins [Schizosaccharomyces pombe] (L39639) kievitone hydratase [Fusarium solani]	
19554	ENU03348	ANI61C41:20	44-64	1025-1044	NAP	g1171641	795	316	1.00E-85	59	96
			88..1046								
19555	ENU03349	ANI61C7807:	64-84	1044-1065	NAP	g417748	807	150	4.00E-77	62	90
			1969..3013							protein transport protein SEC13; SEC13 protein - yeast (Saccharomyces cerevisiae); (L05929) Sec13p [Saccharomyces cerevisiae]; (U14913) Sec13p [Saccharomyces cerevisiae] (AL034583) related to yeast zds family proteins [Schizosaccharomyces pombe] (L39639) kievitone hydratase [Fusarium solani]	
19556	ENU03350	ANI61C4411:	37-56	1014-1038	NAP	g4056558	130	74	2.00E-12	35	18
			1439..396								
19557	ENU03351	ANI61C3627:	53-73	1032-1054	NAP	g755011	496	217	1.00E-55	36	92

Seq num	Seq id	Contig Source	Primer 3 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat	Blast Score	Blast Prob	% id	% cvrg	Description
19558	ENU03352	ANI61C5159:	22-47	1008-2737..1690	NAP	g1171024	542	169	9.00E-49	46	87	"mitochondrial RNA splicing protein MRS3 ; splicing protein MRS3, mitochondrial - yeast (Saccharomyces cerevisiae) ; (X56445) MRS3 protein [Saccharomyces cerevisiae] ; (X87371) mitochondrial splicing unit [Saccharomyces cerevisiae] ; (Z49408) ORF YJL133w [Saccharomyces cerevisiae]"	
19559	ENU03353	ANI61C1040	23-45	1009-93163..2116	1028	NAP	g3024013	949	203	6.00E-57	66	94	eukaryotic translation initiation factor 2 alpha subunit (EIF-2-alpha) ; (AL021046) translational initiation factor 2 alpha [Schizosaccharomyces pombe]
19560	ENU03354	ANI61C2163:	53-72	1027-580..1631	1060	NAP	g1523784	140	83	1.00E-25	32	38	(Z79750) acid phosphatase [Emericella nidulans]
19561	ENU03355	ANI61C766:1	22-49	1008-329..279	1030	NAP	g2414631	65	61	0.000000	28	48	[Schizosaccharomyces pombe] (AL023589) hypothetical protein [Schizosaccharomyces pombe]
19562	ENU03356	ANI61C8382:	64-83	1052-3380..2329	1072	NAP	g3135990	765	167	2.00E-50	41	64	[Schizosaccharomyces pombe] Thioredoxin reductase ; 72k broad-range disulfide reductase (NADPH) (EC 1..--.) - <i>Pencillium chrysogenum</i> ; (X76119) thioredoxin reductase [Penicillium chrysogenum]
19563	ENU03357	ANI61C9268:	22-55	1011-688..1739	1031	NAP	g1351310	1415	514	e-145	83	96	MAK16 protein ; MAK16 protein - yeast (Saccharomyces cerevisiae) ; (J03852) MAK16 protein [Saccharomyces cerevisiae] ; (U12980) Mak16p : putative nuclear protein [Saccharomyces cerevisiae]
19564	ENU03358	ANI61C6529:	22-47	1012-556..6607	1031	NAP	g127112	758	204	6.00E-57	56	97	"Casein kinase II, alpha chain (CK II) (CK2-alpha) ; casein kinase II (EC 2.7.1.-) alpha chain - maize ; Protein Kinase Ck2 (Catalytic Subunit) From Zea Mays ; (X61387) casein kinase II alpha subunit [Zea mays]"

Seq num	Seq id	Contig Source	Primer 3 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat	Blast Score	Blast Prob	% id	% cvrg	Description
19566	ENU03360	ANI61C8693:	59-91	1048-76..1129	NAP	g1170603	1038	375	e-103	53	32	probable serine/threonine-protein kinase	
19567	ENU03361	ANI61C51:26	47-68	1040-..1080	NAP	g558311	1144	254	e-118	65	82	[Schizosaccharomyces pombe] (L35487) mannanase [Aspergillus aculeatus]	
19568	ENU03362	ANI61C980:5	22-57	1001-747..4693	NAP	g3342268	95	57	0.000000	38	14	(AF054824) delta 5 microsomal desaturase [Mortierella alpina]	
19569	ENU03363	ANI61C5185:	22-47	1020-1040..2099	NAP	g121087	556	217	5.00E-57	2	GCY protein ; GCY1 protein - yeast (Saccharomyces cerevisiae); (X13228) GCY protein (AA 1-312)		
19570	ENU03364	ANI61C1024	65-84	1022-9:1587..527	NAP	g417431	604	254	1.00E-66	[Saccharomyces cerevisiae]; (X90518) ORF O31567 [Saccharomyces cerevisiae]; (X94335) YOR3269w [Saccharomyces cerevisiae]; (X96740) GCY protein [Saccharomyces cerevisiae]; (Z75028) ORF YOR120w [Saccharomyces cerevisiae]			
													NADPH dehydrogenase 1 (old yellow enzyme 1); NADPH dehydrogenase (EC 1.6.99.1) chain OYE1 - yeast (Saccharomyces cerevisiae); Old Yellow Enzyme (Oxidized) (Oye) (E.C.1.6.99.1) Complexed With P-Hydroxybenzaldehyde ; Old Yellow Enzyme (Reduced) (Oye) (E.C.1.6.99.1); Old Yellow Enzyme (Oxidized) (Oye) (E.C.1.6.99.1); (X53597) NADPH dehydrogenase [Saccharomyces pastorianus] (Z11701) putative protein kinase [Saccharomyces cerevisiae] (Y14766) alk8 [Candida albicans]
19571	ENU03365	ANI61C8885:	32-51	1024-3652..2592	NAP	g3836	697	186	2.00E-76	47	29		
19572	ENU03366	ANI61C8063:	22-50	1013-1..1062	NAP	g3395458	212	56	1.00E-22	39	35		

Seq num	Seq id	Contig Source	Primer 3 pos	Primer 3 pos	Selection	aat	Blast Score	Blast Prob	% id	% cvrg	Description
19573	ENU03367	ANI61C5331:	1285..223	1056	NAP	g17178	2183	640	0	85	68 Benzoate 4-monoxygenase (benzoate-parahydroxylase) (cytochrome P450 53); benzoate 4-monoxygenase (EC 1.14.13.12) cytochrome P450 53 - Aspergillus niger; (X52521) benzoate 4-monoxygenase [Aspergillus niger] hypothetical protein 48.7 KD protein C6G10.03C in chromosome I; (Z98603) hypothetical protein [Schizosaccharomyces pombe] hypothetical protein (MEL3-10 3' region) - yeast (Saccharomyces cerevisiae); (Z37509) ORF near MEL [Saccharomyces cerevisiae] (Z97992) zuotin like protein [Schizosaccharomyces pombe] Salicylate hydroxylase (salicylate 1-monoxygenase); salicylate 1-monoxygenase (EC 1.14.13.1) - Pseudomonas putida (strain PpG7); (M60055) salicylate hydroxylase [Pseudomonas putida] (AL023534) putative methionine aminopeptidase 1
19574	ENU03368	ANI61C9104:	49..68	1049..1830..2897	NAP	g3183387	608	109	3.00E-37	40	71
19575	ENU03369	ANI61C2888:	24..42	1029..4069..5135	NAP	g1077195	884	136	3.00E-31	34	56
19576	ENU03370	ANI61C2922:	22..53	1020..130..1198	NAP	g2276350	899	290	1.00E-77	56	99
19577	ENU03371	ANI61C6515:	38..57	1032..274..1342	NAP	g1346660	77	4.00E-22			
19578	ENU03372	ANI61C9024:	29..61	1034..3033..1965	NAP	g3130036	1225	299	e-115	61	87 [Schiosaccharomyces pombe] Salicylate hydroxylase (salicylate 1-monoxygenase); salicylate 1-monoxygenase (EC 1.14.13.1) - Pseudomonas putida (strain PpG7); (M60055) salicylate hydroxylase [Pseudomonas putida]
19579	ENU03373	ANI61C6515:	44..63	1038..274..1342	NAP	g1346660	77	4.00E-22			
19580	ENU03374	ANI61C860:	2..46	1036..594..1524	NAP	g1078613	1726	301	e-171	88	74 stearoyl-CoA desaturase (EC 1.14.99.5) - Ajellomyces capsulata; (X85963) delta-9 fatty acid desaturase [Ajellomyces capsulatus]

Seq num	Seq id	Contig Source	Primer 3 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat	Blast Score	Blast Prob	% id	% cvrg	Description
19581	ENU03375	ANI61C6203:	25-45	1031-1033	NAP	g4503653	590	211	8.00E-54	40	52	"fatty-acid-Coenzyme A ligase, very long-chain 1; very-long-chain acyl-CoA synthetase (very-long-chain-fatty-acid-CoA ligase); (D88308) very-long-chain acyl-CoA synthetase [Homo sapiens]; (AF096290) very long-chain acyl-CoA synthetase [Homo sapiens]"	
19582	ENU03376	ANI61C5100:	70-90	1077-1151..81	NAP	g3859693	75	7.00E-13					(AL033497) transport protein [Candida albicans]
19583	ENU03377	ANI61C3804:	50-69	1052-3421..4492	NAP	g731684	590	192	2.00E-52	42	98	hypothetical 35.1 KD protein in NAM8-GAR1 intergenic region ; hypothetical protein YHR088w - yeast (Saccharomyces cerevisiae) ; (U00060) Yhr088wp [Saccharomyces cerevisiae] (U62917) glucose transporter TGTP2 [Taenia solium]	
19584	ENU03378	ANI61C9031:	63-82	1072-342..579	NAP	g1480799	37	0.000000					[AB011211] pectin methyl esterase [Aspergillus oryzae]
19585	ENU03379	ANI61C3234:	52-71	1063-725..1797	NAP	g4514622	469	107	4.00E-44	41	89	hypothetical 37.0 KD protein in SPO11R-GLYC intergenic region ; SUA5 homolog ipc-29d - Bacillus subtilis ; (Z38002) Similar to Saccharomyces cerevisiae SUA5 protein [Bacillus subtilis] ; (Z99122) alternate gene name: ipc-29d; similar to hypothetical proteins [Bacillus subtilis] ; ipc-29d gene [Bacillus subtilis]	
19587	ENU03381	ANI61C1139	65-84	1079-7..730..1805	NAP	g4506223	545	205	5.00E-52	36	84	"proteasome (prosome, macropain) 26S subunit, non-ATPase, 13 ; (AB009398) 26S proteasome subunit p40.5 [Homo sapiens]"	
19588	ENU03382	ANI61C7637:	50-72	1060-1107..2184	NAP	g3005839	410	110	1.00E-23	45	31	(AJ001732) rAsp f 4 [Aspergillus fumigatus]	
19589	ENU03383	ANI61C7016:	63-83	1068-6581..5505	NAP	g2493012	538	99	5.00E-34	41	17	probable calcium-transporting ATPase 9 ; probable membrane protein YOR291w - yeast (Saccharomyces cerevisiae) ; (Z75199) ORF YOR291w [Saccharomyces cerevisiae] (AC000133) ORF [Emericella nidulans]	
19590	ENU03384	ANI61C5673	26-48	1029-434..4511	NAP	g1870209	46	0.0004					

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Primer NAP	Selection Basis	Database Hit	ncbi gi	aat	Blast Score	Blast Prob	% id	% covg	Description	
19591	ENU03385	ANI61C8963:	26-45	1044-	1063		g2132210	665	268	4.00E-71	41	98		(Saccharomyces cerevisiae); (Z73508) ORF YPL152w [Saccharomyces cerevisiae]; (X96770) P2591 protein [Saccharomyces cerevisiae]	
19592	ENU03386	ANI61C4714:	40-61	1053-	1077	NAP	g1836161	530	212	1.00E-56	38	64		"(S83194) Ca2+/calmodulin-dependent protein kinase IV kinase isoform, CaM-kinase kinase alpha [rats, brain, Peptide, 505 aa] [Rattus sp.]; (AB023658) Ca/calmodulin-dependent protein kinase kinase alpha, CaM-kinase kinase alpha [Rattus norvegicus]"	
19593	ENU03387	ANI61C129:3	29-48	1036-	NAP		g2340046	2589	326	e-105	79	42		(L48074) secreted dipeptidyl peptidase [Aspergillus fumigatus]	
19594	ENU03388	ANI61C5996:	22-42	1031-	NAP		g2650534	128	74	2.00E-12	29	54		(AE001098) conserved hypothetical protein [Archaeoglobus fulgidus]	
19595	ENU03389	ANI61C7595:	23-51	1039-	NAP		g2131398	463	120	2.00E-45	37	92		hypothetical protein YDR214w - yeast (Saccharomyces cerevisiae); (Z68195) unknown [Saccharomyces cerevisiae]; (Z68194) unknown [Saccharomyces cerevisiae]	
19596	ENU03390	ANI61C1118	47-66	1063-	1084	NAP	g1723555	83	2.00E-15					hypothetical 27.0 KD protein C12B10.13 in chromosome 1; (Z70721) conserved hypothetical protein. [Schizosaccharomyces pombe] (AL049522) putative dolichol kinase [Schizosaccharomyces pombe]	
19597	ENU03391	ANI61C8085:	52-71	1074-	NAP		g4539603	263	91	1.00E-17	36	37		[Schizosaccharomyces pombe] (AL049522) putative dolichol kinase [Schizosaccharomyces pombe]	
19598	ENU03392	ANI61C1118:	22-53	1043-	NAP		g2498094	348	162	4.00E-39	34	93		2-nitropropane dioxygenase precursor (nitroalkane oxidase) (2-NPD); (U22530) 2-nitropropane dioxygenase precursor [Neurospora crassa]	
19599	ENU03393	ANI61C4327:	27-47	1047-	1150..2235	NAP	g1351597	376	203	2.00E-51	40	72		hypothetical 48.0 KD protein C4G8.06C in chromosome 1; hypothetical protein SPAC4G8.06c - fission yeast (Schizosaccharomyces pombe); (Z56276) hypothetical protein [Schizosaccharomyces pombe] (AL023589) membrane transporter [Schizosaccharomyces pombe]	
19600	ENU03394	ANI61C238:1	22-49	0..1096	1047-	1066	NAP	g3135988	201	89	1.00E-19	35	36		

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Primer NAP	Selection Basis	Database Hit	ncbi gi	aat	Blast Score	Blast Prob	% id	% cvrg	Description
19601	ENU03395	ANI61C7744:	33-54	1058-	1077	NAP	g130684	910	314	7.00E-85	66	93	Outer mitochondrial membrane protein (X05824) major protein (AA 1-283) [Neurospora crassa]	
19602	ENU03396	ANI61C3311:	24-55	1050-	1059	NAP	g4581517	83	3.00E-33					porin ; porin - Neurospora crassa ; oxidase [Schizosaccharomyces pombe] (AL049559) putative d-amino acid oxidase [Schizosaccharomyces pombe] Amidase ; amidase (EC 3.5.1.4) - Brevibacterium sp. (strain R312) ; amidase - Rhodococcus sp. (strain N-774) ; (X54074) amidase [Rhodococcus sp.] ; (M60264)
19603	ENU03397	ANI61C2398:	58-77	1084-	1104	NAP	g113712	600	147	6.00E-40	35	61		enantiomer-selective amidase [Brevibacterium sp.] ; (AB016078) amidase [Rhodococcus sp. N-771] "putative 38.2 KD phosphatase 2C in chromosome I ; (Z98762) SPA.C4A.8.03c, putative protein phosphatase, len:339aa , similar eg. to P2C1_SCHPO, P40371, protein phosphatase 2c homolog 1,(347aa), fasta scores, opt:276, E):3.2e-11, (29.4% identity in 282 aa overlap), also simi..."
19604	ENU03398	ANI61C7272:	24-43	1046-	1071	NAP	g3183379	405	144	9.00E-34	36	83		tetratricopeptide repeat domain 2 ; (U46571) tetratricopeptide repeat protein [Homo sapiens] (Z97052) putative ubiquinone biosynthesis methyltransferase [Schizosaccharomyces pombe] (AJ223327) rAsp f9 [Aspergillus fumigatus]
19605	ENU03399	ANI61C1068	50-70	1079-	1098	NAP	g4507713	505	203	4.00E-51	36	69		putative ribokinase ; (AL023554) ribokinase [Schizosaccharomyces pombe]
19606	ENU03400	ANI61C6636:	23-42	1051-	1071	NAP	g2213547	476	183	1.00E-48	52	59		hypothetical 37.5 KD protein in YUH1-URA8 intergenic region ; hypothetical protein YJR100c - yeast (Saccharomyces cerevisiae) ; (Z49600) ORF YJR100c [Saccharomyces cerevisiae]
19607	ENU03401	ANI61C8531:	38-58	1068-	1173..79	NAP	g2879890	627	264	7.00E-70	46	89		
19608	ENU03402	ANI61C6472:	69-88	1090-	1122	NAP	g3914593	236	132	4.00E-30	39	91		
19609	ENU03403	ANI61C2203:	48-67	1083-	1130..34	NAP	g1352904	296	69	1.00E-24	34	84		

Seq num	Seq id	Contig Source	Primer 3 pos	Primer Basis	Selection	aat	Blast Score	Blast Prob	% id	% cvrg	Description
			5 pos	Database Hit	ncbi gi	Score	Prob	e-118	72	95	
19610	ENU03404	ANI61C9708:	58-77	NAP	g1168269	1196	222				"Arabinan endo-1,5-alpha-L-arabinosidase A precursor (endo-1,5-alpha-L-arabinanase A) (ABN A); (L23430) endo-1,5-alpha-L-Arabinanase [Aspergillus niger]; endo-1,5-alpha-L-Arabinanase [Aspergillus niger]"
19611	ENU03405	ANI61C9805:	42-61	1079-	NAP	g4512702	567	70	3.00E-11	35	24
		1380..282	1098								(AC006569) hypothetical protein [Arabidopsis thaliana]
19612	ENU03406	ANI61C1031	63-82	1096-	NAP	g731746	302	130	2.00E-29	36	80
		6..2340..3438	1119								hypothetical 42.4 KD protein in ENO2-STB5 intergenic region ; hypothetical protein YHR176W - yeast
19613	ENU03407	ANI61C1067:	69-88	1104-	NAP	g3024986	129	59	1.00E-10		
		1112..2210	1125								hypothetical zinc-type alcohol dehydrogenase-like protein in AHPF-RNK intergenic region ; (U82598) FadH homolog [Escherichia coli] ; (AE000166) putative oxidoreductase [Escherichia coli] ; (D90701) Glutathione-dependent formaldehyde dehydrogenase (EC 1.2.1.1) (FDH) (FALDH). [Escherichia coli] ; (D90702) Glutathione-dependent formaldehyde dehydrogenase (EC 1.2.1.1) (FDH) (FALDH). [Escherichia coli]
19614	ENU03408	ANI50C1743	37-64	1050-	NAP	g2132293	157	1.00E-37	32	90	hypothetical protein YPR128c - yeast (Saccharomyces cerevisiae) ; (U40829) Similar to mitochondrial ADP/ATP carrier protein (Swiss Prot accession number P12235) and mitochondrial phosphate carrier protein (Swiss Prot accession number Q00325) [Saccharomyces cerevisiae]
		6..1:16..1114	1093								"Leucyl-tRNA synthetase, mitochondrial precursor (leucine-tRNA ligase) (LEURS), leucine-tRNA ligase (EC 6.1.1.4) precursor, mitochondrial - Neurospora crassa; (M30472) leucyl-tRNA synthetase [Neurospora crassa]"
19615	ENU03409	ANI61C7138:	45-65	1082-	NAP	g135142	1945	270	9.00E-72	44	36
		1323..2422	1102								

Seq num	Seq id	Contig Source	Primer 3 pos	Primer 3 pos	Selection Basis	Database Hit	.ncbi gi	aat	Blast Score	Blast Prob	% id	% cvrg	Description
19616	ENU03410	ANI61C7147:	56-83	1093-7618..6518	NAP	g128847	1614	603	e-173	90	69	NADH-ubiquinone oxidoreductase 49 KD subunit precursor (complex I-49KD) (Cl-49KD); NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) 49K chain - <i>Neurospora crassa</i> ; (X54508) NADH dehydrogenase 49 kD subunit [Neurospora crassa] (X53840) mitochondrial ribosomal protein YmL20 [Saccharomyces cerevisiae]	
19617	ENU03411	ANI61C9007:	22-51	1061-2391..3492	NAP	g3976	198	71	1.00E-11	31	59	"putative dihydroxy-acid dehydratase precursor (DAD)(2,3-Dihydroxy acid hydrolyase); (Z69795) unknown [Schizosaccharomyces pombe]" "ATP synthase alpha chain, mitochondrial precursor; H <sup>+</sup> -transporting ATP synthase (EC 3.6.1.34) alpha chain - <i>Neurospora crassa</i> ; (M84191) mitochondrial ATPase alpha-subunit [Neurospora crassa]"	
19618	ENU03412	ANI61C6616:	43-61	1081-2489..1387	NAP	g1708464	1270	222	e-108	67	56	(AJ001909) transcriptional activator [Aspergillus niger]	
19619	ENU03413	ANI61C953:2	55-74	1093-815..1713	NAP	g584806	1920	661	0	88	66	"Exopolygalacturonase precursor (EXOPG) (galacturan 1,4-alpha-D-galacturonidase) (poly(1,4-alpha-D-galacturonide)galacturonohydrolase); (X99795) exopolygalacturonase [Aspergillus tubingensis]" "hypothetical 52.3 KD protein in FRE2 5'region ; hypothetical protein YKL221w - yeast (Saccharomyces cerevisiae); (X75950) ORF4, B473 [Saccharomyces cerevisiae]; (Z28221) ORF YKL221w [Saccharomyces cerevisiae]; ORF 4 [Saccharomyces cerevisiae]" (Z68905) ATP-binding cassette multidrug transporter [Emericella midulans]	
19620	ENU03414	ANI61C1699:	27-47	1065-2563..1461	NAP	g2808634	3172	522	e-147	80	39	"Exopolygalacturonase precursor (EXOPG) (galacturan 1,4-alpha-D-galacturonidase) (poly(1,4-alpha-D-galacturonide)galacturonohydrolase); (X99795) exopolygalacturonase [Aspergillus tubingensis]" "hypothetical 52.3 KD protein in FRE2 5'region ; hypothetical protein YKL221w - yeast (Saccharomyces cerevisiae); (X75950) ORF4, B473 [Saccharomyces cerevisiae]; (Z28221) ORF YKL221w [Saccharomyces cerevisiae]; ORF 4 [Saccharomyces cerevisiae]" (Z68905) ATP-binding cassette multidrug transporter [Emericella midulans]	
19621	ENU03415	ANI61C8652:	34-54	1080-93..1201	NAP	g2499716	226	77	2.00E-13	29	67		
19622	ENU03416	ANI61C1106	33-52	1082-6:144..1255	NAP	g549759	630	185	5.00E-58	31	78		
19623	ENU03417	ANI61C5477:	22-48	1068-81..1191	NAP	g1834342	750	190	3.00E-78	48	21		

Seq num	Seq id	Contig Source	Primer 3 pos	Primer Basis	Selection	aat	Blast Score	Blast Prob	% id	% cvrg	Description
				ncbi gi	Database Hit	g					
19624	ENU03418	ANI61C7673:	5 pos	NAP	g4495126	1033	269	3.00E-71	37	35	(AL035583) putative helicase
19625	ENU03419	ANI61C8010:	1030..2141	1133	1056-	NAP	g1173405	733	169	2.00E-71	[Schizosaccharomyces pombe] "protein phosphataseS PPI regulatory subunit SDS22 ; protein suppressor sds22 - fission yeast
			2230..3341	1091							(Schizosaccharomyces pombe); (Z98762) SPAC4A.8.12c, sds22; protein phosphatases ppl regulat ory subunit, len:332aa, identical to SD22_SCHPO, P22194, (3 32aa), similar eg. to yeast Q15435, SDS22 homolog, (360aa), fasta scores, opt:837, E:0. (47.6% identi... "
19626	ENU03420	ANI61C8479:	62-82	1111-	NAP	g2440180	1508	542	e-153	69	11 (Z99531) ubiquinin system protein [Schizosaccharomyces pombe]
19627	ENU03421	ANI61C9176:	1350..238	1132	NAP	g1653915	415	203	2.00E-51	32	96 (D90917) hypothetical protein [Synechocystis sp.]
19628	ENU03422	ANI61C1899:	1803..691	1072-	NAP	g137043	489	149	4.00E-53	44	84 "uracil-DNA glycosylase precursor (UDG) ; uracil-DNA glycosylase (EC 3.2.2.-) - yeast (Saccharomyces cerevisiae); (I04470) uracil-DNA-glycosylase [Saccharomyces cerevisiae]; (Z46659) UNG1 gene, len: 359, CAI: 0.12, uracil-DNA glycosylase [Saccharomyces cerevisiae]"
			3429..2317	1117							(AL035503) peptide transport protein [Candida albicans] (AL022592) acetamidase [Schizosaccharomyces pombe] probable membrane protein YLL028w -yeast (Saccharomyces cerevisiae); (Z73133) ORF YLL028w [Saccharomyces cerevisiae] putative transporter C11D3.18C; (Z68166) unknown [Schizosaccharomyces pombe]
19632	ENU03426	ANI61C6686:	34-56	1083-	NAP	g1351714	288	90	3.00E-17	25	68
			2749..1635	1106							

Seq num	Seq id	Contig Source	Primer 3 pos	Primer 3 pos	Selection Basis	Database Hit	nebi gi	aat	Blast Score	Blast Score	% id	% cvrg	Description
19633	ENU03427	ANI61C1032	22-50	1076-	NAP	g126918	310	92	9.00E-32	36	95	Mono- and diacylglycerol lipase precursor (MDGL) ; mono- and diacylglycerol lipase (EC 3.1.1.-)	
			0:1321..2437	1096									precursor - <i>Penicillium camembertii</i> ; (D90315) MDGL precursor [ <i>Penicillium camembertii</i> ]
19634	ENU03428	ANI61C2335:	57-75	1111-1132	NAP	g1346703	1482	468	e-142	78	96	Polygalacturonase precursor (pectinase) (PGL) ; polygalacturonase (EC 3.2.1.15) precursor - <i>Aspergillus parasiticus</i> ; (U17167)	
		3069..1952											polygalacturonase precursor [ <i>Aspergillus parasiticus</i> ] ; (L23523) polygalacturonase [ <i>Aspergillus parasiticus</i> ]
19635	ENU03429	ANI61C6897:	66-97	1108-1141	NAP	g3646379	657	161	2.00E-59	41	60	(AJ001540) phenylacetyl-CoA ligase [ <i>Penicillium chrysogenum</i> ]	
		2289..1172											(AL035396) SRG1-like protein [ <i>Arabidopsis thaliana</i> ]
19636	ENU03430	ANI61C22091:	39-58	1087-1114	NAP	g4454019	62	2.00E-12					
		2554..1436											(AL035076) putative carboxylesterase-lipase family member
19637	ENU03431	ANI61C6093:	28-51	1077-1104	NAP	g4107289	467	192	2.00E-50	35	66	[ <i>Schizosaccharomyces pombe</i> ] probable membrane protein YOL107w - yeast ( <i>Saccharomyces cerevisiae</i> ) ; (Z48149) similarity with <i>P. tetraurelia</i> cytochrome C oxidase [ <i>Saccharomyces cerevisiae</i> ] ; (Z74849) ORF YOL107w [ <i>Saccharomyces cerevisiae</i> ]	
		4053..2935											
19638	ENU03432	ANI61C9179:	35-54	1091-1112	NAP	g1077295	175	102	4.00E-21	31	92	[ <i>Schizosaccharomyces pombe</i> ] probable membrane protein YOL107w - yeast ( <i>Saccharomyces cerevisiae</i> ) ; (X81424) Pas7p	
		2067..949											
19639	ENU03433	ANI61C7538:	22-46	1081-1100	NAP	g730272	625	238	3.00E-77	43	92	Peroxisomal targeting signal 2 receptor (PTS2 receptor) (peroxisome import protein PAS7) (peroxin-7) ; PAS7 protein - yeast ( <i>Saccharomyces cerevisiae</i> ) ; (X81424) Pas7p [ <i>Saccharomyces cerevisiae</i> ] ; (X83704) Peb1 [ <i>Saccharomyces cerevisiae</i> ] (AL022103) deoxyribidylate deaminase [ <i>Schizosaccharomyces pombe</i> ] (D45893) acr-2 [ <i>Neurospora crassa</i> ]	
		2343..1223											
19640	ENU03434	ANI61C6107:	62-82	1122-1141	NAP	g2956780	608	108	1.00E-57	46	90		
		3168..4289											
19641	ENU03435	ANI61C9017:	71-91	1133-1151	NAP	g1754596	398	97	2.00E-19	31	54		
		1203..81											

Seq num	Seq id	Contig Source	Primer 3 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat	Blast Score	Blast Prob	% id	% cvrg	Description
19642	ENU03436	ANI61C9774:	5 pos	5 pos	NAP	g549443	8521	690	0	99	18	Conidial green pigment synthase ; probable polyketide synthase -	
			3928..5051	1127-								Emericella nidulans ; (X65866)	
				1146								putative polyketide or fatty acid synthase [Emericella nidulans] ; wA synthase [Emericella nidulans]	
19643	ENU03437	ANI61C1695:	22-52	1069-	NAP	g3559935	425	141	5.00E-47	55	54	(A)005253) CipP protease [Mus musculus]; (A)012249) CipP protease [Mus musculus]	
			1352..1600	1103								[Mus musculus]	
19644	ENU03438	ANI61C6466:	22-57	1085-	NAP	g1171741	1602	512	e-144	92	99	"NMT1" protein homolog ; nmt1 protein - Aspergillus parasiticus ; (UJ15196) the expression of this gene has been shown to be completely inhibited by thiamine as was observed for the Schizosaccharomyces pombe nmt1, Swiss-Prot Accession Number P36597	
			615..1739	1104								[Aspergillus parasiticus] "Aspergillus parasiticus]" cytochrome C PERoxidase precursor (CCP) ; cytochrome-c peroxidase (EC 1.11.1.5) precursor - yeast (Saccharomyces cerevisiae); (X62422) Cytochrome c peroxidase [Saccharomyces cerevisiae]; (Z28291) ORF YKR066c [Saccharomyces cerevisiae]	
19645	ENU03439	ANI61C1045	70-89	1124-	NAP	g543969	593	135	5.00E-61	42	95	cytochrome C PERoxidase precursor (CCP) ; cytochrome-c peroxidase (EC 1.11.1.5) precursor - yeast (Saccharomyces cerevisiae); (X62422) Cytochrome c peroxidase [Saccharomyces cerevisiae]; (Z28291) ORF YKR066c [Saccharomyces cerevisiae]	
			1:4390..3264	1154								chromosome 22 open reading frame 1 ; (U84894) 239AB [Homo sapiens] (U59214) MAP protein kinase MPKA [Emericella nidulans]	
19646	ENU03440	ANI61C7019:	64-83	1128-	NAP	g4502497	280	71	1.00E-11	38	89	(U26643) NADPH-dependent aldehyde reductase [Sporidiobolus salmonicolor] (U41278) contains similarity to G beta repeats (PROsite:PS00670) of the beta-transducin family [Caenorhabditis elegans]	
			5621..4493	1149									
19647	ENU03441	ANI61C3212:	38-58	1104-	NAP	g4580577	2092	412	0	97	81	(U41278) contains similarity to G beta repeats (PROsite:PS00670) of the beta-transducin family [Caenorhabditis elegans]	
			2345..1218	1123									
19648	ENU03442	ANI61C1118	46-65	1114-	NAP	g1142698	719	120	3.00E-50	57	94	(U26643) NADPH-dependent aldehyde reductase [Sporidiobolus salmonicolor] (U41278) contains similarity to G beta repeats (PROsite:PS00670) of the beta-transducin family [Caenorhabditis elegans]	
			2,2717..3848	1135									
19649	ENU03443	ANI61C8239:	22-52	1090-	NAP	g1086900	178	59	9.00E-12	31	39	(U41278) contains similarity to G beta repeats (PROsite:PS00670) of the beta-transducin family [Caenorhabditis elegans]	
			1151..20	1111									
19650	ENU03444	ANI61C1097	60-79	1131-	NAP	g2132958	353	153	1.00E-36	30	65	probable membrane protein YOR380w -yeast (Saccharomyces cerevisiae); (Z75288) ORF YOR380w [Saccharomyces cerevisiae]	
			9..7353..6221	1150									

Seq num	Seq id	Contig Source	Primer 3 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	Score	Score	Blast Prob	% id	% cvrg	Description
19651	ENU03445	ANI61C8387:	72-92	1139-	NAP	g3560241	373	85	4.00E-21	40	26	(AL031532) putative amino acid permease [Schizosaccharomyces pombe]	
19652	ENU03446	ANI61C5168:	25-52	1088-	NAP	g1171946	615	183	1.00E-71	41	93	NADPH dehydrogenase 3 (old yellow enzyme 3); NADPH dehydrogenase (EC 1.6.99.1) OYE3 - yeast (Saccharomyces cerevisiae); (L29279) NADPH dehydrogenase [Saccharomyces cerevisiae]; (Z73527) ORF YPL171c [Saccharomyces cerevisiae]	
19653	ENU03447	ANI61C113	46-65	1110-	NAP	g1730251	724	192	4.00E-84	56	91	GTP cyclohydrolase II; GTP-cyclohydrolase - <i>Pichia guilliermondii</i> ; GTP-cyclohydrolase - <i>Pichia guilliermondii</i> ; (Z49093) GTP-cyclohydrolase [ <i>Pichia guilliermondii</i> ]	
19654	ENU03448	ANI61C2332:	27-50	1094-	NAP	g136053	1099	187	e-111	98	99	Triosephosphate isomerase (TIM); triose-phosphate isomerase (EC 5.3.1.1) - <i>Emericella nidulans</i> ; (D0019) triosephosphate isomerase [ <i>Emericella nidulans</i> ]	
19655	ENU03449	ANI61C6376:	58-77	1131-	NAP	g1723274	275	96	4.00E-19	36	94	hypothetical 30.0 KD protein C13F4.14 in chromosome I ; hypothetical protein - fission yeast ( <i>Schizosaccharomyces pombe</i> ) ; (AL031322) conserved hypothetical protein	
19656	ENU03450	ANI61C2623:	71-89	1145-	NAP	g732190	81	6.00E-16				[ <i>Schizosaccharomyces pombe</i> ] hypothetical 51.6 KD protein in SSB2-SPX18 intergenic region ; hypothetical protein YNL206c - yeast (Saccharomyces cerevisiae); (X78898) possibly expressed during the late G1 /S phase; homology with the SSRP proteins [Saccharomyces cerevisiae]; (Z71482) ORF YNL206c [Saccharomyces cerevisiae]	
19657	ENU03451	ANI61C9329:	69-88	1142-	NAP	g3078001	36	0.66				(AF031376) LIM-domain binding factor 2; LDB2 [Danio rerio]	
19658	ENU03452	ANI61C3576:	55-75	1120-	NAP	g2833327	76	4.00E-13				Hexokinase ; (L04480) hexokinase [Schistosoma mansoni]	
		634..1771	634..1771	1150									

Seq num	Seq id	Contig Source	Primer 3 pos	Primer Basis	Selection	aat	Blast Score	Blast Prob	% id	% cvrg	Description	
			5 pos	Database Hit	ncbi gi	Score	Prob	e-119	58	88		
19659	ENU03453	ANI61C4140:	43-63 135..1273	NAP	g1705465	1079	414	e-119	58	88	Biotin synthetase (biotin synthetase); biotin synthetase - yeast ( <i>Saccharomyces cerevisiae</i> ); (Z23071) ORF YGR286c [ <i>Saccharomyces cerevisiae</i> ]	
19660	ENU03454	ANI61C9438:	31-50 91..1229	1100- 1127	NAP	g3929362	362	174	9.00E-43	32	70	pisatin demethylase (cytochrome P450 57A1); pisatin demethylase - fungus ( <i>Nectria haematococca</i> ); (L20976) pisatin demethylase [ <i>Nectria haematococca mpV1</i> ]
19661	ENU03455	ANI61C6611:	30-57 1466..2605	1105- 1127	NAP	g2492777	604	220	1.00E-56	47	88	hypothetical zinc-type alcohol dehydrogenase-like protein in PRE5-FET4 intergenic region; hypothetical protein YMR318c - yeast ( <i>Saccharomyces cerevisiae</i> ); (Z54141) unknown [ <i>Saccharomyces cerevisiae</i> ] Polygalacturonase precursor (PG) [pectinase]; (L02239) endopolygalacturonase [ <i>Gibberella fujikuroi</i> ] putative disulfide isomerase TIGA precursor; (X98748) tigA [ <i>Aspergillus niger</i> ] (U61983) benzyl alcohol dehydrogenase [ <i>Acinetobacter calcoaceticus</i> ]
19662	ENU03456	ANI61C7326:	23-45 515..1656	1093- 1122	NAP	g385668	807	192	5.00E-48	49	90	(X95720) O6357 [ <i>Saccharomyces cerevisiae</i> ] pectinase precursor; (L22857) Pectin lyase [ <i>Colletotrichum gloeosporioides</i> ]
19663	ENU03457	ANI61C5335:	22-41 2897..4040	1103- 1125	NAP	g2501210	1300	420	e-135	69	99	"glucosidase precursor (glucan 1,4-alpha-glucosidase) (1,4-alpha-D-glucan glucohydrolase); glucan 1,4-alpha-glucosidase (EC 3.2.1.3) precursor - Aspergillus sp.; (D10460) glucosidase [Aspergillus shirousami]"
19664	ENU03458	ANI61C2777:	52-71 1206..2352	1137- 1156	NAP	g1408294	565	220	1.00E-56	39	94	(X95720) O6357 [ <i>Saccharomyces cerevisiae</i> ] Pectin lyase precursor; (L22857) Pectin lyase [ <i>Colletotrichum gloeosporioides</i> ]
19665	ENU03459	ANI61C4098:	72-91 690..1836	1154- 1176	NAP	g1199853	292	140	2.00E-32	36	90	"glucosidase precursor (glucan 1,4-alpha-glucosidase) (1,4-alpha-D-glucan glucohydrolase); glucan 1,4-alpha-glucosidase (EC 3.2.1.3) precursor - Aspergillus sp.; (D10460) glucosidase [Aspergillus shirousami]"
19666	ENU03460	ANI61C3743:	67-86 4765..5912	1152- 1171	NAP	g3914390	685	150	2.00E-35	45	91	(monoamine oxidase) (MAO)
19667	ENU03461	ANI61C1756:	50-79 3030..1882	1134- 1156	NAP	g113792	1500	466	e-130	63	59	Amine oxidase [flavin-containing]
19668	ENU03462	ANI61C9390:	67-94 2443..1293	1149- 1175	NAP	g3915606	251	86	1.00E-24	30	52	

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Prob	% id	% cvrg	Description
19669	ENU03463	ANI61C348:2	23-58	1109-	NAP	g3493591	647	279	3.00E-74	44	56	(AF063231) cytoplasmic dynein intermediate chain 2 [Mus musculus]	
..1154												"probable transporter FEN2; probable membrane protein YCR028c - yeast (Saccharomyces cerevisiae); (X59720) YCR028c, [len:512 [Saccharomyces cerevisiae]"	
19670	ENU03464	ANI61C323:2	25-44	1118-	NAP	g140479	785	148	9.00E-35	36	37	membrane protein YCR028c - yeast (Saccharomyces cerevisiae); (X59720) YCR028c, [len:512 [Saccharomyces cerevisiae]"	
848..1695												"laccase (EC 1.10.3.2) I - Emericella nidulans	
19671	ENU03465	ANI61C103:7	29-50	1121-	NAP	g66290	554	217	9.00E-56	34	59	probable 2-dehydropantoate 2-reductase (ketopantoate reductase) (KPA reductase); (AE000986) thiamine biosynthesis protein (apbA) [Archaeoglobus fulgidus] probable 2-dehydropantoate 2-reductase (ketopantoate reductase) (KPA reductase); (AE000986) thiamine biosynthesis protein (apbA) [Archaeoglobus fulgidus] hypothetical 49.6 KD protein C5D6.04 in chromosome 1; (Z98056) hypothetical protein [Schizosaccharomyces pombe] probable membrane protein YOL137w -yeast (Saccharomyces cerevisiae); (Z74879) ORF YOL137w [Saccharomyces cerevisiae]; (X95465) ORF [Saccharomyces cerevisiae] (U89991) mannose-1-phosphate guanyltransferase [Hypocrea jecorina]	
2..81..1234				1140									
19672	ENU03466	ANI61C843:3	23-46	1111-	NAP	g3913072	143	86	5.00E-16	39	24	probable 2-dehydropantoate 2-reductase (ketopantoate reductase) (KPA reductase); (AE000986) thiamine biosynthesis protein (apbA) [Archaeoglobus fulgidus] probable 2-dehydropantoate 2-reductase (ketopantoate reductase) (KPA reductase); (AE000986) thiamine biosynthesis protein (apbA) [Archaeoglobus fulgidus] hypothetical 49.6 KD protein C5D6.04 in chromosome 1; (Z98056) hypothetical protein [Schizosaccharomyces pombe] probable membrane protein YOL137w -yeast (Saccharomyces cerevisiae); (Z74879) ORF YOL137w [Saccharomyces cerevisiae]; (X95465) ORF [Saccharomyces cerevisiae] (U89991) mannose-1-phosphate guanyltransferase [Hypocrea jecorina]	
768..2614				1134									
19673	ENU03467	ANI61C843:3	41-64	1129-	NAP	g3913072	143	86	5.00E-16	39	24	probable 2-dehydropantoate 2-reductase (ketopantoate reductase) (KPA reductase); (AE000986) thiamine biosynthesis protein (apbA) [Archaeoglobus fulgidus] probable 2-dehydropantoate 2-reductase (ketopantoate reductase) (KPA reductase); (AE000986) thiamine biosynthesis protein (apbA) [Archaeoglobus fulgidus] hypothetical 49.6 KD protein C5D6.04 in chromosome 1; (Z98056) hypothetical protein [Schizosaccharomyces pombe] probable membrane protein YOL137w -yeast (Saccharomyces cerevisiae); (Z74879) ORF YOL137w [Saccharomyces cerevisiae]; (X95465) ORF [Saccharomyces cerevisiae] (U89991) mannose-1-phosphate guanyltransferase [Hypocrea jecorina]	
768..2614				1152									
19674	ENU03468	ANI61C954:2	28-53	1120-	NAP	g3183308	392	143	2.00E-33	37	38	probable membrane protein YOL137w -yeast (Saccharomyces cerevisiae); (Z74879) ORF YOL137w [Saccharomyces cerevisiae]; (X95465) ORF [Saccharomyces cerevisiae] (U89991) mannose-1-phosphate guanyltransferase [Hypocrea jecorina]	
45..1198				1139									
19675	ENU03469	ANI61C670:2	36-60	1129-	NAP	g2132851	146	53	9.00E-12	29	44	probable membrane protein YOL137w -yeast (Saccharomyces cerevisiae); (Z74879) ORF YOL137w [Saccharomyces cerevisiae]; (X95465) ORF [Saccharomyces cerevisiae] (U89991) mannose-1-phosphate guanyltransferase [Hypocrea jecorina]	
1884..728				1150									
19676	ENU03470	ANI61C950:2	55-74	1150-	NAP	g3323397	1563	518	e-163	83	92	hypothetical 71.1 KD protein in DSK2-CAT8 intergenic region ; hypothetical protein YMR278w - yeast (Saccharomyces cerevisiae); (Z49704) unknown [Saccharomyces cerevisiae]	
1289..133				1169									
19677	ENU03471	ANI61C546:1	35-55	1129-	NAP	g2499517	578	181	3.00E-66	41	56	hypothetical 71.1 KD protein in DSK2-CAT8 intergenic region ; hypothetical protein YMR278w - yeast (Saccharomyces cerevisiae); (Z49704) unknown [Saccharomyces cerevisiae]	
4..1171				1150									

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Primer Basis	Selection	aat	Blast Score	Blast Prob	% id	% cvrg	Description
19678	ENU03472	AN161C11:71	67-87	3..1872	NAP	g1730840	935	190	1.00E-47	36	45	putative cysteinyl-TRNA synthetase C29E6_06C (cysteine-TRNA ligase) (CYRS) ; probable membrane protein YNL247w - yeast ( <i>Saccharomyces cerevisiae</i> ) ; (X96722) ORF N0885 [Saccharomyces cerevisiae] ; (Z71523) ORF YNL247w [Saccharomyces cerevisiae]
19679	ENU03473	AN161C8853:	29-48	1114-	NAP	g1730193	703	291	5.00E-78			UDP-glucose 4-epimerase (galactowaldenase) (UDP-GAlactose 4-epimerase) ; (X99339) UDP-glucose 4-epimerase [Bacillus subtilis] ; (D83026) highly homologous to UDP-glucose 4-epimerases (SwissProt:GALE_HAEIN and GALE_ECOLI) ; hypothetical [Bacillus subtilis] ; (Z99123) UDP-glucose 4-epimerase [Bacillus subtilis] (M11621) putative [Saccharomyces cerevisiae]
19680	ENU03474	AN161C676:4	44-65	1145-	NAP	g806323	295	93	2.00E-27	39	58	"(AC005970) putative translation initiation factor eIF-2B, alpha subunit [Arabidopsis thaliana]" probable membrane protein YOR306c - yeast ( <i>Saccharomyces cerevisiae</i> ) ; (Z75214) ORF YOR306c [Saccharomyces cerevisiae]
19681	ENU03475	AN161C9629:	22-43	319..3440	NAP	g4006818	832	135	9.00E-80	55	96	(AF007270) contains similarity to syntaxin [Arabidopsis thaliana] (AL033497) unknown hypothetical protein [Candida albicans]
19682	ENU03476	AN161C1097	49-68	1152-	NAP	g2132942	112	4.00E-24				N amino acid transport system protein (methyltryptophan resistance protein) ; neutral amino acid permease - Neurospora crassa ; (L34605) neutral amino acid permease [Neurospora crassa]
19683	ENU03477	AN150C1823	27-46	1128-	NAP	g2191179	72	6.00E-12	31	72		
19684	ENU03478	AN161C5073:	39-58	-62180..3345	NAP	g3859696	361	123	4.00E-38	34	78	(AL033497) unknown hypothetical protein [Candida albicans]
19685	ENU03479	AN161C4357:	53-73	1205..40	NAP	g2507070	383	105	4.00E-38	36	65	N amino acid transport system protein (methyltryptophan resistance protein) ; neutral amino acid permease - Neurospora crassa ; (L34605) neutral amino acid permease [Neurospora crassa]

Seq num	Seq id	Contig Source	Primer 3 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	Score	Score	Blast Prob	% id	% cvrg	Description
19686	ENU03480	ANI61C11:71	67-87	1173-	NAP	g1730840	935	196	2.00E-49	36	45	putative cysteinyl-tRNA synthetase C29E6_06C (cysteine-tRNA ligase) (CYRS) ; probable membrane protein YNL247w - yeast (Saccharomyces cerevisiae) ; (X96722) ORF N0885 [Saccharomyces cerevisiae] ; (Z71523) ORF YNL247w [Saccharomyces cerevisiae]	
19687	ENU03481	ANI61C7427:	32-54	1139-	NAP	g4038613	681	184	8.00E-46	50	91	(Z98602) conserved uncharacterized protein domain-containing protein [Schizosaccharomyces pombe] (AJ009956) alpha-galactosidase 1 [Penicillium simplicissimum] (AF052688) putative transmembrane transporter Liz1p [Schizosaccharomyces pombe] ; (AL023706) transmembrane transporter Liz1p [Schizosaccharomyces pombe] quinate permease (quinate transporter) ; quinate transport protein - Emericella nidulans ; (X13525) quinate permease [Emericella nidulans] (Z98974) putative small nuclear ribonucleoprotein	
19688	ENU03482	ANI61C4324:	71-94	1180-	NAP	g3821271	1076	351	4.00E-96	64	66	[Schizosaccharomyces pombe] (AJ009956) alpha-galactosidase 1 [Penicillium simplicissimum] (AF052688) putative transmembrane transporter Liz1p [Schizosaccharomyces pombe] ; (AL023706) transmembrane transporter Liz1p [Schizosaccharomyces pombe] quinate permease (quinate transporter) ; quinate transport protein - Emericella nidulans ; (X13525) quinate permease [Emericella nidulans] (Z98974) putative small nuclear ribonucleoprotein	
19689	ENU03483	ANI61C9384:	37-63	1148-	NAP	g2981103	375	140	1.00E-32	33	64	[Schizosaccharomyces pombe] ; (AL023706) transmembrane transporter Liz1p [Schizosaccharomyces pombe] quinate permease (quinate transporter) ; quinate transport protein - Emericella nidulans ; (X13525) quinate permease [Emericella nidulans] (Z98974) putative small nuclear ribonucleoprotein [Schizosaccharomyces pombe] (AL033497) transport protein [Candida albicans] (AL033497) transport protein [Candida albicans]	
			2716..1542	1169									

Seq num	Seq id	Contig Source	Primer 3 pos	Primer Basis	Selection	aat	Blast Score	Blast Prob	% id	% cvrg	Description
			5 pos	NAP	Database Hit	ncbi gi	Score	Prob			
19695	ENU03489	ANi61C7187:	65-84	1167-1201	g112940	532	134	1.00E-40			Acyl-coenzyme A:6-aminopenicillanic-acid acyltransferase precursor (isopenicillin N acyltransferase); acyltransferase AAT - Emericella nidulans ; isopenicillin N acyltransferase (EC 2.3.1.-) - Emericella nidulans ; (X53310) Acyl-CoA [Emericella nidulans] ; (M58293) acyl-coenzyme A:isopenicilin N acyltransferase [Emericella nidulans] (AL031603) putative glycosyl transferase [Schizosaccharomyces pombe]
19696	ENU03490	ANi61C9634:	52-71	1165-1189	NAP	g3646449	753	206	3.00E-62	48	69 hypothetical 61.8 KD protein C12B10_03 in chromosome 1; (Z70721) WD repeat protein [Schizosaccharomyces pombe]
19697	ENU03491	ANi61C352:5	22-48	1142-571..6752	NAP	g1723547	701	170	8.00E-80	46	59 YDR331w - yeast membrane protein YDR331w [Saccharomyces cerevisiae]; (U32517) Ydr331wp [Saccharomyces cerevisiae] (Z80108) lipI [Mycobacterium tuberculosis]
19698	ENU03492	ANi61C8306:	60-79	1180-1202	NAP	g1351809	956	397	e-109	53	94 (AL031532) hypothetical protein [Schizosaccharomyces pombe] (AL035707) putative salicylate hydroxylase [Streptomyces coelicolor] hypothetical 47.0 KD protein in PET117-CEM1 intergenic region; hypothetical protein YER059w - yeast (Saccharomyces cerevisiae); (U18813) Yer059wp [Saccharomyces cerevisiae] hypothetical 39.0 KD protein in GLNQ-ANSR intergenic region; (D84432) YqkA [Bacillus subtilis]; (Z99116) yqkA [Bacillus subtilis] (Z93777) hypothetical protein Rv1215c [Mycobacterium tuberculosis] (AB010439) steroid monooxygenase [Rhodococcus rhodochrous]
19703	ENU03497	ANi61C9095:	22-50	1147-1401..215	NAP	g1731087	67	56	0.000000	21	59
19704	ENU03498	ANi61C1082:	63-82	1181-1208	NAP	g1929089	393	133	3.00E-30	30	65
19705	ENU03499	ANi61C4013:	34-55	1161-519..1708	NAP	g2804298	792	241	6.00E-63	36	70

Seq num	Seq id	Contig Source	Primer 3 pos	Primer Basis	Selection	Blast gi	aat	Blast Score	Prob	% id	% cvrg	Description
			5 pos	NAP	Database Hit	g2131476	626	210	7.00E-69	44	89	hypothetical protein YDR415c - yeast (Saccharomyces cerevisiae); (U33007) Ydr415cp; CAI: 0.14 [Saccharomyces cerevisiae]
19707	ENU03501	ANI61C8114:	64..83	1181-1215	NAP	g1706694	609	178	1.00E-46	35	49	"Lanosterol synthase (oxidosqualene—lanosterol cyclase) (2,3-epoxyisqualene-lanosterol cyclase) (OSC); lanosterol synthase (EC 5.4.99.7) - fission yeast (Schizosaccharomyces pombe); (U41368) lanosterol synthase [Schizosaccharomyces pombe] (AL031543) putative amino-acid permease [Schizosaccharomyces pombe]
19708	ENU03502	ANI61C9917:	22..41	1153-2839..1646	NAP	g3581896	443	138	8.00E-32	24	70	[Schizosaccharomyces pombe] (AL031543) putative amino-acid permease [Schizosaccharomyces pombe]
19709	ENU03503	ANI61C6104:	28..47	1158-2458..1265	NAP	g4106687	432	86	6.00E-20	34	97	(AL035065) putative nadh-dependent flavin oxidoreductase [Schizosaccharomyces pombe]
19710	ENU03504	ANI61C6105:	57..75	1190-599..1793	NAP	g3560215	956	252	2.00E-80	49	81	"(AL031536) yeast reduced viability upon starvation protein rvs167 homolog, SH3 domain containing [Schizosaccharomyces pombe]" nuclear pore protein SEH1; SEC13 protein homolog YGL100w - yeast (Saccharomyces cerevisiae); (X90994) Sec13p-like protein [Saccharomyces cerevisiae]; (Z72622) ORF YGL100w [Saccharomyces cerevisiae]
19711	ENU03505	ANI61C650:	3..22..49	1155-29..1525	NAP	g1711370	326	107	5.00E-34	32	96	"(AE000952) 2-hydroxyhepta-2,4-diene-1,7-dioate isomerase (hpcE-2) [Archaeoglobus fulgidus]" (AB019045) OMPdecarboxylase [Rhizomucor pusillus] Flagellin 1; flagellin fltC-1 - Proteus mirabilis; (L07270) flagellin [Proteus mirabilis] hypothetical 50.5 KD protein in MDH1-VMA5 intergenic region; hypothetical protein YKL082c - yeast (Saccharomyces cerevisiae); (Z28082) ORF YKL082c [Saccharomyces cerevisiae]
19712	ENU03506	ANI61C1054	24..43	1148-0..6432..6182	NAP	g2648302	290	108	1.00E-32	42	97	"(AE000952) 2-hydroxyhepta-2,4-diene-1,7-dioate isomerase (hpcE-2) [Archaeoglobus fulgidus]" (AB019045) OMPdecarboxylase [Rhizomucor pusillus] Flagellin 1; flagellin fltC-1 - Proteus mirabilis; (L07270) flagellin [Proteus mirabilis] hypothetical 50.5 KD protein in MDH1-VMA5 intergenic region; hypothetical protein YKL082c - yeast (Saccharomyces cerevisiae); (Z28082) ORF YKL082c [Saccharomyces cerevisiae]
19713	ENU03507	ANI61C8859:	22..41	1153-1375..177	NAP	g4587097	104	65	0.000000	32	67	"(AB019045) OMPdecarboxylase [Rhizomucor pusillus] Flagellin 1; flagellin fltC-1 - Proteus mirabilis; (L07270) flagellin [Proteus mirabilis] hypothetical 50.5 KD protein in MDH1-VMA5 intergenic region; hypothetical protein YKL082c - yeast (Saccharomyces cerevisiae); (Z28082) ORF YKL082c [Saccharomyces cerevisiae]
19714	ENU03508	ANI61C9217:	22..41	1150-1731..2931	NAP	g1169696	36	0.7				
19715	ENU03509	ANI61C6534:	23..47	1166-1344..1248	NAP	g549699	427	41	0.021	27	89	

Seq num	Seq id	Contig Source	Primer 3 pos	Primer Basis	Selection	aat	Blast Score	Blast Prob	% id	% cvrg	Description	
			5 pos	Database Hit	ncbi gi	Score	Prob					
19716	ENU03510	ANI61C6741:	48-67	NAP	g1174552	564	99	1.00E-54	43	95	tryptophanYL-TRNA synthetase (tryptophan-tRNA ligase) (TRPRS); tryptophan-tRNA ligase (EC 6.1.1.2). Haemophilus influenzae (strain Rd KW20); (U32746) tryptophanyl-tRNA synthetase (trpS) [Haemophilus influenzae Rd] (AJ005824) Ufd1 protein [Schizosaccharomyces pombe]; [Schizosaccharomyces pombe]	
19717	ENU03511	ANI61C1046	22-49	1152-1184	NAP	g3123677	610	254	1.00E-66	46	99	(AJ005825) Ufd1 protein
19718	ENU03512	ANI61C8443:	24-55	1154-4113..2909	NAP	g1352074	792	282	3.00E-77			[Schizosaccharomyces pombe] type II proteinS geranylgeranyltransferase beta subunit (type II protein geranylgeranyltransferase beta subunit) (GGTASE-II-beta) (PGGT) (YPT1/SEC4 proteinS geranylgeranyltransferase beta subunit); probable protein prenyltransferase (EC 2..5..1.-) BET2 - yeast (Saccharomyces cerevisiae); (U25842) Protein Geranyl-geranyltransferase beta subunit (Swiss Prot. accession number P20133; P32433) [Saccharomyces cerevisiae] (D43950) KIAA0098 is a human counterpart of mouse chaperonin containing TCP-1 gene. [Homo sapiens] hypothetical 49.3 KD protein C30D11.06C in chromosome I; hypothetical protein SPAC30D11.06c-fission yeast (Schizosaccharomyces pombe); (Z67961) hypothetical protein [Schizosaccharomyces pombe] hypothetical protein YLR114c - yeast (Saccharomyces cerevisiae); (U53878) Ylr114cp [Saccharomyces cerevisiae]; (X89514) putative orf [Saccharomyces cerevisiae]; (Z73286) ORF YLR114c [Saccharomyces cerevisiae]
19719	ENU03513	ANI61C3364:	56-76	1185-1219	NAP	g603955	1280	349	e-122	71	64	
19720	ENU03514	ANI61C5704:	24-50	1159-1187	NAP	g1351659	766	311	5.00E-84	46	88	
19721	ENU03515	ANI61C7052:	67-87	1213-1233	NAP	g2131781	369	102	8.00E-44	35	42	

Seq num	Seq id	Contig Source	Primer 3 pos	Primer Basis	Selection Database Hit	aat	Blast Score	Blast Prob	% id	% cvg	Description	
19722	ENU03516	ANI61C9393:	62-81	NAP	g3261633	452	200	2.00E-50	35	95	(Z79700) fadE13 [Mycobacterium tuberculosis]	
19723	ENU03517	ANI61C8651:	23-44	NAP	g2499591	1035	296	2.00E-79	69	68	mitogen-activated protein kinase HOG1 (MAP kinase HOG1); (X90586) unnamed protein product	
19724	ENU03518	ANI61C9381:	45-67	1194-1213	NAP	g135025	905	297	7.00E-84	69	83	[Candida albicans] "succinyl-CoA ligase (GDP-forming), alpha-chain precursor (succinyl-CoA synthetase, alpha chain (SCS-alpha); succinate--CoA ligase (GDP-forming) (EC 6.2.1.4) alpha chain precursor - rat; (J03621) succinyl-CoA synthetase alpha subunit (EC 6.2.1.4) [Rattus norvegicus]" (AF054512) endoglucanase V [Aspergillus aculeatus]
19725	ENU03519	ANI61C6226:	44-63	1193-1212	NAP	g2997731	992	229	3.00E-59	64	92	[Aspergillus aculeatus]
19726	ENU03520	ANI61C1227:	69-95	1216-1238	NAP	g1723554	619	237	1.00E-61	39	60	putative DNA repair protein C12B10.12C; (Z70721) putative dna repair protein [Schizosaccharomyces pombe] (AL031536) hypothetical zinc finger protein [Schizosaccharomyces pombe] (Z75532) similar to mitochondrial carrier protein; cDNA EST yk264h5.5 comes from this gene [Caenorhabditis elegans] (X16609) alt. ankyrin (variant 2.2) [Homo sapiens]
19727	ENU03521	ANI50C7567	22-54	1172-1192	NAP	g3560212	68	5.00E-25	29	20	hypothetical 70.5 KD protein in AGP3-DAK3 intergenic region; probable membrane protein YFL054c - yeast (Saccharomyces cerevisiae); (D50617) YFL054C [Saccharomyces cerevisiae]; (D44603) unknown [Saccharomyces cerevisiae]	
19729	ENU03523	ANI61C1056	71-90	1223-1243	NAP	g747710	231	117	1.00E-25	30	20	(AC000132) F21M12.7 gene product [Arabidopsis thaliana]
19730	ENU03524	ANI61C1086:	41-60	1194-1213	NAP	g1175958	571	233	1.00E-60	36	55	(AL034565) putative transcription initiation factor tif1f small subunit [Schizosaccharomyces pombe]
19731	ENU03525	ANI61C5132:	22-51	1170-1195	NAP	g2160161	43	0.003				
19732	ENU03526	ANI61C1064	63-88	1209-1237	NAP	g4049527	391	71	1.00E-30	45	97	



Seq num	Seq id	Contig Source	Primer 3 pos	Primer Basis	Selection	aat	Blast Score	Blast Prob	% id	% cvrg	Description		
			5 pos	NAP	Database Hit	ncbi gi							
19741	ENU03535	ANI61C2490:	35-54	1199-1218	g2507436	922	333	1.00E-90	49	46	glutaminyl-tRNA synthetase (glutamine--tRNA ligase) (GLNRS); yeast (Saccharomyces cerevisiae); (U55021) Gln4p [Saccharomyces cerevisiae]; (Z75076) ORF YOR168w [Saccharomyces cerevisiae]		
19742	ENU03536	ANI61C5804:	22-47	1183-1205	NAP	g125886	618	169	2.00E-53	41	86	lactate 2-monoxygenase (lactate oxidase); lactate 2-monoxygenase (EC 1.13.12.4) -Mycobacterium smegmatis; (J05402) L-lactate 2-monoxygenase [Mycobacterium smegmatis]	
19743	ENU03537	ANI61C1809:	22-47	1174-1207	NAP	g2498337	722	242	2.00E-64	42	78	squalene monoxygenase (squalene epoxidase) (SE); (D88252) squalene epoxidase [Candida albicans]; (U69674) squalene epoxidase [Candida albicans] (Z99162) ER protein-translocation complex subunit [Schizosaccharomyces pombe]	
19744	ENU03538	ANI61C7512:	64-84	1228-1251	NAP	g2408022	357	125	8.00E-28	47	35	cytochrome B2 precursor (L-lactate dehydrogenase (cytochrome)) (L-lactate ferricytochrome C oxidoreductase) (L-LCR); L-lactate dehydrogenase (cytochrome) (EC 1.1.2.3) precursor - yeast (Pichia anomala); (X16051) L-Lactate:cytochrome c oxidoreductase preprotein [Pichia anomala]	
19745	ENU03539	ANI61C7486:	57-75	1225-1246	NAP	g117803	1224	452	e-126	62	67	RNA-binding protein EWS; RNA-binding protein EWS - human; (X66899) RNA binding protein [Homo sapiens]; (X72990) EWS [Homo sapiens]; (Y07848) RNA binding protein [Homo sapiens]; EWS gene [Homo sapiens]	
19746	ENU03540	ANI61C676:1	32-51	1203-800..3031	1221	NAP	g544261	46	0.0006			ferrichrome siderophore peptide synthetase; (U62738) ferrichrome siderophore peptidase synthetase [Ustilago maydis]	
19747	ENU03541	ANI61C5627:	55-74	1227-5260..4027	1246	NAP	g3914984	208	113	3.00E-24	25	10	

Seq num	Seq id	Contig Source	Primer 3 pos	Primer Basis	Selection	aat	Blast Score	Blast Prob	% id	% cvrg	Description	
19748	ENU03542	ANI61C164:1	36-55 024..2255	NAP	g1750122	1071	163	3.00E-64	42	75	"(U66480) xylose beta-1,4-xylanase [Bacillus subtilis]; (Z99113) xylan beta-1,4-xylosidase [Bacillus subtilis]; (M38434) S-adenosylmethionine decarboxylase PROenzyme (ADOMETDC); adenosylmethionine decarboxylase (EC 4.1.1.50) precursor - yeast (Saccharomyces cerevisiae); (M38434) S-adenosylmethionine decarboxylase [Saccharomyces cerevisiae]; (X91067) adenosylmethionine decarboxylase [Saccharomyces cerevisiae]; (Z74794) ORF YOL052c [Saccharomyces cerevisiae]	
19749	ENU03543	ANI61C9610:	72-96 1578..347	1244- 1264	NAP	g118298	463	200	2.00E-50			
19750	ENU03544	ANI61C5499:	57-77 269..1504	1215- 1250	NAP	g2132395	346	150	3.00E-48	36	71	polyadenylated RNA-binding protein PUB1 - yeast [Saccharomyces cerevisiae]; (Z71292) ORF YNL016w [Saccharomyces cerevisiae]
19751	ENU03545	ANI61C3215:	72-91 1248..12	1247- 1266	NAP	g730251	626	208	5.00E-64	49	89	protein phosphatase 2C homolog 1 (PP2C-1); phosphoprotein phosphatase (EC 3.1.3.16) 2C - fission yeast (Schizosaccharomyces pombe); (L26970) protein phosphatase 2C [Schizosaccharomyces pombe] stearoyl-CoA desaturase (EC 1.14.99.5) - Ajellomyces capsulata; (X8563) delta-9 fatty acid desaturase [Ajellomyces capsulatus]
19752	ENU03546	ANI61C9596:	22-56 2267..3504	1196- 1216	NAP	g1078613	1662	534	e-151	69	80	DNA-directed RNA polymerase mitochondrial precursor; (L25087) mitochondrial RNA polymerase [Neurospora crassa]; cyt-5 gene [Neurospora crassa]
19753	ENU03547	ANI61C6355:	38-57 17..1253	1207- 1232	NAP	g730615	978	393	e-108	47	28	hypothetical 80.0 KD protein in SNF4-TAF60 intergenic region; probable membrane protein YGL114w - yeast (Saccharomyces cerevisiae); (Z72636) ORF YGL114w [Saccharomyces cerevisiae]
19754	ENU03548	ANI61C1028	33-55 1:47..1284	1207- 1228	NAP	g1723906	542	206	3.00E-52	39	48	

Seq num	Seq id	Contig	Source	Primer 5 pos	Primer 3 pos	Primer Basis	Selection	aat	Blast Score	Blast Prob	% id	% cvrg	Description	
19755	ENU03549	ANI61C1118:	69-88	4267..3029	1264	NAP	ncbi gi	g2132958	354	110	2.00E-23	26	73	probable membrane protein YOR380w - yeast ( <i>Saccharomyces cerevisiae</i> ); (Z75288) ORF YOR380w
19756	ENU03550	ANI61C5525:	26-45	420..1657	1221	NAP	g2271503	247	83	1.00E-20	30	91	[ <i>Saccharomyces cerevisiae</i> ] (AF009672) unknown [Acinetobacter sp. ADP1]	
19757	ENU03551	ANI61C8624:	47-68	150..1387	1223-	NAP	g114699	158	85	9.00E-16	29	67	ATP10 protein ; (I05463) ATP10 protein [ <i>Saccharomyces cerevisiae</i> ] (U78597) kinesin light chain	
19758	ENU03552	ANI61C1080	72-92	1242-	1269	NAP	g2645229	358	95	1.00E-18	34	29	[Plectonema boryanum] hypothetical 102.3 KD protein in DAL82-RFA2 intergenic region ; hypothetical protein YNL313c - yeast ( <i>Saccharomyces cerevisiae</i> ) ; (Z46259) NO364 [ <i>Saccharomyces cerevisiae</i> ] ; (Z71589) ORF YNL313c	
19759	ENU03553	ANI61C431:3	22-44	9..396..1635	219..1979	1220	NAP	g1176586	579	157	1.00E-37	36	36	[ <i>Saccharomyces cerevisiae</i> ] (Yhr169wp [ <i>Saccharomyces cerevisiae</i> ] (AL023780) DNA binding protein [Schizosaccharomyces pombe] alcohol dehydrogenase II ; alcohol dehydrogenase (EC 1.1.1.) II - Emericella nidulans ; (Z48000) alcohol dehydrogenase II [Emericella nidulans] ; alcohol dehydrogenase II [Emericella nidulans] (AL031603) conserved hypothetical protein. [Schizosaccharomyces pombe] zinc finger protein 207 ; (AF046001) zinc finger transcription factor [Homo sapiens]
19760	ENU03554	ANI61C1007	44-63	4..898..2138	1223-1242	NAP	g731740	990	363	1.00E-99	50	91	probable ATP-dependent RNA helicase DBP8 ; helicase homolog - yeast ( <i>Saccharomyces cerevisiae</i> ) ; (U00027) Yhr169wp [ <i>Saccharomyces cerevisiae</i> ] (AL023780) DNA binding protein [Schizosaccharomyces pombe] alcohol dehydrogenase II ; alcohol dehydrogenase (EC 1.1.1.) II - Emericella nidulans ; (Z48000) alcohol dehydrogenase II [Emericella nidulans] ; alcohol dehydrogenase II [Emericella nidulans]	
19761	ENU03555	ANI61C1111:	66-88	1711..2952	1232-1265	NAP	g3184115	634	250	1.00E-65	35	80	(AL023780) DNA binding protein [Schizosaccharomyces pombe]	
19762	ENU03556	ANI61C3965:	66-86	1636..394	1242-1265	NAP	g1703172	1802	433	e-163	98	93	alcohol dehydrogenase II ; alcohol dehydrogenase (EC 1.1.1.) II - Emericella nidulans ; (Z48000) alcohol dehydrogenase II [Emericella nidulans] ; alcohol dehydrogenase II [Emericella nidulans]	
19763	ENU03557	ANI61C290:9	26-47	99..2241	1207-1226	NAP	g3646450	1005	148	9.00E-35	41	53	(AL031603) conserved hypothetical protein. [Schizosaccharomyces pombe]	
19764	ENU03558	ANI61C7312:	66-85	1222..2467	1250-1269	NAP	g4508017	242	58	4.00E-18	27	76	zinc finger transcription factor [Homo sapiens]	

Seq num	Seq id	Contig Source	Primer 3 pos	Primer Basis	Selection	aat	Blast Score	Blast Prob	% id	% cvrg	Description	
19765	ENU03559	ANI61C1036	25-55	NAP	g549077	974	375	e-103	51	98	"3-ketoacyl-COA thiolase peroxisomal precursor (beta-ketothiolase) (acetyl-CoA acyltransferase) (peroxisomal 3-oxoacyl-CoA thiolase); acetyl-CoA C-acyltransferase (EC 2.3.1.16), peroxisomal - yeast ( <i>Yarrowia lipolytica</i> ); ( <i>X69988</i> ) acetyl-CoA acyltransferase [ <i>Yarrowia lipolytica</i> ] (Z79750) acid phosphatase [ <i>Emericella nidulans</i> ] Uroporphyrinogen decarboxylase (UPD); uroporphyrinogen decarboxylase (EC 4.1.1.37) - yeast ( <i>Saccharomyces cerevisiae</i> ); ( <i>X63721</i> ) uroporphyrinogen decarboxylase [ <i>Saccharomyces cerevisiae</i> ]; ( <i>Z19089</i> ) uroporphyrinogen decarboxylase [ <i>Saccharomyces cerevisiae</i> ]; ( <i>Z49209</i> ) HemL2p [ <i>Saccharomyces cerevisiae</i> ] (AL035076) putative glutamate-1-semialdehyde ammonotransferase [Schizosaccharomyces pombe] (Y16748) malate dehydrogenase [Promyces sp. E2] (AL034393) predicted using Genefinder; cDNA EST <i>yk433c12.5</i> comes from this gene; cDNA EST <i>yk402e12.5</i> comes from this gene; cDNA EST <i>yk457e8.5</i> comes from this gene; cDNA EST <i>yk470f2.5</i> comes from this gene; cDNA EST <i>yk281e3.5</i> com...".	
19766	ENU03560	ANI61C170:3	55-74	1232-1250	NAP	g1523784	2260	840	0	97	67	"3-ketoacyl-COA thiolase peroxisomal precursor (beta-ketothiolase) (acetyl-CoA acyltransferase) (peroxisomal 3-oxoacyl-CoA thiolase); acetyl-CoA C-acyltransferase (EC 2.3.1.16), peroxisomal - yeast ( <i>Yarrowia lipolytica</i> ); ( <i>X69988</i> ) acetyl-CoA acyltransferase [ <i>Yarrowia lipolytica</i> ] (Z79750) acid phosphatase [ <i>Emericella nidulans</i> ] Uroporphyrinogen decarboxylase (UPD); uroporphyrinogen decarboxylase (EC 4.1.1.37) - yeast ( <i>Saccharomyces cerevisiae</i> ); ( <i>X63721</i> ) uroporphyrinogen decarboxylase [ <i>Saccharomyces cerevisiae</i> ]; ( <i>Z19089</i> ) uroporphyrinogen decarboxylase [ <i>Saccharomyces cerevisiae</i> ]; ( <i>Z49209</i> ) HemL2p [ <i>Saccharomyces cerevisiae</i> ] (AL035076) putative glutamate-1-semialdehyde ammonotransferase [Schizosaccharomyces pombe] (Y16748) malate dehydrogenase [Promyces sp. E2] (AL034393) predicted using Genefinder; cDNA EST <i>yk433c12.5</i> comes from this gene; cDNA EST <i>yk402e12.5</i> comes from this gene; cDNA EST <i>yk457e8.5</i> comes from this gene; cDNA EST <i>yk470f2.5</i> comes from this gene; cDNA EST <i>yk281e3.5</i> com...".
19767	ENU03561	ANI61C9890:	23-44	1195-1251..4	NAP	g416894	1069	392	e-112			
19768	ENU03562	ANI61C8571:	71-94	1257-1770..523	NAP	g4107288	922	216	5.00E-84	52	88	"3-ketoacyl-COA thiolase peroxisomal precursor (beta-ketothiolase) (acetyl-CoA acyltransferase) (peroxisomal 3-oxoacyl-CoA thiolase); acetyl-CoA C-acyltransferase (EC 2.3.1.16), peroxisomal - yeast ( <i>Yarrowia lipolytica</i> ); ( <i>X69988</i> ) acetyl-CoA acyltransferase [ <i>Yarrowia lipolytica</i> ] (Z79750) acid phosphatase [ <i>Emericella nidulans</i> ] Uroporphyrinogen decarboxylase (UPD); uroporphyrinogen decarboxylase (EC 4.1.1.37) - yeast ( <i>Saccharomyces cerevisiae</i> ); ( <i>X63721</i> ) uroporphyrinogen decarboxylase [ <i>Saccharomyces cerevisiae</i> ]; ( <i>Z19089</i> ) uroporphyrinogen decarboxylase [ <i>Saccharomyces cerevisiae</i> ]; ( <i>Z49209</i> ) HemL2p [ <i>Saccharomyces cerevisiae</i> ] (AL035076) putative glutamate-1-semialdehyde ammonotransferase [Schizosaccharomyces pombe] (Y16748) malate dehydrogenase [Promyces sp. E2] (AL034393) predicted using Genefinder; cDNA EST <i>yk433c12.5</i> comes from this gene; cDNA EST <i>yk402e12.5</i> comes from this gene; cDNA EST <i>yk457e8.5</i> comes from this gene; cDNA EST <i>yk470f2.5</i> comes from this gene; cDNA EST <i>yk281e3.5</i> com...".
19769	ENU03563	ANI61C3737:	51-70	1236-2726..3975	NAP	g4029338	627	112	5.00E-41	49	95	"3-ketoacyl-COA thiolase peroxisomal precursor (beta-ketothiolase) (acetyl-CoA acyltransferase) (peroxisomal 3-oxoacyl-CoA thiolase); acetyl-CoA C-acyltransferase (EC 2.3.1.16), peroxisomal - yeast ( <i>Yarrowia lipolytica</i> ); ( <i>X69988</i> ) acetyl-CoA acyltransferase [ <i>Yarrowia lipolytica</i> ] (Z79750) acid phosphatase [ <i>Emericella nidulans</i> ] Uroporphyrinogen decarboxylase (UPD); uroporphyrinogen decarboxylase (EC 4.1.1.37) - yeast ( <i>Saccharomyces cerevisiae</i> ); ( <i>X63721</i> ) uroporphyrinogen decarboxylase [ <i>Saccharomyces cerevisiae</i> ]; ( <i>Z19089</i> ) uroporphyrinogen decarboxylase [ <i>Saccharomyces cerevisiae</i> ]; ( <i>Z49209</i> ) HemL2p [ <i>Saccharomyces cerevisiae</i> ] (AL035076) putative glutamate-1-semialdehyde ammonotransferase [Schizosaccharomyces pombe] (Y16748) malate dehydrogenase [Promyces sp. E2] (AL034393) predicted using Genefinder; cDNA EST <i>yk433c12.5</i> comes from this gene; cDNA EST <i>yk402e12.5</i> comes from this gene; cDNA EST <i>yk457e8.5</i> comes from this gene; cDNA EST <i>yk470f2.5</i> comes from this gene; cDNA EST <i>yk281e3.5</i> com...".
19770	ENU03564	ANI61C8574:	24-48	1204-85..1333	NAP	g3979938	105	36	0.73	34	31	"3-ketoacyl-COA thiolase peroxisomal precursor (beta-ketothiolase) (acetyl-CoA acyltransferase) (peroxisomal 3-oxoacyl-CoA thiolase); acetyl-CoA C-acyltransferase (EC 2.3.1.16), peroxisomal - yeast ( <i>Yarrowia lipolytica</i> ); ( <i>X69988</i> ) acetyl-CoA acyltransferase [ <i>Yarrowia lipolytica</i> ] (Z79750) acid phosphatase [ <i>Emericella nidulans</i> ] Uroporphyrinogen decarboxylase (UPD); uroporphyrinogen decarboxylase (EC 4.1.1.37) - yeast ( <i>Saccharomyces cerevisiae</i> ); ( <i>X63721</i> ) uroporphyrinogen decarboxylase [ <i>Saccharomyces cerevisiae</i> ]; ( <i>Z19089</i> ) uroporphyrinogen decarboxylase [ <i>Saccharomyces cerevisiae</i> ]; ( <i>Z49209</i> ) HemL2p [ <i>Saccharomyces cerevisiae</i> ] (AL035076) putative glutamate-1-semialdehyde ammonotransferase [Schizosaccharomyces pombe] (Y16748) malate dehydrogenase [Promyces sp. E2] (AL034393) predicted using Genefinder; cDNA EST <i>yk433c12.5</i> comes from this gene; cDNA EST <i>yk402e12.5</i> comes from this gene; cDNA EST <i>yk457e8.5</i> comes from this gene; cDNA EST <i>yk470f2.5</i> comes from this gene; cDNA EST <i>yk281e3.5</i> com...".
19771	ENU03565	ANI61C1023	33-56	1220-1239	NAP	g3367626	867	163	7.00E-87	59	94	"3-ketoacyl-COA thiolase peroxisomal precursor (beta-ketothiolase) (acetyl-CoA acyltransferase) (peroxisomal 3-oxoacyl-CoA thiolase); acetyl-CoA C-acyltransferase (EC 2.3.1.16), peroxisomal - yeast ( <i>Yarrowia lipolytica</i> ); ( <i>X69988</i> ) acetyl-CoA acyltransferase [ <i>Yarrowia lipolytica</i> ] (Z79750) acid phosphatase [ <i>Emericella nidulans</i> ] Uroporphyrinogen decarboxylase (UPD); uroporphyrinogen decarboxylase (EC 4.1.1.37) - yeast ( <i>Saccharomyces cerevisiae</i> ); ( <i>X63721</i> ) uroporphyrinogen decarboxylase [ <i>Saccharomyces cerevisiae</i> ]; ( <i>Z19089</i> ) uroporphyrinogen decarboxylase (EC 4.1.1.37) - yeast ( <i>Saccharomyces cerevisiae</i> ); ( <i>X63721</i> ) uroporphyrinogen decarboxylase [ <i>Saccharomyces cerevisiae</i> ]; ( <i>Z19089</i> ) uroporphyrinogen decarboxylase [ <i>Saccharomyces cerevisiae</i> ]; ( <i>Z49209</i> ) HemL2p [ <i>Saccharomyces cerevisiae</i> ] (AL035076) putative glutamate-1-semialdehyde ammonotransferase [Schizosaccharomyces pombe] (Y16748) malate dehydrogenase [Promyces sp. E2] (AL034393) predicted using Genefinder; cDNA EST <i>yk433c12.5</i> comes from this gene; cDNA EST <i>yk402e12.5</i> comes from this gene; cDNA EST <i>yk457e8.5</i> comes from this gene; cDNA EST <i>yk470f2.5</i> comes from this gene; cDNA EST <i>yk281e3.5</i> com...".
19772	ENU03566	ANI61C6252:	31-52	1219-1239	NAP	g3687502	605	65	3.00E-20	48	90	"3-ketoacyl-COA thiolase peroxisomal precursor (beta-ketothiolase) (acetyl-CoA acyltransferase) (peroxisomal 3-oxoacyl-CoA thiolase); acetyl-CoA C-acyltransferase (EC 2.3.1.16), peroxisomal - yeast ( <i>Yarrowia lipolytica</i> ); ( <i>X69988</i> ) acetyl-CoA acyltransferase [ <i>Yarrowia lipolytica</i> ] (Z79750) acid phosphatase [ <i>Emericella nidulans</i> ] Uroporphyrinogen decarboxylase (UPD); uroporphyrinogen decarboxylase (EC 4.1.1.37) - yeast ( <i>Saccharomyces cerevisiae</i> ); ( <i>X63721</i> ) uroporphyrinogen decarboxylase [ <i>Saccharomyces cerevisiae</i> ]; ( <i>Z19089</i> ) uroporphyrinogen decarboxylase (EC 4.1.1.37) - yeast ( <i>Saccharomyces cerevisiae</i> ); ( <i>X63721</i> ) uroporphyrinogen decarboxylase [ <i>Saccharomyces cerevisiae</i> ]; ( <i>Z19089</i> ) uroporphyrinogen decarboxylase [ <i>Saccharomyces cerevisiae</i> ]; ( <i>Z49209</i> ) HemL2p [ <i>Saccharomyces cerevisiae</i> ] (AL035076) putative glutamate-1-semialdehyde ammonotransferase [Schizosaccharomyces pombe] (Y16748) malate dehydrogenase [Promyces sp. E2] (AL034393) predicted using Genefinder; cDNA EST <i>yk433c12.5</i> comes from this gene; cDNA EST <i>yk402e12.5</i> comes from this gene; cDNA EST <i>yk457e8.5</i> comes from this gene; cDNA EST <i>yk470f2.5</i> comes from this gene; cDNA EST <i>yk281e3.5</i> com...".
19773	ENU03567	ANI61C1155:	22-48	1211-4035..2784	NAP	g1708616	896	175	3.00E-82	57	48	"3-ketoacyl-COA thiolase peroxisomal precursor (beta-ketothiolase) (acetyl-CoA acyltransferase) (peroxisomal 3-oxoacyl-CoA thiolase); acetyl-CoA C-acyltransferase (EC 2.3.1.16), peroxisomal - yeast ( <i>Yarrowia lipolytica</i> ); ( <i>X69988</i> ) acetyl-CoA acyltransferase [ <i>Yarrowia lipolytica</i> ] (Z79750) acid phosphatase [ <i>Emericella nidulans</i> ] Uroporphyrinogen decarboxylase (UPD); uroporphyrinogen decarboxylase (EC 4.1.1.37) - yeast ( <i>Saccharomyces cerevisiae</i> ); ( <i>X63721</i> ) uroporphyrinogen decarboxylase [ <i>Saccharomyces cerevisiae</i> ]; ( <i>Z19089</i> ) uroporphyrinogen decarboxylase (EC 4.1.1.37) - yeast ( <i>Saccharomyces cerevisiae</i> ); ( <i>X63721</i> ) uroporphyrinogen decarboxylase [ <i>Saccharomyces cerevisiae</i> ]; ( <i>Z19089</i> ) uroporphyrinogen decarboxylase [ <i>Saccharomyces cerevisiae</i> ]; ( <i>Z49209</i> ) HemL2p [ <i>Saccharomyces cerevisiae</i> ] (AL035076) putative glutamate-1-semialdehyde ammonotransferase [Schizosaccharomyces pombe] (Y16748) malate dehydrogenase [Promyces sp. E2] (AL034393) predicted using Genefinder; cDNA EST <i>yk433c12.5</i> comes from this gene; cDNA EST <i>yk402e12.5</i> comes from this gene; cDNA EST <i>yk457e8.5</i> comes from this gene; cDNA EST <i>yk470f2.5</i> comes from this gene; cDNA EST <i>yk281e3.5</i> com...".

Seq num	Seq id	Contig Source	Primer 3 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19774	ENU03568	ANI61C4414:	22-40	2075..3328	NAP	g1077358	523	196	6.00E-55	37	66	probable membrane protein YLR361c-yeast (Saccharomyces cerevisiae); (U19103) Yf361cp [Saccharomyces cerevisiae]	
19775	ENU03569	ANI61C7023:	59-78	2774..4030	1254-	NAP	g1351643	674	161	2.00E-70	41	93	hypothetical 43.0 KD protein C8A4.09C in chromosome 1; hypothetical protein SPAC8A4.09c - fission yeast (Schizosaccharomyces pombe); (Z66569) unknown [Schizosaccharomyces pombe]; (AL032824) hypothetical protein [Schizosaccharomyces pombe] (AL033385) conserved hypothetical protein [Schizosaccharomyces pombe] (X58121) SMP3 protein [Saccharomyces cerevisiae]
19776	ENU03570	ANI61C8693:	37-56	1232-	NAP	g3850069	254	85	1.00E-15	32	95	protein [Schizosaccharomyces pombe] (AL033385) conserved hypothetical protein [Schizosaccharomyces pombe] (X58121) SMP3 protein [Saccharomyces cerevisiae]	
19777	ENU03571	ANI61C6252:	60-83	1257-	NAP	g4498	445	163	3.00E-45	35	69	(AL031743) putative protein transport protein [Schizosaccharomyces pombe] "(AL033388) hypothetical integral membrane protein, putative involvement in lipid metabolism [Schizosaccharomyces pombe]" hypothetical zinc-type alcohol dehydrogenase-like protein in GDH3-CNE1 intergenic region ; FUN49 protein - yeast (Saccharomyces cerevisiae); (U12980) Yal060wp [Saccharomyces cerevisiae] (AF104312) glycolate oxidase; short-chain alpha-hydroxy acid oxidase [Mus musculus]	
19778	ENU03572	ANI61C3740:	55-75	1242-	NAP	g3650391	831	201	1.00E-50	50	78	(AL031743) putative protein transport protein [Schizosaccharomyces pombe] "(AL033388) hypothetical integral membrane protein, putative involvement in lipid metabolism [Schizosaccharomyces pombe]" hypothetical zinc-type alcohol dehydrogenase-like protein in GDH3-CNE1 intergenic region ; FUN49 protein - yeast (Saccharomyces cerevisiae); (U12980) Yal060wp [Saccharomyces cerevisiae] (AF104312) glycolate oxidase; short-chain alpha-hydroxy acid oxidase [Mus musculus]	
19779	ENU03573	ANI61C672:4	36-59	405..3143	1235-	NAP	g3850111	561	94	2.00E-45	41	98	"(AL033388) hypothetical integral membrane protein, putative involvement in lipid metabolism [Schizosaccharomyces pombe]" hypothetical zinc-type alcohol dehydrogenase-like protein in GDH3-CNE1 intergenic region ; FUN49 protein - yeast (Saccharomyces cerevisiae); (U12980) Yal060wp [Saccharomyces cerevisiae] (AF104312) glycolate oxidase; short-chain alpha-hydroxy acid oxidase [Mus musculus]
19780	ENU03574	ANI61C2194:	46-65	1966..704	1246-	NAP	g731293	286	138	1.00E-31	33	90	"(AL033388) hypothetical integral membrane protein, putative involvement in lipid metabolism [Schizosaccharomyces pombe]" hypothetical zinc-type alcohol dehydrogenase-like protein in GDH3-CNE1 intergenic region ; FUN49 protein - yeast (Saccharomyces cerevisiae); (U12980) Yal060wp [Saccharomyces cerevisiae] (AF104312) glycolate oxidase; short-chain alpha-hydroxy acid oxidase [Mus musculus]
19781	ENU03575	ANI61C5263:	32-51	139..1401	1231-	NAP	g4585221	330	101	3.00E-24	39	88	"(AL033388) hypothetical integral membrane protein, putative involvement in lipid metabolism [Schizosaccharomyces pombe]" hypothetical zinc-type alcohol dehydrogenase-like protein in GDH3-CNE1 intergenic region ; FUN49 protein - yeast (Saccharomyces cerevisiae); (U12980) Yal060wp [Saccharomyces cerevisiae] (AF104312) glycolate oxidase; short-chain alpha-hydroxy acid oxidase [Mus musculus]
19782	ENU03576	ANI61C1054	42-61	1243-	NAP	g4377376	462	165	1.00E-52	39	94	[Chlamydia pneumoniae] probable serine/threonine-protein kinase C24B11.11C ; hypothetical protein SPAC24B11.11C - fission yeast (Schizosaccharomyces pombe); (Z67757) unknown [Schizosaccharomyces pombe]	

Seq num	Seq id	Contig Source	Primer 3 pos	Primer Basis	Selection	aat	Blast Score	Blast Prob	% id	% cvrg	Description
				NAP	Database Hit	ncbi gi	Score	Prob			
19784	ENU03578	ANI61C4008:	58-77	1259-	g2276351	329	93	4.00E-18	55	42	(Z97992) putative transcriptional regulator [Schizosaccharomyces pombe]
19785	ENU03579	ANI61C1160:	32-51	1225-	NAP	g5855007	63	57	0.000000	2	cell division protein kinase 2 homolog CRK1 ; protein kinase (EC 2.7.1.37) cdc2-related CRK1 - Leishmania mexicana ; (X60385) cdc2-like protein [Leishmania mexicana]
19786	ENU03580	ANI61C4268:	22-42	1228-1247	NAP	g400766	447	201	1.00E-50	36	62 phenol 2-monoxygenase (phenol hydroxylase); phenol 2-monoxygenase (EC 1.14.13.7) Pseudomonas sp. plasmid EST1412 (AL031534) protein kinase kin1 [Schizosaccharomyces pombe]
19787	ENU03581	ANI61C8771:	22-48	1213-1247	NAP	g3560139	157	50	0.00003	27	39 maackiain detoxification protein 1 - fungus (Nectria haematoxocca); (U35892) predicted flavin-containing mono-oxygenase [Nectria haematoxocca]
19788	ENU03582	ANI61C4868:	71-90	1279-1299	NAP	g2133295	1263	182	4.00E-96	54	77 Meiotic recombination protein DLH1 (DMC1 homolog); DMC1/LIM15 homolog 1 - yeast (Candida albicans); (U39808) Dh1lp [Candida albicans] hypothetical 40.0 KD protein C4G8.14C in chromosome 1; hypothetical protein SPAC4G8.14c - fission yeast (Schizosaccharomyces pombe)
19789	ENU03583	ANI61C1074	22-46	1230-1250	NAP	g1706446	876	208	5.00E-90	63	99 (SACCHAROMYCES CEREVISIAE) mitogen-activated protein kinase [Nectria haematoxocca var. brevicornata]
19790	ENU03584	ANI61C1113	22-46	1225-1250	NAP	g1351604	337	123	2.00E-35	35	96 hypothetical 40.0 KD protein C4G8.14C in chromosome 1; hypothetical protein SPAC4G8.14c - fission yeast (Schizosaccharomyces pombe)
19791	ENU03585	ANI61C9449:	29-48	1235-1259	NAP	g1279911	1596	555	e-167	91	99 (U52063) mitogen-activated protein kinase [Nectria haematoxocca var. brevicornata]
19792	ENU03586	ANI61C6804:	50-77	1262-7842..6567	NAP	g1034946	276	96	4.00E-25	29	83 hypothetical protein YPR023c - yeast (Saccharomyces cerevisiae); (Z49274) unknown [Saccharomyces cerevisiae]; (Z71255) unknown [Saccharomyces cerevisiae]
19793	ENU03587	ANI61C1101:	26-51	1235-1341..68	NAP	g434759	1403	232	e-147	64	41 (D21163) similar to human elongation factor 2 mRNA (HSEF2). [Homo sapiens]
19794	ENU03588	ANI61C1171:	25-52	1240-4..1281	NAP	g3184099	637	193	5.00E-51	36	69 (AL023777) hypothetical protein [Schizosaccharomyces pombe]

Seq num	Seq id	Contig Source	Primer 3 pos	Primer 1234-	Selection Basis	Database Hit	ncbi gi	aat	Blast Score	Blast Prob	% id	% cvrg	Description
19795	ENU03589	ANI61C7713:	22-43	6808..5530	NAP	g3183342	519	135	5.00E-31	38	96	hypothetical protein C14C4.09 in chromosome I; (Z98596)	
19796	ENU03590	ANI61C8371:	22-46	1235-1861..3140	NAP	g1805251	366	166	4.00E-40	29	74	[Schizosaccharomyces pombe] (U58946) transposase [Aspergillus awamori]	
19797	ENU03591	ANI61C1137	25-47	1241-7..5545..4266	NAP	g2388971	1133	260	e-119	57	99	(Z98979) hypothetical protein [Schizosaccharomyces pombe] (AF032386) aldose-1-epimerase-like protein [Nicotiana tabacum] (AJ001330) orfT [Lactobacillus sakei]	
19798	ENU03592	ANI61C822:1	22-45	1228-1260	NAP	g2739168	229	148	7.00E-35	31	98	alpha-amylase (EC 3.2.1.1) precursor - yeast (Lipomyces kononenkiae) NADH-ubiquinone oxidoreductase 51 KD subunit precursor (complex I-51KD) (CI-51KD); (X64402) NADH dehydrogenase [Aspergillus niger] (AL024353) probable metabolite transport protein	
19799	ENU03593	ANI61C1918:	22-55	1241-3246..4527	NAP	g2764614	510	128	7.00E-58	40	98	[Schizosaccharomyces pombe] (Y14749) MDM10 [Podospora anserina]	
19800	ENU03594	ANI61C9032:	22-41	1242-4163..2881	NAP	g2144467	1212	135	2.00E-84	59	52	(AF016448) Similar to glycolate oxidase; coded for by <i>C. elegans</i> cDNA yki151h10.5; coded for by <i>C. elegans</i> cDNA yki151h10.3 [Caenorhabditis elegans]	
19801	ENU03595	ANI61C5905:	70-89	1292-524...1807	NAP	g2499312	2312	591	e-168	92	77	"3-ketoacyl-CoA thiolase peroxisomal A precursor (beta-ketothiolate A) (acetyl-CoA acyltransferase A) (peroxisomal 3-oxoacyl-CoA thiolase A); acetyl-CoA C-acyltransferase (EC 2.3.1.16) A precursor, peroxisomal - rat ; (D90058) 3-ketoacyl-CoA thiolase A [Rattus norvegicus]" (AF032443) ABC1 transporter; ABC-type ATPase [Magnaporthe grisea]	
19802	ENU03596	ANI61C6334:	63-83	1272-1851..3134	NAP	g3925778	835	78	1.00E-17	44	26	[Schizosaccharomyces pombe] (AL021428) hypothetical protein Rv0068 [Mycobacterium tuberculosis] (Y14749)	
19803	ENU03597	ANI61C3320:	35-55	1246-1285..2	NAP	g2808725	159	78	1.00E-13	34	53	[Mycobacterium tuberculosis] (Y14749) MDM10 [Podospora anserina]	
19804	ENU03598	ANI61C2332:	64-87	1283-3982..2697	NAP	g2407968	415	164	9.00E-40	35	87	[Podospora anserina]	
19805	ENU03599	ANI61C3370:	23-42	1237-1552..266	NAP	g2315453	463	123	5.00E-43	40	98	[Caenorhabditis elegans]	
19806	ENU03600	ANI61C6496:	22-56	1247-4395..5681	NAP	g135746	730	182	2.00E-83	46	93	"3-ketoacyl-CoA thiolase peroxisomal A precursor (beta-ketothiolate A) (acetyl-CoA acyltransferase A) (peroxisomal 3-oxoacyl-CoA thiolase A); acetyl-CoA C-acyltransferase (EC 2.3.1.16) A precursor, peroxisomal - rat ; (D90058) 3-ketoacyl-CoA thiolase A [Rattus norvegicus]" (AF032443) ABC1 transporter; ABC-type ATPase [Magnaporthe grisea]	
19807	ENU03601	ANI61C1837:	71-90	1296-1607..321	NAP	g2625138	2012	190	5.00E-94	48	23		

Seq num	Seq id	Contig Source	Primer 3 pos	Primer Basis	Selection	aat	Blast Score	Blast Prob	% id	% cvrg	Description		
				NAP	Database Hit	ncbi gi							
19808	ENU03602	ANI61C9767:	23-56	1248-1257	g1723533	220	109	4.00E-23	38	39	hypothetical 33.6 KD protein		
		3929..2643									C25G10.01 in chromosome 1; (Z70691) rna binding protein		
19809	ENU03603	ANI61C263:1	22-41	1242-1257	NAP	g3875242	181	66	3.00E-22	30	96	[Schizosaccharomyces pombe] (Z75532) similar to mitochondrial carrier protein; cDNA EST yk264h5.5 comes from this gene [Caenorhabditis elegans]	
19810	ENU03604	ANI61C526:3	72-93	1290-333..2046	NAP	g125935	165	65	0.000000	26	64	lactose permease ; lactose permease - yeast (Kluyveromyces marxianus var. lactic) ; (X06997) lactose permease (AA 1-587) [Kluyveromyces lactic] " (D83732) endo-1,4-beta-glucanase [Aspergillus oryzae]"	
19811	ENU03605	ANI61C1086	24-56	1243-1269	NAP	g2467375	1275	527	e-149	63	98	probable membrane protein YOR161c - yeast (Saccharomyces cerevisiae) ; (U55021) O3568p [Saccharomyces cerevisiae] ; (Z75069) ORF YOR161c [Saccharomyces cerevisiae]	
19812	ENU03606	ANI61C3295:	31-52	1255-10..1297	NAP	g2132901	833	178	4.00E-75	40	78	probable membrane protein YOR161c - yeast (Saccharomyces cerevisiae) ; (U55021) O3568p [Saccharomyces cerevisiae] ; (Z75069) ORF YOR161c [Saccharomyces cerevisiae]	
19813	ENU03607	ANI61C435:4	49-68	1269-685..3397	1295	NAP	g1723809	380	152	7.00E-36	27	78	hypothetical 56.4 KD protein in RPL32-CWH41 intergenic region precursor ; probable membrane protein YGL028c - yeast (Saccharomyces cerevisiae) ; (Z72550) ORF YGL028c [Saccharomyces cerevisiae] (AL033391) hypothetical membrane protein [Candida albicans]
19814	ENU03608	ANI61C2205:	64-84	1290-2001..712	NAP	g3850125	458	131	9.00E-31	33	76	Arginine metabolism regulation protein III ; regulatory protein ARGRIII - yeast (Saccharomyces cerevisiae) ; (X05328) ARGRIII protein (AA 1-355) [Saccharomyces cerevisiae] ; (Z46727) Arg3p [Saccharomyces cerevisiae] (AE001015) acyl-CoA dehydrogenase (acd-9) [Archaeoglobus fulgidus]	
19815	ENU03609	ANI61C80:12	55-74	1283-1302	NAP	g114134	236	93	4.00E-18	33	86	RPL18A1 intergenic region ; hypothetical 34.2 KD protein in CUS1-hypothetical protein YMR241w - yeast (Saccharomyces cerevisiae) ; (Z48756) unknown [Saccharomyces cerevisiae]	
19816	ENU03610	ANI61C9725:	53-72	1282-1421..131	NAP	g2649289	300	118	8.00E-26	33	88	(Acyl-CoA dehydrogenase (acd-9)) [Archaeoglobus fulgidus]	
19817	ENU03611	ANI61C6152:	45-64	1273-1746..3037	NAP	g2497200	1006	332	1.00E-92	70	97	hypothetical protein YMR241w - yeast (Saccharomyces cerevisiae) ; (Z48756)	

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat	Blast Score	Blast Prob	% id	% cvrg	Description
19818	ENU03612	ANI61C1077	67-86	1295-	NAP	g1363051	468	I13	2.00E-24	28	76	P58	protein - bovine ; (U04631) PKR inhibitor P58 [Bos taurus]
19819	ENU03613	ANI61C8876:	43-63	1316	NAP	g1170767	1490	383	e-154	77	96	26S	protease regulatory subunit 8 homolog (LET1 protein) ; transcription factor SUG1 homolog - fission yeast
		1019..2313	1271-	1295									(Schizosaccharomyces pombe) ; (U02280) Let1 [Schizosaccharomyces pombe] ; (AL035065) 26s protease regulatory subunit 8 homolog
19820	ENU03614	ANI61C59:19	26-45	1259-	NAP	g2492825	374	141	5.00E-41	32	96	"N"-carboxy-L-amino acid amidohydrolase : N-carbamyl-L-amino acid amidohydrolase (EC 3.5.-.-)	
		80..3274	1278	1278	NAP	g2492825	374	141	5.00E-41	32	96	Bacillus stearothermophilus (strain NS1122A) ; (S67784) N-carbamyl-L-amino acid amidohydrolase [Bacillus stearothermophilus, NS1122A, Peptide, 409 aa] [Bacillus stearothermophilus] "N"-carbamyl-L-amino acid amidohydrolase ; N-carbamyl-L-amino acid amidohydrolase (EC 3.5.-.-)	
19821	ENU03615	ANI61C59:19	26-45	1259-	NAP	g2492825	374	141	5.00E-41	32	96	Bacillus stearothermophilus (strain NS1122A) ; (S67784) N-carbamyl-L-amino acid amidohydrolase [Bacillus stearothermophilus, NS1122A, Peptide, 409 aa] [Bacillus stearothermophilus] "D83970) CPRD8 protein [Vigna unguiculata]	
19822	ENU03616	ANI61C1100	29-49	1256-	NAP	g1854443	474	180	2.00E-44	39	92	Myo-inositol transporter 1 ; (X98622) Myo-inositol transporter	
19823	ENU03617	ANI61C9270:	26-51	1283	NAP	g2500938	115	71	2.00E-11	32	42	[Schizosaccharomyces pombe] Myo-inositol transporter 1 ; (X98622) myo-inositol transporter	
19824	ENU03618	ANI61C9270:	26-51	1249-	NAP	g2500938	115	71	2.00E-11	32	42	[Schizosaccharomyces pombe] Myo-inositol transporter 1 ; (X98622) myo-inositol transporter	
19825	ENU03619	ANI61C3627:	22-42	1257-	NAP	g4240421		99	1.00E-22			[Schizosaccharomyces pombe] (AF080235) reductase homolog [Streptomyces cyanogenus]	
		1747..450	1277										

Seq num	Seq id	Contig Source	Primer 3 pos	Primer Basis	Selection Database Hit	aat	Blast Score	Blast Prob	% id	% cvrg	Description	
19826	ENU03620	ANI61C9039:	28-51	NAP	g2330781	972	328	e-103	51	84	"(Z98559) SPAC23C11.17; len:485aa, similar eg. to YPR125W, Q06493, chromosome xvi orf, (454aa), fasta scores, opt:1063, EO:0, (43.5% identity in 418 aa overlap)	
19827	ENU03621	ANI61C3441: 705..2002	1292-1327	NAP	g731716	646	270	4.00E-73	42	88	[Schizosaccharomyces pombe]" hypothetical 49.8 KD protein in ACT3-YCK1 intergenic region precursor ; hypothetical protein YHR132c - yeast (Saccharomyces cerevisiae); (U10398) Ecm14p [Saccharomyces cerevisiae]	
19828	ENU03622	ANI61C1057 2-2746..1446	1262-1281	NAP	g731846	159	53	0.000003	27	70	"hypothetical 39.4 KD protein in SGA1-KTR7 intergenic region ; hypothetical protein YIL096c - yeast (Saccharomyces cerevisiae); (Z38125) orf, len: 336, CAI: 0.14	
19829	ENU03623	ANI50C1282 7_1:1701..400	50-69	1277-1309	NAP	g137471	134	1.00E-30	38	94	[Saccharomyces cerevisiae]" "vacuolar ATP synthase subunit C (V-ATPase C subunit) ; H+-transporting ATPase (EC 3.6.1.35) chain C, vacuolar - bovine ; (J05681) H+-ATPase C subunit [Bos taurus]" probable ATP-dependent RNA helicase PRH1 ; PRH1 protein - fission yeast (Schizosaccharomyces pombe) ; (Z54354) probable atp-dependent maize helicase prh1 [Schizosaccharomyces pombe]	
19830	ENU03624	ANI61C5190: 2421..1118	68-90	1310-1329	NAP	g1172616	1087	326	2.00E-88	49	54	(Y16748) malate dehydrogenase [Phytomyces sp. E2] (AB016720) carboxylesterase precursor [Aphis gossypii]
19831	ENU03625	ANI61C8056: 65-84	1306-641..1944	NAP	g4029338	632	145	6.00E-65	57	96	putative polyketide biosynthesis protein PKS1 ; (U11039) unknown [Bacillus subtilis] ; (Z99112) pksJ [Bacillus subtilis] ; (Z99113) pksJ [Bacillus subtilis]	
19834	ENU03628	ANI61C1029 4-4056..2745	22-42	1271-1290	NAP	g3043694	243	137	2.00E-31	29	64	(AB011157) KIAA0585 protein [Homo sapiens]
19835	ENU03629	ANI61C2332: 3982..2670	64-87	1315-1334	NAP	g2407968	415	164	9.00E-40	34	88	(Y14749) MDM10 [Podospora anserina]

Seq num	Seq id	Contig Source	Primer 3 pos	Primer 3 pos	Selection Basis	Database Hit	.ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19836	ENU03630	ANI61C8090:	22-41	1277-	NAP	g2984184	398	157	2.00E-37	29	82	(AE00763) N-methylhydantoinase B [Aquifex aeolicus]	
19837	ENU03631	ANI61C4285:	46-68	1206	NAP	g2664292	1594	447	e-171	81	95	(Y15744) cellular aspartic protease [Aspergillus fumigatus]; (AJ132504)	
19838	ENU03632	ANI61C7950:	57-77	1304-	NAP	g2493391	96	4.00E-19				aspartic protease [Aspergillus fumigatus]	
19839	ENU03633	ANI61C4230:	47-75	1289-	NAP	g1351673	367	113	6.00E-32	38	96	probable sterigmatocystin biosynthesis P450 monooxygenase STCB (cytochrome P450 62); (U34740) putative p450 monooxygenase [Emericella nidulans]	
19840	ENU03634	ANI61C3599:	29-52	1288-	NAP	g522302	4000	589	e-167	63	36	hypothetical 37.7 KD protein C1F7.12 in chromosome I; hypothetical protein SPAC1F7.12 - fission yeast (Schizosaccharomyces pombe); (Z67998) unknown	
19841	ENU03635	ANI61C4299:	57-80	1316-	NAP	g1351606	196	67	3.00E-10	29	25	[Schizosaccharomyces pombe] (L35053) endonuclease [Magnaporthe grisea]	
19842	ENU03636	ANI61C406:2	30-57	1290-	NAP	g135184	2357	266	e-118	54	38	hypothetical 54.3 KD protein C23D3.03C in chromosome I; hypothetical protein SPAC23D3.03c - fission yeast (Schizosaccharomyces pombe); (Z64354) unknown	
		706..1384		1310								"Valyl-tRNA synthetase, mitochondrial precursor (valine-tRNA ligase) (VALRS); valine-tRNA ligase (EC 6.1.1.9) - Neurospora crassa"	
19843	ENU03637	ANI61C4412:	45-65	1307-	NAP	g1469396	692	226	8.00E-75	43	94	(U43775) secreted aspartic proteinase precursor [Glomerella cingulata]	
19844	ENU03638	ANI61C1527:	25-56	1326	NAP	g730338	1840	565	e-160	58	72	Lysophospholipase precursor (phospholipase B); lysophospholipase (EC 3.1.1.5) - <i>Penicillium notatum</i> (fragment); (X60348)	
		2982..4308		1309								lysophospholipase [Penicillium chrysogenum]	
19845	ENU03639	ANI61C188:1	56-77	1321-	NAP	g1346290	802	166	2.00E-81	45	69	high-affinity glucose transporter; (U22525) high affinity glucose transporter [Kluyveromyces lactis]	
		375..49		1340									

Seq num	Seq id	Contig Source	Primer 3 pos	Primer Basis	Selection	aat	Blast Score	Blast Prob	% id	% cvrg	Description	
			5 pos	Database Hit	nebi gi	Score	cvrg					
19846	ENU03640	ANI61C118	71-94	NAP	g2621739	762	227	2.00E-87	51	68	(AE00845) long-chain-fatty-acid-CoA ligase [Methanobacterium thermoautotrophicum]	
19847	ENU03641	ANI61C3898:	65-90	1331-	NAP	g2498971	627	130	3.00E-29	34	75	putative sterigmatocystin biosynthesis monooxygenase STCW ; (U34740) putative FAD-containing
19848	ENU03642	ANI61C1085	22-51	1282- 7:1133..2463	1310	NAP	g3738167	452	173	2.00E-42	41	100 (AL031856) putative golgi uridine diphosphate-N-acetylglucosamine transporter [Schizosaccharomyces pombe]
19849	ENU03643	ANI61C1018	44-63	1314- 7:4272..2941	1333	NAP	g1723948	1150	469	e-131	55	95 probable histone DEacetylase HOS2 ; probable transcription regulator YGL194c - yeast (Saccharomyces cerevisiae) ; (Z72716) ORF YGL194c [Saccharomyces cerevisiae] (AB010714) salicylate hydroxylase [Pseudomonas putida]
19850	ENU03644	ANI61C8914:	51-70	1315- 1895..3227	1341	NAP	g2826168	62	7.00E-13			hypothetical protein YDR322w - yeast (Saccharomyces cerevisiae) ; (U32517) Ydr322wp [Saccharomyces cerevisiae] (AL023596) hypothetical protein MLCB2407.16c [Mycobacterium leprae]
19851	ENU03645	ANI61C1926:	22-42	1295- 59..1393	1314	NAP	g2131429	236	119	4.00E-26	25	96
19852	ENU03646	ANI61C8043:	65-84	1340- 2221..884	1360	NAP	g3150104	251	129	4.00E-29	36	33
19853	ENU03647	ANI61C7152:	40-61	1314- 4223..2886	1335	NAP	g2132817	222	75	2.00E-21	33	41 probable membrane protein YOL003c - yeast (Saccharomyces cerevisiae) ; (U43491) hypothetical protein UNE378 [Saccharomyces cerevisiae] ; (Z74745) ORF YOL003c [Saccharomyces cerevisiae]
19854	ENU03648	ANI61C3804:	22-41	1299- 2043..705	1318	NAP	g1711632	2083	396	e-149	62	65 putative glycyl-tRNA synthetase (glycine--tRNA ligase) (GLYRS) ; (Z69369) glycyl tRNA synthetase [Schizosaccharomyces pombe]

Seq num	Seq id	Contig Source	Primer 3 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19855	ENU03649	ANI61C4864:	57-76	1333-1353	NAP	g1176339	517	136	4.00E-57	37	87	"hypothetical 50.8 KD protein in MIR1-STE18 intergenic region ; indoleamine-pyrrole 2,3-dioxygenase homolog YJR078w - yeast	
													(Saccharomyces cerevisiae); (Z49578) ORF YJR078w [Saccharomyces cerevisiae]; (L47993) ORF YJR078w [Saccharomyces cerevisiae] ; (AL033524) carbamoyl-phosphate synthase [Schizosaccharomyces pombe]
19856	ENU03650	ANI61C7945:	72-91	1349-1416..2755	NAP	g3873545	3360	293	e-150	66	36	(AL033524) carbamoyl-phosphate synthase [Schizosaccharomyces pombe]	
19857	ENU03651	ANI61C1092	47-66	1323-1345	NAP	g2462982	244	103	8.00E-35	34	23	(Y13975) phospholipase C [Candida albicans]	
19858	ENU03652	ANI61C9031:	63-82	1335-342..579	NAP	g1480799	37	0.000000	04			[Taenia solium] hypothetical protein YDR322w - yeast	
19859	ENU03653	ANI61C1926:	22-42	1302-59..1401	NAP	g2131429	236	119	4.00E-26	25	96	(Saccharomyces cerevisiae); (U32517) Ydr322wp [Saccharomyces cerevisiae] ; (U62928) multidrug resistance protein, ABC transporter protein [Aureobasidium pullulans]; (U85909) multidrug resistance-like protein [Aureobasidium pullulans]"	
19860	ENU03654	ANI61C6211:	49-71	1324-1869..3212	NAP	g4097503	1671	313	2.00E-84	42	34	(U31348) G4p1 [Saccharomyces cerevisiae]	
19861	ENU03655	ANI61C3588:	64-84	1347-2903..2660	NAP	g1002712	351	64	0.000000	54	12	(X81067) probable mitochondrial protein; nearly identical to YME1 [Saccharomyces cerevisiae]	
19862	ENU03656	ANI61C4066:	58-77	1342-1651..306	NAP	g531752	1288	418	e-116	56	57	Galactose-1-phosphate uridylyltransferase ; UDP-glucose--hexose-1-phosphate uridylyltransferase (EC 2.7.7.12) - yeast (Kluyveromyces marxianus var. lactis); (X07039) epimerase (GAL7) (AA 1 - 370) [Kluyveromyces lactis]	
19863	ENU03657	ANI61C7448:	22-48	1305-1277..2623	NAP	g120909	856	314	2.00E-92	51	96	(AB025252) reverse transcriptase [Magnaporthe grisea]	
19864	ENU03658	ANI61C5998:	50-69	1334-5415..4069	NAP	g4586458	151	108	1.00E-22	32	62		

Seq num	Seq id	Contig Source	Primer 3 pos	Primer 3 pos	Selection Basis	Database Hit	aat	Blast Score	Blast Prob	% id	% cvrg	Description
19865	ENU03659	ANI61C8751:	22-45	4049..5395	NAP	g2498440	926	297	4.00E-99	48	88	"Homogentisate 1,2-dioxygenase (homogenitase) (homogentisate oxygenase); 3,4-dihydroxyphenylacetate 2,3-dioxygenase (EC 1.13.11.15) - Emericella nidulans; (U30797) 2,5 dihydroxyphenylacetate oxidase [Emericella nidulans]; (A001836) homogenitate dioxygenase [Emericella nidulans]"
19866	ENU03660	ANI61C2872:	28-50	1630..282	1315-1334	NAP	g1717973	1184	499	e-140	61	56 "Glycogen (starch) synthase, isoform 2 ; UDP-glucose--starch glucosyltransferase (EC 2.4.1.11) 2 - yeast (Saccharomyces cerevisiae); (U17244) Gsy2p; Glycogen Synthase (UDP-glucose--starch glucosyltransferase) [Saccharomyces cerevisiae]"
19867	ENU03661	ANI61C5204:	42-61	1325-1104..2453	NAP	g45558826	2307	553	e-156	99	98 (AF076691) aureobasidin-resistance protein; AurA [Emericella nidulans] hypothetical 37.6 KD protein in GNTR-HTPG intergenic region; (AB005524) see SWISS_PROT ACC#: P42106 [Bacillus subtilis]; (Z99124) yxaG [Bacillus subtilis] (AF009036) NAD(+) Isocitrate dehydrogenase subunit I [A]ellomyces capsulatus]	
19869	ENU03663	ANI61C236:1	45-65	622..272	1328-1353	NAP	g2266941	1681	559	e-168	87	93 "Hypothetical 50.8 KD protein in MIR1-STE18 intergenic region; indoleamine-pyrrole 2,3-dioxygenase homolog YJR078w - yeast (Saccharomyces cerevisiae); (Z49578) ORF YJR078w [Saccharomyces cerevisiae]; (L47993) ORF YJR078w [Saccharomyces cerevisiae]"
19870	ENU03664	ANI61C4864:	57-76	1333-1365	NAP	g1176339	517	136	4.00E-57	35	88	

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Primer NAP	Selection Basis	Database Hit	ncbi gi	aat	Blast Score	Blast Prob	% id	% cvrg	Description
19871	ENU03665	ANI61C8878:	23-42	1307-	1335		g1351651	784	220	1.00E-56	45	99		hypothetical 43.7 KD protein C24B11.08C in chromosome I;
			2850..1496											hypothetical protein SPA.C24B11.08c - fission yeast ( <i>Schizosaccharomyces pombe</i> ) ; (Z67757) unknown [Schizosaccharomyces pombe] (AC000133) ORF [Emericella nidulans] (AL021748) major facilitator superfamily protein
19872	ENU03666	ANI61C3420:	37-56	1326-	NAP		g1870209	419	158	7.00E-38	95	13		
			1372..18	1349			g2842516	589	83	1.00E-34	30	66		
19873	ENU03667	ANI61C6436:	57-76	1350-	NAP									
			2965..1611	1369										
19874	ENU03668	ANI61C6064:	22-41	1315-	NAP		g2494171	80	3.00E-14					
			92..1449	1337										
19875	ENU03669	ANI61C313:2	22-41	1319-	NAP		g1711561	105	3.00E-27					
			655..1296	1338										
19876	ENU03670	ANI61C8049:	69-90	1357-	NAP		g2832659	249	100	2.00E-20	27	71		(AL021710) hypothetical protein [Arabidopsis thaliana]
19877	ENU03671	ANI61C8377:	50-69	1386	NAP		g117803	591	262	3.00E-69	39	71		cytochrome B2 precursor (L-lactate dehydrogenase (cytochrome)) (L-lactate ferricytochrome C oxidoreductase) (L-LCR) ; L-lactate dehydrogenase (cytochrome) (EC 1.1.2.3) precursor - yeast ( <i>Pichia anomala</i> ) ; (X16051) L-lactate:cytochrome c oxidoreductase preprotein [ <i>Pichia anomala</i> ]
19878	ENU03672	ANI61C722:3	42-61	1342-	NAP		g2499576	2827	357	e-177	85	35		protein kinase C-like ; protein kinase C homolog PKCA - <i>Aspergillus niger</i> ; (U10349) protein kinase C [ <i>Aspergillus niger</i> ]
			078..1715	1362										

Seq num	Seq id	Contig Source	Primer 3 pos	Primer Basis	Selection	aat	Blast Score	Blast Prob	% id	% cvrg	Description
					Database Hit	ncbi gi					(Z98981) putative pyridoxal kinase
19879	ENU03673	ANI61C9491:	27-46	NAP	g4154089	286	98	2.00E-32	35	100	[Schizosaccharomyces pombe] (AF12185) origin recognition complex subunit 4-related protein
19880	ENU03674	ANI61C9160:	68-95	NAP	g4512109	470	176	2.00E-43	36	40	Orp4p [Schizosaccharomyces pombe] Arginine permease ; arginine transport protein - yeast (Saccharomyces cerevisiae); (M11724) amino acid permease [Saccharomyces cerevisiae]; (U18795) Can1p: arginine permease [Saccharomyces cerevisiae]
19881	ENU03675	ANI61C2242:	56-75	NAP	g729014	1043	146	1.00E-95	46	74	(AL023589) membrane transporter [Schizosaccharomyces pombe] (Z99753) hypothetical protein [Schizosaccharomyces pombe] (Y12693) oxysterol-binding protein [Neurospora crassa] (Z79700) fadE13 [Mycobacterium tuberculosis]
19882	ENU03676	ANI61C7470:	65-84	NAP	g3135990	1056	287	1.00E-76	42	78	[Neurospora crassa] (Z79700) fadE13 [Mycobacterium tuberculosis] histidinol dehydrogenase (HDH); (AE000809) histidinol dehydrogenase [Methanobacterium thermoautotrophicum] (U64852) coded for by C. elegans cDNA cm17d4; Similar to epoxide hydrolase. [Caenorhabditis elegans] uracil permease ; (X98696) uracil permease [Schizosaccharomyces pombe]
19887	ENU03681	ANI61C4094:	22-55	NAP	g1465805	274	87	7.00E-21	32	85	"Exoglucanase II precursor (exocellobiohydrolase II) (CBHII) (1,4-beta-cellulobiosidase (EC 3.2.1.91) II precursor - fungus (Trichoderma reesei) ; cellulose 1,4-beta-cellulobiosidase (EC 3.2.1.91) II - fungus (Trichoderma viride); (M16190) cellobiohydrolase II [Trichoderma reesei] ; cellobiohydrolase II [Trichoderma reesei]"
19888	ENU03682	ANI61C3456:	1626..246	NAP	g2492816	582	156	5.00E-62	32	73	
19889	ENU03683	ANI61C7433:	35-54	NAP	g121855	1110	182	7.00E-76			
			2206..826	1373							

Seq num	Seq id	Contig Source	Primer 3 pos	Primer Basis	Selection	Blast gi	aat Score	Blast Score	Prob %	% id	% cvrg	Description
19890	ENU03684	ANI61C1092	57-76	NAP		g461915	829	108	2.00E-43			Dipeptidyl aminopeptidase A (DPAP A) (YSCIV); dipeptidyl aminopeptidase (EC 3.4.14.-) - yeast (Saccharomyces cerevisiae); (L21944) dipeptidyl aminopeptidase [Saccharomyces cerevisiae]; (U08230) dipeptidyl aminopeptidase A [Saccharomyces cerevisiae]; (X92441) YOR50-9 [Saccharomyces cerevisiae]; (Z75127) ORF YOR219c [Saccharomyces cerevisiae] (AF016452) Similar to aldehyde dehydrogenase; coded for by C. elegans cDNA yk144e3.3; coded for by C. elegans cDNA CESAC55R; coded for by C. elegans cDNA yk144e3.5 [Caenorhabditis elegans]
19891	ENU03685	ANI61C2498:	47-67 402..1785	1367- 1388	NAP	g2315524	682	129	1.00E-67	37	81	(AF140505) DEAD box RNA helicase [Candida albicans] "Endo-1,4-beta-xylanase (xylanase) (1,4-beta-D-xylan xylanohydrolase)" "ARG6 protein precursor (contains: N-acetyl-gamma-glutamyl-phosphate reductase (N-acetyl-gamma-glutamate reductase (N-acetyl-gamma-dehydrogenase) (NAGSA dehydrogenase), and acetylglutamate kinase (NAG kinase) (AGK) (N-acetyl)-L-glutamate 5-...; acetylglutamate kinase (EC 2.7.2.8) / N-acetyl-gamma-glutamyl-phosphate reductase (EC 1.2.1.38) precursor, mitochondrial - Neurospora crassa ; (L27746) arg-6 gene product [Neurospora crassa]"
19892	ENU03686	ANI61C8615:	23-42 471..1854	1329- 1364	NAP	g2132083	929	353	2.00E-96	49	95	[Saccharomyces cerevisiae]; (Z75105) ORF YOR197w [Saccharomyces cerevisiae] (AF140505) DEAD box RNA helicase [Candida albicans] "Endo-1,4-beta-xylanase (xylanase) (1,4-beta-D-xylan xylanohydrolase)" "ARG6 protein precursor (contains: N-acetyl-gamma-glutamyl-phosphate reductase (N-acetyl-gamma-glutamate reductase (N-acetyl-gamma-dehydrogenase) (NAGSA dehydrogenase), and acetylglutamate kinase (NAG kinase) (AGK) (N-acetyl)-L-glutamate 5-...; acetylglutamate kinase (EC 2.7.2.8) / N-acetyl-gamma-glutamyl-phosphate reductase (EC 1.2.1.38) precursor, mitochondrial - Neurospora crassa ; (L27746) arg-6 gene product [Neurospora crassa]"
19893	ENU03687	ANI61C8941:	64-83 2802..1417	1388- 1407	NAP	g4589366	542	226	3.00E-58	39	65	[Drosophila hydei]; transposase [Drosophila hydei]
19894	ENU03688	ANI61C7867:	69-88 425..1811	1391- 1413	NAP	g3123294	781	79	2.00E-70	61	97	
19895	ENU03689	ANI61C1061	35-56 9.2216..830	1360- 1380	NAP	g1703361	1592	467	e-169			

Seq num	Seq id	Contig Source	Primer 3 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19897	ENU03691	ANI61C3244:	25-46	1344-1371	NAP	g1708319	820	349	4.00E-95	45	82		cell cycle protein kinase HSK1 ; protein kinase hsk1 (EC 2.7.1.-) ; fission yeast (Schizosaccharomyces pombe) ; (D50493) hsk1+ protein kinase [Schizosaccharomyces pombe] ; (AL035263) cell cycle protein kinase hsk1 [Schizosaccharomyces pombe] (Z22902) putative transposase [Drosophila hydei] ; transposase
19898	ENU03692	ANI61C9575:	22-56	1337-1368	NAP	g436466	143	64	0.000000	24	89		[Drosophila hydei]
19899	ENU03693	ANI61C9932:	32-59	1359-1379	NAP	g417432	613	280	1.00E-74	40	91		NADPH dehydrogenase 2 (old yellow enzyme 2) ; NADPH dehydrogenase (EC 1.6.99.1) chain OYE2 - yeast (Saccharomyces cerevisiae) ; (L06124) NAD(P)H:oxidoreductase [Saccharomyces cerevisiae] ; (U00027) Oye2p: NAD(P)H oxidoreductase (Old Yellow Enzyme) [Saccharomyces cerevisiae]
19900	ENU03694	ANI61C7763:	26-45	1353-59..1451	NAP	g134270	146	54	0.000003	33	31		Conidiium-specific protein ; SpoCI-C1D protein - <i>Emericella nidulans</i> ; (X54668) SpoCI-C1D product [Emericella nidulans] (AE00955) 2-nitropropane dioxygenase (ncd2) [Archaeoglobus fulgidus]
19901	ENU03695	ANI61C1560:	44-64	1376-3104..1711	NAP	g2648355	167	60	0.000000	38	96		Zn/Cd resistance gene [Saccharomyces cerevisiae]
19902	ENU03696	ANI61C410:5	41-62	1371-030..6425	NAP	g227157	333	107	2.00E-22	32	85		hypothetical protein YDR330w - yeast (Saccharomyces cerevisiae) ; (U32517) Ydr330wp [Saccharomyces cerevisiae] ATP-dependent bile acid permease ; probable membrane protein YLL048c - yeast (Saccharomyces cerevisiae) ; (Z73153) ORF YLL048c [Saccharomyces cerevisiae]
19903	ENU03697	ANI61C1048	59-79	1387-2159..200	NAP	g2131432	441	155	5.00E-37	32	83		
19904	ENU03698	ANI61C1128	67-87	1401-3193..544	NAP	g3915963	742	159	3.00E-73	38	26		

Seq num	Seq id	Contig Source	Primer 3 pos	Primer Basis	Selection	aat	Blast Score	Blast Prob	% id	% cvrg	Description	
				NAP	Database Hit	ncbi gi	Score	Prob				
19905	ENU03699	ANI61C2134:	26-45	1347-1379	g730893	283	54	7.00E-13			tryptophan permease (tryptophan transport protein - yeast)	
						(Saccharomyces cerevisiae); (L33461)					amino acid transporter); tryptophan	
						tryptophan permease [Saccharomyces cerevisiae]; (X79150) tryptophan					cerevisiae); (X79150) tryptophan	
						amino acid permease [Saccharomyces cerevisiae]; (Z74762) ORF YOL020w					amino acid permease [Saccharomyces cerevisiae]; (Z74762) ORF YOL020w	
						[Saccharomyces cerevisiae]; (U66834)					[Saccharomyces cerevisiae]; (U66834)	
						suppressor of ABF1 [Saccharomyces cerevisiae]					suppressor of ABF1 [Saccharomyces cerevisiae]	
19906	ENU03700	ANI61C2438:	72-93	1407-1426	NAP	g731880	520	191	8.00E-48	27	64	"hypothetical 80.5 KD protein in SLN1-RAD25 intergenic region;
			160..1556			hypothetical protein YIL144w - yeast						
						(Saccharomyces cerevisiae); (Z38059)					(Saccharomyces cerevisiae); (Z38059)	
						orf, len: 691, CAI: 0.15, possible					orf, len: 691, CAI: 0.15, possible	
						coiled-coil [Saccharomyces cerevisiae]					coiled-coil [Saccharomyces cerevisiae]	
19907	ENU03701	ANI61C2438:	72-93	1407-1426	NAP	g731880	520	191	8.00E-48	27	64	"hypothetical 80.5 KD protein in SLN1-RAD25 intergenic region;
			160..1556			hypothetical protein YIL144w - yeast						
						(Saccharomyces cerevisiae); (Z38059)					(Saccharomyces cerevisiae); (Z38059)	
						orf, len: 691, CAI: 0.15, possible					orf, len: 691, CAI: 0.15, possible	
						coiled-coil [Saccharomyces cerevisiae]					coiled-coil [Saccharomyces cerevisiae]	
						"vacuolar aminopeptidase I precursor					"vacuolar aminopeptidase I precursor	
						(polypeptidase) (leucine					(polypeptidase) (leucine	
						aminopeptidase IV) (LAPIV)					aminopeptidase IV) (LAPIV)	
						(aminopeptidase III) (aminopeptidase					(aminopeptidase III) (aminopeptidase	
						YSCI); aminopeptidase ysci (EC					YSCI); aminopeptidase ysci (EC	
						3.4.11.-) precursor, vacuolar - yeast					3.4.11.-) precursor, vacuolar - yeast	
						(Saccharomyces cerevisiae); (M25548)					(Saccharomyces cerevisiae); (M25548)	
						aminopeptidase I [Saccharomyces					aminopeptidase I [Saccharomyces	
						cerevisiae]; (X71133) vacuolar					cerevisiae]; (X71133) vacuolar	
						aminopeptidase YSCI) [Saccharomyces					aminopeptidase YSCI) [Saccharomyces	
						cerevisiae]; (Z28103) ORF YKL103c					cerevisiae]; (Z28103) ORF YKL103c	
						[Saccharomyces cerevisiae]"					[Saccharomyces cerevisiae]"	
						(AL03453) putative major facilitator					(AL03453) putative major facilitator	
						family multi-drug resistance protein					family multi-drug resistance protein	
						[Schizosaccharomyces pombe]					[Schizosaccharomyces pombe]	

Seq num	Seq id	Contig Source	Primer 3 pos	Primer Basis	Selection	aat	Blast Score	Blast Prob	% id	% cvrg	Description	
19910	ENU03704	ANI61C3294:	58-77	NAP	g3201958	368	159	4.00E-40	39	62	(AF058116) eIF4E-like protein 4E-LP [Mus musculus]	
19911	ENU03705	ANI61C3573:	68-90	NAP	g1078218	961	195	3.00E-80	45	93	probable membrane protein YDR105c - yeast (Saccharomyces cerevisiae); (Z4746) unknown [Saccharomyces cerevisiae]; (Z48758) unknown [Saccharomyces cerevisiae] ; (Z35875) ORF YBR006w	
19912	ENU03706	ANI61C7316:	30-57	1375-1524..118	NAP	g4388565	1265	424	e-125	52	91	[Saccharomyces cerevisiae] " (D89173) similar to Saccharomyces cerevisiae hypothetical 36.4KD protein in SOD1-CPA2 intergenic region, SWISS-PROT Accession Number P47143 [Schizosaccharomyces pombe] ; (AL023781) adenosine kinase [Schizosaccharomyces pombe] " (AL03856) putative mitochondrial protein import protein - DNAJ protein [Schizosaccharomyces pombe] hypothetical 44.5 KD protein C14C4.09 in chromosome I; (Z98596) hypothetical protein
19913	ENU03707	ANI61C2435:	51-71	1386-2680..1272	NAP	g1749554	618	213	7.00E-64	47	95	[Schizosaccharomyces pombe] " (Z95334) Cdc15p [Schizosaccharomyces pombe] cell division control protein 15 ; cell division control protein cdc15 - fission yeast (Schizosaccharomyces pombe); (Z95334) Cdc15p
19914	ENU03708	ANI61C9254:	23-52	1370-1564..156	NAP	g3738169	1087	314	7.00E-99	58	97	[Schizosaccharomyces pombe] " (AL023781) adenosine kinase [Schizosaccharomyces pombe] " (AL03856) putative mitochondrial protein import protein - DNAJ protein [Schizosaccharomyces pombe] hypothetical 44.5 KD protein C14C4.09 in chromosome I; (Z98596) hypothetical protein
19915	ENU03709	ANI61C1115	22-48	1370-64986..3576	NAP	g3183342	353	130	2.00E-29	38	96	[Schizosaccharomyces pombe] cell division control protein 15 ; cell division control protein cdc15 - fission yeast (Schizosaccharomyces pombe); (Z95334) Cdc15p
19916	ENU03710	ANI61C3949:	66-85	1415-3655..2245	NAP	g1345704	233	62	0.000000	27	33	[Schizosaccharomyces pombe] cell division control protein 15 ; cell division control protein cdc15 - fission yeast (Schizosaccharomyces pombe); (Z95334) Cdc15p
19917	ENU03711	ANI61C9367:	22-42	1362-131..1492	NAP	g131828	998	282	5.00E-98	44	79	[Schizosaccharomyces pombe] LOW-affinity glucose transporter ; glucose transport protein RA G1 - yeast (Kluyveromyces marxianus var. lactis); (X53752) putative sugar transporter [Kluyveromyces lactis]
19918	ENU03712	ANI61C212:3	23-42	1367-273..1861	NAP	g2996008	1881	666	0	85	99	(AF055983) translation release factor subunit 1 [Podospora anserina]
19919	ENU03713	ANI61C7848:	37-55	1384-669..2082	NAP	g3023951	470	205	5.00E-52	30	43	Histone transcription regulator 1 homolog ; (Z97204) putative histone protein; histone transcription regulator [Schizosaccharomyces pombe] (AF009631) AP47/50p [Arabidopsis thaliana]
19920	ENU03714	ANI61C9794:	23-50	1367-151..1564	NAP	g2271477	1012	194	e-106	49	97	

Seq num	Seq id	Contig	Source	5' pos	Primer 3' pos	Primer Basis	Selection	aat	Blast Score	Blast Prob	% id	% cvrg	Description
19921	ENU03715	ANI61C7561:		45-64	1391-	NAP	g117619	135	50	0.00004	34	18	choline transport protein ; choline transport protein - yeast (Saccharomyces cerevisiae) ; (J05603)
				258..87	1421								[Saccharomyces cerevisiae] ; (Z72599) ORF YGL077c [Saccharomyces cerevisiae] ; (AL01543) putative amino-acid permease [Schizosaccharomyces pombe]
19922	ENU03716	ANI61C9917:	22-41	1380-	1399	NAP	g3581896	443	138	9.00E-32	24	75	(AL01543) putative amino-acid permease [Schizosaccharomyces cerevisiae]
				2839..1420									
19923	ENU03717	ANI61C7944:	36-55	1392-	1414	NAP	g1077336	466	127	2.00E-52	35	96	hypothetical protein YLR380w - yeast (Saccharomyces cerevisiae) ; (U19104) Ylr380wp [Saccharomyces cerevisiae]
				3165..4585									hypothetical 50.8 KD protein in COQ1-FLR1 intergenic region precursor ; probable membrane protein YBR004c-yeast (Saccharomyces cerevisiae) ; (Z35873) ORF YBR004c [Saccharomyces cerevisiae]
19924	ENU03718	ANI61C2369:	22-44	1380-	1402	NAP	g586465	233	88	2.00E-20	26	94	(AF04640) similar to peptidase family C19 (ubiquitin carboxyl-terminal hydrolase) [Caenorhabditis elegans]
				861..2283									mevalonate kinase (MVK) ; mevalonate kinase (EC 2.7.1.36) - yeast (Saccharomyces cerevisiae) ; (X55875) mevalonate kinase [Saccharomyces cerevisiae] ; (X06114) ORF1 (put. RAR1 protein) (AA 1-443) [Saccharomyces cerevisiae] ; (Z49809) Rar1p [Saccharomyces cerevisiae] alpha-galactosidase precursor (melipinase) (alpha-D-galactoside galactosidase [Coffea arabica])
19925	ENU03719	ANI61C1133	22-44	1383-	1403	NAP	g2746775	414	139	9.00E-37	36	82	"DLTE protein ; hypothetical protein - Bacillus subtilis ; dltE product[putative cytosolic oxidoreductase [Bacillus subtilis, Peptide, 252 aa] ; (X73124) ipa-1t [Bacillus subtilis] ; (Z99123) alternate gene name: ipa-1r [Bacillus subtilis]"
				0-963..2385									
19926	ENU03720	ANI61C7948:	42-61	1391-	1424	NAP	g125407	523	179	1.00E-47	36	95	
				2803..4226									
19927	ENU03721	ANI61C316:3	58-84	1423-	1442	NAP	g2492782	551	219	5.00E-56	38	97	
				290..1864									
19928	ENU03722	ANI61C1271:	22-44	1379-	1408	NAP	g729344	45	0.000000				
				2312..2792									

Seq num	Seq id	Contig Source	Primer 3 pos	Primer Basis	Selection	Blast aat	Blast Score	Blast Prob	% id	% cvrg	Description	
19929	ENU03723	ANI61C8203:	5 pos	NAP	g4249560	1229	291	e-133	52	96	(AB003109) beta-glucosidase	
19930	ENU03724	ANI61C1036	1190..2622	1459	NAP	g1730771	1269	330	1.00E-89	41	[Humicola grisea var. thermotolerans] hypothetical 110.9 KD protein in SPC98-TOM70 intergenic region ; probable membrane protein YNL123w	
19931	ENU03725	ANI61C8805:	24..49	1396- NAP	g4105567	184	105	9.00E-22	31	93	-yeast (Saccharomyces cerevisiae); (Z69382) N1897 [Saccharomyces cerevisiae]; (Z71399) ORF YNL123w	
19932	ENU03726	ANI61C1038	698..2133	1417 NAP	g2894272	351	141	1.00E-32	38	76	[AF047707] UDP-glucose:ceramide glycosyltransferase [Rattus norvegicus] (AL021839) hypothetical protein	
19933	ENU03727	ANI61C9835:	23..42	1397- 0:1152..2587	1416 NAP	g2132357	148	84	2.00E-15	40	[Schizosaccharomyces pombe] NBP2 protein - yeast (Saccharomyces cerevisiae); (Z50046) Nbp2p [Saccharomyces cerevisiae]; (D43693) Nap1-binding protein [Saccharomyces cerevisiae]	
19934	ENU03728	ANI61C8985:	1370..86	1425- 3019..4455	NAP	g3915140	562	127	2.00E-54	34	94	isotrichodermin C-15 hydroxylase (cytochrome P450 65A1); (AF011355) isotrichodermin C-15 hydroxylase
19935	ENU03729	ANI61C7943:	833..1185	1419- 1438 NAP	g632081	103	3.00E-21				[Fusarium sporotrichioides] hypothetical protein 4 - Xanthobacter sp.; (X79863) orf4 [Xanthobacter sp. Py2]	
19936	ENU03730	ANI61C9526:	34..1474	1401- 1420 NAP	g2501674	185	61	2.00E-18	39	20	DRAP deaminase ; RIB2 protein - yeast (Saccharomyces cerevisiae); (Z21618) DRAP deaminase [Saccharomyces cerevisiae]; (Z74808) ORF YOL066c [Saccharomyces cerevisiae]	
19937	ENU03731	ANI61C8286:	55..74	1426- 1439..1357 NAP	g1172703	484	191	8.00E-48	44	32	"peptide transporter PTR2-A; (U01171) similar to S. cerevisiae PTR2 gene, GenBank Accession Number L11994 [Arabidopsis thaliana]" (X63029) Uhu [Drosophila heteroneura]	
19938	ENU03732	ANI61C408:7	296..8739	1425- 1453 NAP	g7464	75	1.00E-12				(Z98529) putative RNA-binding protein [Schizosaccharomyces pombe]	
19939	ENU03733	ANI61C9882:	22..49	1405- 1424 NAP	g2462671	413	129	4.00E-29	33	97		

Seq num	Seq id	Contig Source	Primer 3 pos	Primer Basis	Selection	aat	Blast Score	Blast Prob	% id	% cvrg	Description
			5 pos	NAP	Database Hit	ncbi gi	Score	Prob	59	59	probable mitochondrial intermediate peptidase precursor (MIP) ; (Z70690) unknown [Schizosaccharomyces pombe]
19941	ENU03735	ANI61C6436:	57-76	1436-1463	NAP	g2842516	589	92	3.00E-37	30	72 (AL021748) major facilitator superfamily protein [Schizosaccharomyces pombe] (Z99126) hypothetical protein.
19942	ENU03736	ANI61C8998:	39-58	1427-1446	NAP	g2398820	524	221	8.00E-57	34	43 [Schizosaccharomyces pombe] (Z99126) hypothetical protein.
19943	ENU03737	ANI61C8998:	39-58	1427-1446	NAP	g2398820	524	221	8.00E-57	34	43 [Schizosaccharomyces pombe] (Z99126) hypothetical protein.
19944	ENU03738	ANI61C7853:	22-48	1411-1430	NAP	g1345707	387	108	6.00E-42	38	73 CCC1 protein ; CCC1 protein - yeast (Saccharomyces cerevisiae) ; (U19027) CCC1p: putative transmembrane Ca2+ transporter [Saccharomyces cerevisiae] ; (L24112) Ccc1p [Saccharomyces cerevisiae]
19945	ENU03739	ANI61C5260:	62-81	1441-1474	NAP	g1709784	955	347	8.00E-95		gamma-glutamyl phosphate reductase (GPR) (glutamate-5-semialdehyde dehydrogenase) (glutamyl-gamma-semialdehyde dehydrogenase) ; glutamate-5-semialdehyde dehydrogenase (EC 1.2.1.4) - yeast (Saccharomyces cerevisiae) ; (X90565) orf0155 [Saccharomyces cerevisiae] ; (U43565) gamma-glutamyl phosphate reductase [Saccharomyces cerevisiae] ; (Z75231) ORF YOR323c [Saccharomyces cerevisiae] (AF127176) trichothecene 3-O-acetyltransferase [Fusarium sporotrichoides]
19946	ENU03740	ANI61C7017:	22-55	1409-1434	NAP	g4378882	150	3.00E-35			hypothetical 42.3 KD protein in YTA2-DIT1 intergenic region ; hypothetical protein YDR400w - yeast (Saccharomyces cerevisiae) ; (U32274) Ydr400wp; CAI: 0.14 [Saccharomyces cerevisiae]
19947	ENU03741	ANI61C6489:	24-50	1417-1437	NAP	g2497466	344	73	3.00E-34	35	98

Seq num	Seq id	Contig Source	Primer 3 pos	Primer Basis	Selection	aat	Blast Score	Blast Prob	% id	% cvrg	Description	
19948	ENU03742	ANI61C1056	22..41	NAP	g3881508	259	75	1.00E-12	33	91	(Z47357) cDNA EST EMBL:T00822 comes from this gene; cDNA EST EMBL:T00823 comes from this gene [Caenorhabditis elegans]	
19949	ENU03743	ANI61C7184:	32..53	1428-3218..4678	NAP	g1710597	292	121	2.00E-30	33	73	"mitochondrial 60S ribosomal protein L7 precursor (YML7) ; ribosomal protein YmL7, mitochondrial - yeast (Saccharomyces cerevisiae); (Z49701) unknown [Saccharomyces cerevisiae]" (AF095898) siderophore biosynthesis repressor SREA [Emericella nidulans] "3'-ketoadyl-COA thiolase peroxisomal precursor (beta-ketothiolase) (acetyl-CoA acyltransferase) (peroxisomal 3-oxoacyl-CoA thiolase); acetyl-CoA C-acyltransferase (EC 2.3.1.16), peroxisomal - yeast (Yarrowia lipolytica); (X69988) acetyl-CoA acyltransferase [Yarrowia lipolytica]" choline transport protein ; choline transport protein - yeast (Saccharomyces cerevisiae); (J05603) choline transport protein [Saccharomyces cerevisiae]; (Z72599) ORF YGL077c [Saccharomyces cerevisiae]
19950	ENU03744	ANI61C9446:	67..86	1452-3377..4838	NAP	g4585213	2852	484	0	99	81	(AF095898) siderophore biosynthesis repressor SREA [Emericella nidulans] "3'-ketoadyl-COA thiolase peroxisomal precursor (beta-ketothiolase) (acetyl-CoA acyltransferase) (peroxisomal 3-oxoacyl-CoA thiolase); acetyl-CoA C-acyltransferase (EC 2.3.1.16), peroxisomal - yeast (Yarrowia lipolytica); (X69988) acetyl-CoA acyltransferase [Yarrowia lipolytica]" choline transport protein ; choline transport protein - yeast (Saccharomyces cerevisiae); (J05603) choline transport protein [Saccharomyces cerevisiae]; (Z72599) ORF YGL077c [Saccharomyces cerevisiae]
19951	ENU03745	ANI61C6203:	68..87	1455-5604..7069	NAP	g549077	840	275	1.00E-75	53	95	"3'-ketoadyl-COA thiolase peroxisomal precursor (beta-ketothiolase) (acetyl-CoA acyltransferase) (peroxisomal 3-oxoacyl-CoA thiolase); acetyl-CoA C-acyltransferase (EC 2.3.1.16), peroxisomal - yeast (Yarrowia lipolytica); (X69988) acetyl-CoA acyltransferase [Yarrowia lipolytica]" choline transport protein ; choline transport protein - yeast (Saccharomyces cerevisiae); (J05603) choline transport protein [Saccharomyces cerevisiae]; (Z72599) ORF YGL077c [Saccharomyces cerevisiae]
19952	ENU03746	ANI61C3969:	29..48	1420-238..1703	NAP	g117619	632	213	2.00E-54	33	82	"3'-ketoadyl-COA thiolase peroxisomal precursor (beta-ketothiolase) (acetyl-CoA acyltransferase) (peroxisomal 3-oxoacyl-CoA thiolase); acetyl-CoA C-acyltransferase (EC 2.3.1.16), peroxisomal - yeast (Yarrowia lipolytica); (X69988) acetyl-CoA acyltransferase [Yarrowia lipolytica]" choline transport protein ; choline transport protein - yeast (Saccharomyces cerevisiae); (J05603) choline transport protein [Saccharomyces cerevisiae]; (Z72599) ORF YGL077c [Saccharomyces cerevisiae]
19953	ENU03747	ANI61C1041	69..90	1467-72853..2916	NAP	g2507070	369	88	1.00E-18	35	61	"3'-ketoadyl-COA thiolase peroxisomal precursor (beta-ketothiolase) (acetyl-CoA acyltransferase) (peroxisomal 3-oxoacyl-CoA thiolase); acetyl-CoA C-acyltransferase (EC 2.3.1.16), peroxisomal - yeast (Yarrowia lipolytica); (X69988) acetyl-CoA acyltransferase [Yarrowia lipolytica]" choline transport protein ; choline transport protein - yeast (Saccharomyces cerevisiae); (J05603) choline transport protein [Saccharomyces cerevisiae]; (Z72599) ORF YGL077c [Saccharomyces cerevisiae]
19954	ENU03748	ANI61C9290:	55..86	1460-3960..2492	NAP	g1237183	434	146	2.00E-53	33	83	(D43773) 4-coumarate:coenzyme A ligase [Nicotiana tabacum] (AL034381) transcriptional regulator [Schizosaccharomyces pombe] (L24441) kinesin light chain [Loligo pealii]
19955	ENU03749	ANI61C6471:	24..50	1432-6161..7630	NAP	g3947853	663	232	9.00E-65	53	73	
19956	ENU03750	ANI61C222:1	23..43	1430-257..1567	NAP	g403179	263	129	5.00E-29	37	25	

Seq num	Seq id	Contig Source	Primer 3 pos	Primer Basis	Selection	aat	Blast Score	Blast Prob	% id	% cvrg	Description	
					Database Hit	ncbi gi						
19957	ENU03751	ANI61C7471:	65-84	NAP	g2507070	442	113	1.00E-50	35	83	N amino acid transport system protein (methyltryptophan resistance protein); neutral amino acid permease -	
		6428..4957	1494								Neurospora crassa ; (L34605) neutral amino acid permease [Neurospora crassa]	
19958	ENU03752	ANI61C1144	35-64	1442-1465	NAP	g127024	1418	417	e-163	60	93	homoserine O-acetyltransferase (homoserine O-trans-acetylase); homoserine O-acetyltransferase (EC 2.3.1.31) - fungus ( <i>Ascobolus immersus</i> ) ; ( <i>M26662</i> ) met2
		6-2721..1249									[ <i>Ascobolus immersus</i> ]	
19959	ENU03753	ANI61C2369:	58-77	1467-1489	NAP	g586465	233	88	2.00E-20	26	94	hypothetical 50.8 KD protein in COQ1-FLR1 intergenic region precursor; probable membrane protein YBR004c-yeast ( <i>Saccharomyces cerevisiae</i> ) ; (Z35873) ORF YBR004c
		810..2283									[ <i>Saccharomyces cerevisiae</i> ] (Z47357) cDNA EST EMBL:T00822	
19960	ENU03754	ANI61C1056	62-81	1474-1494	NAP	g3881508	259	76	7.00E-13	32	96	comes from this gene; cDNA EST EMBL:T00823 comes from this gene
		5:1164..2638									[ <i>Caenorhabditis elegans</i> ] DNA repair and recombination protein RAD52 ; ( <i>X75086</i> ) <i>K.lactis</i> Rad52	
19961	ENU03755	ANI61C5215:	27-54	1440-1459	NAP	g1172824	337	57	0.000000	56	11	[ <i>Kluyveromyces lactis</i> ] (D43773) 4-coumarate:coenzyme A ligase [ <i>Nicotiana tabacum</i> ]
		4956..3482									"hypothetical 47.3 KD protein in OMPX-MOEB intergenic region ; (AE000184) orf, hypothetical protein [ <i>Escherichia coli</i> ] ; (D90719) ORF ID:o207#4 [Escherichia coli] ; (D90720) ORF ID:o207#4 [Escherichia coli]"	
19962	ENU03756	ANI61C9290:	55-86	1470-1489	NAP	g1237183	434	146	2.00E-53	33	84	(A006219) clathrin-associated protein [ <i>Drosophila melanogaster</i> ]
		3960..2484									(Z98980) hypothetical protein [ <i>Schizosaccharomyces pombe</i> ]	
19963	ENU03757	ANI61C1118	22-53	1438-1457	NAP	g3025028	482	217	2.00E-55	33	83	
		5:6237..4760										
19964	ENU03758	ANI61C9356:	23-42	1440-1460	NAP	g3150152	1177	372	e-121	70	78	
		1498..19									(A006219) clathrin-associated protein	
19965	ENU03759	ANI61C3300:	22-41	1440-1459	NAP	g2388977	152	56	0.000000	39	16	
		478..1957										

Seq num	Seq id	Contig Source	Primer 3 pos	Primer Basis	Selection Database Hit	aat ncbi gi	blast Score	blast Prob	% id	% cvrg	Description
19966	ENU03760	ANI61C7237:	42-63	NAP	g1708578	63	0.000000				myo-inositol transporter 1 ; myo-inositol transport protein [ITR1] - yeast (Saccharomyces cerevisiae) ; (U33057)
		3570..5051	1481						006		Itr1p: myo-inositol transporter, YDR497C;CAI: 0.19 [Saccharomyces cerevisiae]
19967	ENU03761	ANI61C8669:	46-68	1453-1485	NAP	g1176670	262	90	4.00E-17	33	96 hypothetical 37.7 KD protein
		2812..1331									C08B11.7 in chromosome II ; (Z46676) similar to thioesterase; cDNA EST yk221d9.5 comes from this gene [Caenorhabditis elegans] (U59421) Band 17 [Gallus gallus]
19968	ENU03762	ANI61C9412:	54-74	1471-1494	NAP	g2795769	36	0.0004			dicarboxylic amino acid permease ; dicarboxylic amino acid permease DIP5 - yeast (Saccharomyces cerevisiae) ; (X95802) dicarboxylic amino acids Dip5p permease [Saccharomyces cerevisiae]; (Z73621) ORF YPL265w [Saccharomyces cerevisiae]
19969	ENU03763	ANI61C3441:	37-59	1450-1480	NAP	g1706439	1343	469	e-131	56	DIP5 - yeast (Saccharomyces cerevisiae) ; (X95802) dicarboxylic amino acids Dip5p permease [Saccharomyces cerevisiae]; (Z73621) ORF YPL265w [Saccharomyces cerevisiae]
19970	ENU03764	ANI61C5996:	30-55	1454-1475	NAP	g2507070	323	101	1.00E-35	28	93 N amino acid transport system protein (methyltryptophan resistance protein); neutral amino acid permease - Neurospora crassa ; (L34605) neutral amino acid permease [Neurospora crassa]
19971	ENU03765	ANI61C3862:	68-95	1495-1515	NAP	g4204312	652	271	1.00E-71	38	42 (AC003027) lcl prt_seq No definition line found [Arabidopsis thaliana] probable eukaryotic initiation factor C17C9.03 ; (Z73099) probable initiation factor [Schizosaccharomyces pombe]
19972	ENU03766	ANI61C2424:	72-96	1503-1522	NAP	g1723562	778	291	2.00E-81	46	30 (U59234) biotin carboxylase [Synechococcus PCC7942] (A006487) propionyl-CoA carboxylase [Homo sapiens] (AL031825) putative membrane transport protein [Schizosaccharomyces pombe]
19973	ENU03767	ANI61C2430:	39-58	1470-1489	NAP	g1399818	863	337	1.00E-96	45	98
19974	ENU03768	ANI61C276:1	72-94	1505-1524	NAP	g4127990	375	142	5.00E-33	34	83
19975	ENU03769	ANI61C7856:	26-49	1449-1478	NAP	g3702646	458	81	5.00E-26		

Seq num	Seq id	Contig Source	Primer 3 pos	Primer Basis	Selection	Blast aat	Blast Score	Blast Prob	% id	% cvrg	Description	
			5 pos	NAP	Database Hit	ncbi gi	Score	e-127				
19976	ENU03770	ANI61C113	38-57	1476-1495	g416582	1318	276				actin-like protein ARP2 ; actin-like protein ACT2 - yeast (Saccharomyces cerevisiae) (strain X2180) ; (X61502)	
			3:1690..192								actin-like protein [Saccharomyces cerevisiae] ; (Z71781) actin-like protein ACT2 [Saccharomyces cerevisiae] ; (Z74077) ORF YDL029w [Saccharomyces cerevisiae] ; actin-like protein ACT2 [Saccharomyces cerevisiae]	
19977	ENU03771	ANI61C1093	53-79	1480-1510	NAP	g3006137	942	324	9.00E-88	44	53	(AL022299) Cut+-transporting ATPase [Schizosaccharomyces pombe]
19978	ENU03772	ANI61C3308:	58-77	1495-2458..957	NAP	g1293655	880	347	1.00E-94	41	73	(U51327) versicolorin B synthase [Aspergillus parasiticus] ; (U51328) versicolorin B synthase [Aspergillus parasiticus]
19979	ENU03773	ANI61C6810:	32-60	1473-6538..8040	NAP	g138595	57	41	0.02	26	8	Vitellogenin II precursor (major vitellogenin) [contains: lipovitelillin I (LVII); phosvitin (PV); lipovitelillin II (LVII); YGP40]; vitellogenin II precursor - chicken ; (X13607)
19980	ENU03774	ANI61C5895:	43-63	1474-1504	NAP	g2497105	546	166	4.00E-40	38	97	"hypothetical 43.7 KD protein in OST6-PSP2 intergenic region; probable membrane protein YML018c -yeast (Saccharomyces cerevisiae); (Z46659) unknown orf, len:393, CAI: 0.13 [Saccharomyces cerevisiae]"
19981	ENU03775	ANI61C9701:	65-84	1501-1526	NAP	g2133295	664	187	2.00E-73	38	96	maackian detoxification protein 1 - fungus (Nectria haematococca); (U35892) predicted flavin-containing mono-oxygenase [Nectria haematococca]
19982	ENU03776	ANI61C3368:	22-41	1467-1486	NAP	g417337	77	3.00E-13				nuclear polyadenylated RNA-binding protein NAB2 ; RNA-binding protein NAB2 - yeast (Saccharomyces cerevisiae) ; (L10288) RNA-binding protein [Saccharomyces cerevisiae] ; (Z72644) ORF YGL122c [Saccharomyces cerevisiae]

Seq num	Seq id	Contig	Source	Primer 3 pos	Primer Basis	Selection	aat	Blast Score	Blast Prob	% id	% cvrg	Description
					NAP	Database Hit	ncbi gi	Score	Prob			
19983	ENU03777	ANI61C7316:	2847	1463-1493	NAP	g2132651	161	2.00E-45				probable membrane protein YLL028w -yeast (Saccharomyces cerevisiae); (Z73133) ORF YLL028w [Saccharomyces cerevisiae]
19984	ENU03778	ANI61C4256:	52-71	1497-1517	NAP	g2143220	1826	681	0	79	93	[Aspergillus fumigatus] (AE001323) S13 Ribosomal Protein [Chlamydia trachomatis]
19985	ENU03779	ANI61C905:2	22-53	1458-1489	NAP	g3328946	155	80	4.00E-14	34	30	p-aminobenzoate synthase (EC 4.1.3.-) -yeast (Saccharomyces cerevisiae); (Z71648) ORF YNR033w [Saccharomyces cerevisiae]
19986	ENU03780	ANI61C6340:	22-48	1472-2069..557	NAP	g2132374	501	205	5.00E-52	34	57	"aldehyde dehydrogenase 6; aldehyde dehydrogenase (NAD+)(EC 1.2.1.3) 6 precursor, salivary - human ; (U07919) aldehyde dehydrogenase 6 [Homo sapiens]" (M95300) csgA [Stigmatella aurantiaca]
19987	ENU03781	ANI61C1036	47-65	1499-1520	NAP	g4502041	818	147	1.00E-75	44	83	(J62028) negative acting factor [Fusarium solani f. sp. pis] serine/threonine-protein kinase COT-1 ; probable protein kinase cot-1 (EC 2.7.1.) - Neurospora crassa "met-10+ protein - Neurospora crassa ; (L40806) Restriction enzyme inactivation of met-10 complementation in this region. Sequence similarity to S. cerevisiae chromosome VIII cosmid 9205, accession no. U10556 CDS residues 22627-24126 [Neurospora crassa]; met-10 gene [Neurospora crassa]" "glutathione reductase (GR)(GRASE); glutathione reductase (NADPH)(EC 1.6.4.2) - yeast (Saccharomyces cerevisiae); (U43281) Glr1p,Lpg17p [Saccharomyces cerevisiae]" fumarate hydratase (EC 4.2.1.2) - Rhizopus oryzae
19988	ENU03782	ANI61C1098	26-51	1483-1503	NAP	g152650	54	0.00000009				
19989	ENU03783	ANI61C6204:	71-90	1525-1549	NAP	g1470090	243	64	0.000000030	72		
19990	ENU03784	ANI61C5953:	68-88	1520-1547	NAP	g729186	474	194	2.00E-51	38	52	
19991	ENU03785	ANI61C9152:	61-80	1522-1541	NAP	g2133315	914	330	2.00E-89	45	94	
19992	ENU03786	ANI61C800:1	22-56	1476-1502	NAP	g1708060	1088	179	e-107	53	94	
19993	ENU03787	ANI61C6075:	72-91	1535-1554	NAP	g2118296	1531	550	e-159	69	87	

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat	Blast Score	Blast Prob	% id	% cvrg	Description
19994	ENU03788	ANI61C357:2	2747	1491-	NAP	g4160574	528	127	3.00E-49	33	83	(AL035226) major facilitator	
251..726				1510								superfamily protein	
19995	ENU03789	ANI61C7020:	49-69	1520-	NAP	g1351917	422	68	8.00E-20	41	24	[Schizosaccharomyces pombe] probable amidase ; amidase (EC 3.5.1.4) - yeast (Saccharomyces cerevisiae); (Z49701) Amdyp [Saccharomyces cerevisiae]	
6795..5263				1539								(AB010714) salicylate hydroxylase [Pseudomonas putida]	
19996	ENU03790	ANI61C7125:	24-53	1484-	NAP	g2826168	67	57	0.000000	45	10	"(AC002131) Similar to gbl[41670 from <i>Emericella nidulans</i> . fumarylacetate hydrolase, "Arabidopsis thaliana]"	
1703..166				1519								"(AC002131) Similar to fumarylacetate hydrolase, gbl[41670 from <i>Emericella nidulans</i> . fumarylacetate hydrolase, "Arabidopsis thaliana]"	
19997	ENU03791	ANI61C3681:	22-53	1496-	NAP	g3157928	455	152	4.00E-45	38	96	"(AC002131) Similar to fumarylacetate hydrolase, gbl[41670 from <i>Emericella nidulans</i> . fumarylacetate hydrolase, "Arabidopsis thaliana]"	
2420..2906				1518								"(AC002131) Similar to fumarylacetate hydrolase, gbl[41670 from <i>Emericella nidulans</i> . fumarylacetate hydrolase, "Arabidopsis thaliana]"	
19998	ENU03792	ANI61C3681:	24-55	1498-	NAP	g3157928	455	152	4.00E-45	38	96	"(AC002131) Similar to fumarylacetate hydrolase, gbl[41670 from <i>Emericella nidulans</i> . fumarylacetate hydrolase, "Arabidopsis thaliana]"	
2420..2906				1520								"(AC002131) Similar to fumarylacetate hydrolase, gbl[41670 from <i>Emericella nidulans</i> . fumarylacetate hydrolase, "Arabidopsis thaliana]"	
19999	ENU03793	ANI61C59:17	23-42	1501-	NAP	g2492825	374	141	7.00E-41	32	88	"N-carbamyl-L-amino acid amidohydrolase ; N-carbamyl-L-amino acid amidohydrolase (EC 3.5.-.-)-Bacillus stearothermophilus (strain NS1122A) ; (S67784) N-carbamyl-L-amino acid amidohydrolase [Bacillus stearothermophilus, NS1122A, Peptide, 409 aa] [Bacillus stearothermophilus], geranylgeranyl pyrophosphate synthetase (GGPP synthetase) (Dimethylallyltransferase / geranyltransferase / farnesyltransferase ; geranylgeranyl pyrophosphate synthetase - <i>Neurospora crassa</i> ; (U20940) geranylgeranyl pyrophosphate synthetase [Neurospora crassa]	
35..3274				1520								"(AL031856) STAM-like protein, VHS domain containing, putative signal transducing adaptor [Schizosaccharomyces pombe]"	
20000	ENU03794	ANI61C7924:	50-69	1529-	NAP	g121146	766	162	5.00E-80	45	94	"(AL031856) STAM-like protein, VHS domain containing, putative signal transducing adaptor [Schizosaccharomyces pombe]"	
618..2163				1553									
20001	ENU03795	ANI61C2480:	24-43	1502-	NAP	g37378166	561	172	4.00E-50	41	97	"(AL031856) STAM-like protein, VHS domain containing, putative signal transducing adaptor [Schizosaccharomyces pombe]"	
4201..5746				1527									

Seq num	Seq id	Contig Source	Primer 3 pos	Primer Basis	Selection	aat	Blast Score	Blast Prob	% id	% cvrg	Description	
20002	ENU03796	ANI61C3788:	72-96	NAP	Database Hit	ncbi gi	g1351102	1128	342	4.00E-93	65	57
20003	ENU03797	ANI61C7597:	45-64	1527-1548..1	NAP	g549620	349	122	7.00E-27	33	85	"agmatine ureohydrolase" (AUH); (Z68166) unknown
20004	ENU03798	ANI61C9849:	24-54	1513-2809..4358	NAP	g3122249	687	296	3.00E-79	41	97	[Schizosaccharomyces pombe] hypothetical 46.5 KD protein in MRS4-DYN1 intergenic region ; hypothetical protein YKR053c - yeast (Saccharomyces cerevisiae); (Z28278) ORF YKR053c [Saccharomyces cerevisiae]
20005	ENU03799	ANI61C1077	24-43	1512-8549..2098	NAP	g2239243	1343	374	e-103	64	82	"D-hydantoinase (dihydropyrimidinase) (DHPS); dihydropyrimidinase (EC 3.5.2.2) - Bacillus stearothermophilus; (S73773) hydantoinase [Bacillus stearothermophilus, NS1122A, Peptide, 471 aa] [Bacillus stearothermophilus]; hydantoinase [Bacillus stearothermophilus]" (Z97211) probable inosine-5'-monophosphate dehydrogenase [Schizosaccharomyces pombe]
20006	ENU03800	ANI61C1086	42-62	1521-6.956..2507	NAP	g3024434	1475	344	e-151	69	99	26S protease regulatory subunit 6A homolog (TAT-binding protein homolog 1) (TBP-1); (D88663) Tat binding protein 1 [Brassica rapa] hypothetical 61.1 KD protein C11D3.05 in chromosome 1; (Z68166) unknown [Schizosaccharomyces pombe]
20007	ENU03801	ANI61C821:4	25-48	1520-..1563	NAP	g1351702	608	149	2.00E-62	35	84	"aldehyde dehydrogenase (ALDDH); aldehyde dehydrogenase (NAD+) (EC 1.2.1.3) - Emericella nidulans; (M16197) aldehyde dehydrogenase [Emericella nidulans]; dehydrogenase,aldehyde [Emericella nidulans]" tubulin alpha-2 chain ; tubulin alpha-2 chain - Emericella nidulans (AL031543) stxbp-unc-18-sec1 family protein [Schizosaccharomyces pombe]
20008	ENU03802	ANI61C5992:	47-66	1547-2851..4414	NAP	g118498	1272	437	e-142	54	96	"aldehyde dehydrogenase (ALDDH); aldehyde dehydrogenase (NAD+) (EC 1.2.1.3) - Emericella nidulans; (M16197) aldehyde dehydrogenase [Emericella nidulans]; dehydrogenase,aldehyde [Emericella nidulans]" tubulin alpha-2 chain ; tubulin alpha-2 chain - Emericella nidulans (AL031543) stxbp-unc-18-sec1 family protein [Schizosaccharomyces pombe]
20009	ENU03803	ANI61C5357:	57-76	1560-587..2151	NAP	g135407	1608	455	e-156	73	94	"aldehyde dehydrogenase (ALDDH); aldehyde dehydrogenase (NAD+) (EC 1.2.1.3) - Emericella nidulans; (M16197) aldehyde dehydrogenase [Emericella nidulans]; dehydrogenase,aldehyde [Emericella nidulans]" tubulin alpha-2 chain ; tubulin alpha-2 chain - Emericella nidulans (AL031543) stxbp-unc-18-sec1 family protein [Schizosaccharomyces pombe]
20010	ENU03804	ANI61C1612:	22-57	1522-3035..1470	NAP	g3581893	1005	336	e-112	51	70	"aldehyde dehydrogenase (ALDDH); aldehyde dehydrogenase (NAD+) (EC 1.2.1.3) - Emericella nidulans; (M16197) aldehyde dehydrogenase [Emericella nidulans]; dehydrogenase,aldehyde [Emericella nidulans]" tubulin alpha-2 chain ; tubulin alpha-2 chain - Emericella nidulans (AL031543) stxbp-unc-18-sec1 family protein [Schizosaccharomyces pombe]

Seq num	Seq id	Contig Source	Primer 3 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat	Blast Score	Blast Prob	% id	% cvrg	Description
20011	ENU03805	ANI61C2135:	32-52	1543-	NAP	g2493387	804	261	1.00E-93	43	96	probable sterigmatocystin biosynthesis P450 monooxygenase STCS (cytochrome P450 59); (U34740) putative p450 monooxygenase [Emericella nidulans]	
20012	ENU03806	ANI61C486:1	35-58	1537-	NAP	g4530579	1474	483	e-151	71	79	(AF130355) Pad-1 [Neurospora crassa]	
20013	ENU03807	ANI61C1046	26-46	1532-	NAP	g2245570	437	89	1.00E-36	32	63	"(AF005035) alpha 1,2-mannosidase [Spodoptera frugiperda]"	
20014	ENU03808	ANI61C385:3	45-64	1538-	NAP	g3122623	1340	511	e-144	56	98	PRL1/PRL2-like protein ; (AB004535) PRL1 [Schizosaccharomyces pombe] (Z98951) hypothetical protein [Schizosaccharomyces pombe]; (AL031546) putative dna-binding protein [Schizosaccharomyces pombe] (D49827) alpha-mannosidase [Aspergillus phoenicis]	
20015	ENU03809	ANI61C474:1	22-47	1534-	NAP	g2370467	1132	441	e-123	49	75	hypothetical protein YLL057c - yeast (Saccharomyces cerevisiae); (Z47973) ORF L0572 [Saccharomyces cerevisiae]; (Z73162) ORF YLL057c [Saccharomyces cerevisiae]	
20016	ENU03810	ANI61C1035	70-89	1583-	NAP	g1171477	1118	724	0	72	95	[Mycobacterium tuberculosis] hypothetical 54.2 KD TRP-ASP repeats containing protein C29A4_08C in chromosome 1 ; (Z97210) beta-transducin [Schizosaccharomyces pombe]	
20017	ENU03811	ANI61C537:8	22-52	1606	NAP	g2497056	557	202	5.00E-51	44	35	hypothetical protein YLL057c - yeast (Saccharomyces cerevisiae); (Z47973) ORF L0572 [Saccharomyces cerevisiae]; (Z73162) ORF YLL057c [Saccharomyces cerevisiae]	
			6:1872..2880	1679..1447	1540-								
					1559								
20018	ENU03812	ANI61C9607:	25-46	1544-	NAP	g2105061	180	85	2.00E-15	30	40	[L07339] serine/threonine-protein kinase PRP4; [Schizosaccharomyces pombe]; (AL031532) mRNA splicing-associated serine-threonine protein kinase [Schizosaccharomyces pombe]	
20019	ENU03813	ANI61C1014	36-55	1563-	NAP	g3219948	474	123	4.00E-43	33	96	hypothetical 54.2 KD TRP-ASP repeats containing protein C29A4_08C in chromosome 1 ; (Z97210) beta-transducin [Schizosaccharomyces pombe]	
			5:1689..1205		1552-								
					1574								
20020	ENU03814	ANI61C1559:	64-82	1585-	NAP	g2851498	1058	386	e-109	49	90	hypothetical 51.9 KD protein C27F1.04C in chromosome 1 ; (Z69368) unknown [Schizosaccharomyces pombe]	
			2644..1063		1604								
20021	ENU03815	ANI61C7:410	25-46	1548-	NAP	g1723245	419	131	1.00E-29	28	89	[Schizosaccharomyces pombe]	
			1..5688		1570								

Seq num	Seq id	Contig	Source	5 pos	3 pos	Basis	Database	Hit	ncbi_gi	Score	Score	Prob	% id	% cvrg	Description
20022	ENU03816	ANI61C318:8	22-41	1548-	1572	NAP	g1063421	412	95	5.00E-28	27	89	(L48797) toxin pump [Cochliobolus carbonum]		
20023	ENU03817	ANI61C778:5:	53-72	1583-	1604	NAP	g4507707	330	144	1.00E-33	37	60	thiosulfate sulfurtransferase (rhodanese); 3-mercaptoppyruvate sulfurtransferase (MST); thiosulfate sulfurtransferase (EC 2.8.1.1) - human; (X59434) rhodanese [Homo sapiens] Nucleolar protein NOP5; hypothetical protein YOR310c - yeast (Saccharomyces cerevisiae); (X90565) orf06108 [Saccharomyces cerevisiae]; (Z75217) ORF YOR310c		
20024	ENU03818	ANI61C1069	33-52	1557-	1585	NAP	g2833225	1329	275	e-113	60	85	[Saccharomyces cerevisiae]; (AF056070) nucleolar protein Nop5p putative transporter YGR260W; probable membrane protein YGR260w - yeast (Saccharomyces cerevisiae); (Z73044) ORF YGR260w [Saccharomyces cerevisiae]; (Y07777) YGR260w ORF [Saccharomyces cerevisiae] (Z99295)		
20025	ENU03819	ANI61C7618:	34-54	1570-	1589	NAP	g1723769	363	82	3.00E-15	29	81	[Schizosaccharomyces pombe] (AB006052) RNA polymerase I second-largest subunit [Neurospora crassa] [putative GTP-binding protein C1B3_04C; (Z98598) putative gtp binding protein, gtpase; Elongation factor Tu family [Schizosaccharomyces pombe]" (AL01743) conserved hypothetical protein [Schizosaccharomyces pombe] (AC000133) ORF [Emericella nidulans]		
20026	ENU03820	ANI61C6527:	22-48	1557-	1579	NAP	g2414603	443	89	3.00E-31	38	99	aminoalcoholphosphotransferase [Schizosaccharomyces pombe]		
20027	ENU03821	ANI61C30-82	23-47	1561-	1580	NAP	g3668171	2167	531	e-150	69	41	second-largest subunit [Neurospora crassa] [putative GTP-binding protein C1B3_04C; (Z98598) putative gtp binding protein, gtpase; Elongation factor Tu family [Schizosaccharomyces pombe]" (AL01743) conserved hypothetical protein [Schizosaccharomyces pombe] (AC000133) ORF [Emericella nidulans]		
20028	ENU03822	ANI61C1185:	69-88	1599-	1629	NAP	g3219963	1564	235	e-135	53	78	tubulin-specific chaperone e ; (U61232) cofactor E [Homo sapiens] (AL031907) trp-asp repeat containing protein [Schizosaccharomyces pombe]		
20029	ENU03823	ANI61C1894:	36-64	1566-	1598	NAP	g3650387	510	170	3.00E-41	35	20			
20030	ENU03824	ANI61C1794:	22-49	1570-	1594	NAP	g1870209	1025	324	e-102	42	94			
20031	ENU03825	ANI61C7709:	43-64	1594-	1618	NAP	g4507375	255	65	8.00E-19	30	84			
20032	ENU03826	ANI61C4819:	62-82	1609-	1637	NAP	g3766367	1267	338	e-125	52	97			

Seq num	Seq id	Contig Source	Primer 3 pos	Primer Basis	Selection	aat	Blast Database	Blast Hit	blast gi	Score	Score Prob	% id	% cvrg	Description
20033	ENU03827	ANI61C6841:	26-47	NAP	g3702646	681	280	2.00E-74	33	98	(AL031825) putative membrane transport protein			
20034	ENU03828	ANI61C9043:	22-45	NAP	g1346290	750	282	2.00E-80	40	82	[Schizosaccharomyces pombe] high-affinity glucose transporter ; (U22525) high affinity glucose transporter [Kluyveromyces lactis]			
20035	ENU03829	ANI61C3809:	48-76	NAP	g2956784	549	228	1.00E-58	44	79	(AL022103) hypothetical protein [Schizosaccharomyces pombe]			
20036	ENU03830	ANI61C896:1	34-54	NAP	g114555	2077	439	0	86	83	"ATP synthase beta chain, mitochondrial precursor; H <sup>+</sup> -transporting ATP synthase (EC 3.6.1.34) beta chain - Neurospora crassa ; (X53720) F(1)-ATPase beta-subunit precursor (519 AA)			
20037	ENU03831	ANI61C1139	22-53	NAP	g1346290	456	125	3.00E-50	31	88	[Neurospora crassa]; (M84192) mitochondrial ATPase beta-subunit [Neurospora crassa]" high-affinity glucose transporter ; (U22525) high affinity glucose transporter [Kluyveromyces lactis]			
20038	ENU03832	ANI61C6331:	59-78	NAP	g126694	225	103	4.00E-21	27	62	Maltose permease MAL6T (maltose transport protein MAL6T); maltose transport protein MAL61 - yeast (Saccharomyces cerevisiae); (X17391) maltose permease [Saccharomyces cerevisiae]; (M27823) maltose permease [Saccharomyces carlsbergensis]			
					g2495096	629	250	2.00E-65	39	98	glutathione synthetase (glutathione synthase) (GSH synthetase) (GSH-S); hypothetical protein YOL049w - yeast (Saccharomyces cerevisiae); (Z74791) ORF YOL049w [Saccharomyces cerevisiae]; (Y13804) Glutathione synthetase [Saccharomyces cerevisiae]			
20040	ENU03834	ANI61C1188:	72-91	NAP	g4049539	85	57	0.000000	34	18	(AL034664) hypothetical protein [Schizosaccharomyces pombe] (AF094417) cytochrome P450 [Myrothecium roridum]			
20041	ENU03835	ANI61C3095:	61-80	NAP	g2267601	723	233	1.00E-74	34	93				

Seq num	Seq id	Contig Source	Primer 3 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat	Blast Score	Blast Prob	% id	% cvrg	Description
20042	ENU03836	ANI61C9933:	2847	1607-	NAP	g127289	1692	458	0	73	99	mitochondrial processing peptidase	
		1111..2751	1626										(ubiquinol-cytochrome C reductase complex CORE protein I) ; mitochondrial processing peptidase (EC 3.4.99.41) beta chain precursor - Neurospora crassa ; (M20928)
20043	ENU03837	ANI61C2470:	52-71	1632-	NAP	g3395585	735	129	5.00E-65	49	86	beta subunit precursor (beta-MPP)	
		1830..3471	1651										[Schizosaccharomyces pombe]
20044	ENU03838	ANI61C1647:	72-94	1651-	NAP	g1169291	1259	277	e-116	54	96	aldehyde dehydrogenase (ALDDH) ; (M32351) aldehyde dehydrogenase [Aspergillus niger]	
		2502..860	1672										probable membrane protein YLL031c - yeast (Saccharomyces cerevisiae); (Z73136) ORF YLL031c [Saccharomyces cerevisiae]
20045	ENU03839	ANI61C3493:	22-48	1594-	NAP	g2132652	1240	222	7.00E-57	34	41	probable membrane protein YLL031c - yeast (Saccharomyces cerevisiae); (Z73136) ORF YLL031c [Saccharomyces cerevisiae]	
		971..5613	1622										(Z98529) mating and morphogenesis protein Scd1p. [Schizosaccharomyces pombe]
20046	ENU03840	ANI61C6338:	23-47	1606-	NAP	g2330697	400	52	0.000000	24	43	putative transporter C11D3.18C ; (Z68166) unknown	
		5664..4020	1625										[Schizosaccharomyces pombe]
20047	ENU03841	ANI61C9837:	69-89	1649-	NAP	g1351714	588	146	2.00E-60	33	94	Trichodiene oxygenase (cytochrome P450 58) ; trichodiene oxygenase 4 - fungus (Fusarium sporotrichioides); (U22462) trichodiene oxygenase [Fusarium sporotrichioides]	
		48..1696	1675										potential transcriptional adaptor ; probable transcriptional adaptor ADA2 - yeast (Saccharomyces cerevisiae) ; (M95396) ADA2 [Saccharomyces cerevisiae] ; (U33007) Ada2p; probable transcriptional adaptor; YDR448W; CAI:0.12 [Saccharomyces cerevisiae] (AL021815) hypothetical protein [Schizosaccharomyces pombe]; (AL035675) adducin N terminal domain protein [Schizosaccharomyces pombe]
20049	ENU03843	ANI61C7279:	30-60	1621-	NAP	g399006	844	232	3.00E-64	48	98		
		1692..39	1641										
20050	ENU03844	ANI61C1109	44-64	1639-	NAP	g2879861	59	1.00E-10					
		9:4929..6584	1657										

Seq num	Seq id	Contig Source	Primer 3 pos	Primer 3 pos	Selection Basis	Database Hit	nebi gi	aat	Blast Score	Blast Prob	% id	% cvrg	Description
20051	ENU03845	ANI61C1085	46-66	1640-	NAP	g2132080	918	230	1.00E-71	37	29		hypothetical protein YOR191w - yeast (Saccharomyces cerevisiae); (Z75099) ORF YOR191w [Saccharomyces cerevisiae]
20052	ENU03846	ANI61C1145	22-50	1616-21..1658	NAP	g3560233	582	182	5.00E-45	32	54	(AL031530) putative b-zip transcription factor	
20053	ENU03847	ANI61C8860:	40-61	1638-	NAP	g3184114	344	61	0.000000	34	17	[Schizosaccharomyces pombe] (AL023780) hypothetical protein	
20054	ENU03848	ANI61C3943:	50-69	1647-1430..1779	NAP	g3874345	84	48	0.0001			[Schizosaccharomyces pombe] (Z81035) predicted using Genefinder; Similarity to dehydrogenases; cDNA EST EMBL:D65800 comes from this gene; cDNA EST EMBL:D76184 comes from this gene; cDNA EST EMBL:D69322 comes from this gene; cDNA EST EMBL:C08158 comes from...	
20055	ENU03849	ANI61C6208:	51-70	1650-1216..2876	NAP	g4502169	673	189	4.00E-69	34	95	unknown ; (U50939) amyloid precursor protein-binding protein 1 [Homo sapiens]; (AC004638) amyloid precursor protein-binding protein 1 (APP-B1) [Homo sapiens] (AC000133) ORF [Emericella nidulans]	
20056	ENU03850	ANI61C9150:	23-44	1606-851..2511	NAP	g1870209	2694	1027	0	94	99	(AC000133) ORF [Emericella nidulans]	
20057	ENU03851	ANI61C1229:	23-44	1606-	NAP	g1870209	2917	1107	0	99	99	(AC000133) ORF [Emericella nidulans]	
20058	ENU03852	ANI61C6693:	24-47	1621-4549..2888	NAP	g3702646	66	2.00E-29				(AL031825) putative membrane transport protein	
20059	ENU03853	ANI61C5910:	67-95	1665-3284..3411	NAP	g4493738	35	1.3				[Schizosaccharomyces pombe] (AL034358) predicted using hexExon; L4830.1, Hypothetical protein, len: 1107 [Leishmania major]"	
20060	ENU03854	ANI61C5282:	42-69	1641-	NAP	g3258635	526	218	3.00E-60	32	97	(AF041049) 4-coumarate:CoA ligase [Populus tremuloides]	
20061	ENU03855	ANI61C1045	22-47	1621-8.6523..6683	NAP	g1255728	1081	195	1.00E-94	56	96	(U33265) complement fixation antigen [Coccidioides immitis] ; (U51271) complement-fixation antigen [Coccidioides immitis]	

Seq num	Seq id	Contig Source	Primer 3 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat	Blast Score	Blast Prob	% id	% cvrg	Description
20062	ENU03856	ANI61C1000:	23-48	1619-	NAP	g2498883	821	363	2.00E-99	43	50	50	Spliceosome associated protein 145 (SAP145) (SF3B150); (U41371) spliceosome associated protein [Homo sapiens]
20063	ENU03857	ANI61C4380:	38-59	1643-	NAP	g2791647	700	168	3.00E-78	41	90	90	(AL021287) hypothetical protein Rv3049c [Mycobacterium tuberculosis] (Z99120) yu1l [Bacillus subtilis]
20064	ENU03858	ANI61C6812:	25-44	1623-	NAP	g2635698	234	74	3.00E-25	37	49	49	"vacuolar ATP synthase catalytic subunit A (V-ATPase 67 KD subunit); H+-transporting ATPase (EC 3.6.1.35), vacuolar, 67K chain - Neurospora crassa; (J03955) vacuolar ATPase vma-1 [Neurospora crassa]" (AB010439) steroid monooxygenase [Rhodococcus rhodochrous]
20065	ENU03859	ANI61C6552:	60-79	1606-	NAP	g137461	2306	363	0	80	80	80	"vacuolar ATP synthase catalytic subunit A (V-ATPase 67 KD subunit); H+-transporting ATPase (EC 3.6.1.35), vacuolar, 67K chain - Neurospora crassa; (J03955) vacuolar ATPase vma-1 [Neurospora crassa]" (AB010439) steroid monooxygenase [Rhodococcus rhodochrous]
20066	ENU03860	ANI61C5299:	61-81	1671-	NAP	g2804298	813	261	2.00E-88	38	94	94	"vacuolar ATP synthase catalytic subunit A (V-ATPase 67 KD subunit); H+-transporting ATPase (EC 3.6.1.35), vacuolar, 67K chain - Neurospora crassa; (J03955) vacuolar ATPase vma-1 [Neurospora crassa]" (AB010439) steroid monooxygenase [Rhodococcus rhodochrous]
20067	ENU03861	ANI61C4054:	31-50	1644-	NAP	g1176239	470	207	2.00E-52	36	62	62	"vacuolar ATP synthase catalytic subunit A (V-ATPase 67 KD subunit); H+-transporting ATPase (EC 3.6.1.35), vacuolar, 67K chain - Neurospora crassa; (J03955) vacuolar ATPase vma-1 [Neurospora crassa]" (AB010439) steroid monooxygenase [Rhodococcus rhodochrous]
20068	ENU03862	ANI61C7785:	27-47	1639-	NAP	g3850071	823	260	3.00E-74	48	56	56	"vacuolar ATP synthase catalytic subunit A (V-ATPase 67 KD subunit); H+-transporting ATPase (EC 3.6.1.35), vacuolar, 67K chain - Neurospora crassa; (J03955) vacuolar ATPase vma-1 [Neurospora crassa]" (AB010439) steroid monooxygenase [Rhodococcus rhodochrous]
20069	ENU03863	ANI61C9135:	40-59	1654-	NAP	g171085	1225	276	e-121	66	96	96	"vacuolar ATP synthase catalytic subunit A (V-ATPase 67 KD subunit); H+-transporting ATPase (EC 3.6.1.35), vacuolar, 67K chain - Neurospora crassa; (J03955) vacuolar ATPase vma-1 [Neurospora crassa]" (AB010439) steroid monooxygenase [Rhodococcus rhodochrous]
20070	ENU03864	ANI61C1100:	22-48	1623-	NAP	g1703220	57	38	0.2	30	38	38	"vacuolar ATP synthase catalytic subunit A (V-ATPase 67 KD subunit); H+-transporting ATPase (EC 3.6.1.35), vacuolar, 67K chain - Neurospora crassa; (J03955) vacuolar ATPase vma-1 [Neurospora crassa]" (AB010439) steroid monooxygenase [Rhodococcus rhodochrous]
20071	ENU03865	ANI61C6552:	23-43	1641-	NAP	g2131358	588	166	3.00E-40	52	28	28	"vacuolar ATP synthase catalytic subunit A (V-ATPase 67 KD subunit); H+-transporting ATPase (EC 3.6.1.35), vacuolar, 67K chain - Neurospora crassa; (J03955) vacuolar ATPase vma-1 [Neurospora crassa]" (AB010439) steroid monooxygenase [Rhodococcus rhodochrous]
20072	ENU03866	ANI61C1117:	22-54	1638-	NAP	g3560142	651	167	2.00E-40	31	83	83	"vacuolar ATP synthase catalytic subunit A (V-ATPase 67 KD subunit); H+-transporting ATPase (EC 3.6.1.35), vacuolar, 67K chain - Neurospora crassa; (J03955) vacuolar ATPase vma-1 [Neurospora crassa]" (AB010439) steroid monooxygenase [Rhodococcus rhodochrous]
			5555..7234	1659									"vacuolar ATP synthase catalytic subunit A (V-ATPase 67 KD subunit); H+-transporting ATPase (EC 3.6.1.35), vacuolar, 67K chain - Neurospora crassa; (J03955) vacuolar ATPase vma-1 [Neurospora crassa]" (AB010439) steroid monooxygenase [Rhodococcus rhodochrous]

Seq num	Seq id	Contig Source	Primer 3 pos	Primer Basis	Selection	Blast aat	Blast Prob	% id	% cvrg	Description	
			5 pos	NAP	Database Hit	ncbi gi	Score	56	64		
20073	ENU03867	ANI61C8874:	49-76	1667-	g1170324	1662	422	e-170		Heavy metal tolerance protein precursor ; vacuolar membrane protein HMT1 - fission yeast	
		2557..877	1687							(Schizosaccharomyces pombe); (ZJ4055) HMT1	
20074	ENU03868	ANI61C9789:	22-55	1630-	NAP	g543187	46	0.000003		[Schizosaccharomyces pombe] "ankyrin, erythrocyte - mouse; (X69063) erythroid ankyrin [Mus musculus]"	
		3347..5030	1663							(A1223630) homocitrate synthase [Penicillium chrysogenum]	
20075	ENU03869	ANI61C5161:	22-52	1645-	NAP	g4165570	1971	551	0	"hypothetical 23.6 KD protein C23C1.13C in chromosome I ; (Z98559) SPAC23C1.13c; len:206aa; similar eg. to YJR133W, YJ9B _yeast, P47165, hypothetical 23.7 kd protein, (209aa), fasta scores: opt:737, E:0:0, (59.0% identity in 200 aa overlap)	
		880..2565	1664							[Schizosaccharomyces pombe] (AL035076) putative carboxylesterase-lipase family member	
20076	ENU03870	ANI61C6798:	25-45	1650-	NAP	g3183352	490	104	2.00E-32	64	"hypothetical 23.6 KD protein C23C1.13C in chromosome I ; (Z98559) SPAC23C1.13c; len:206aa; similar eg. to YJR133W, YJ9B _yeast, P47165, hypothetical 23.7 kd protein, (209aa), fasta scores: opt:737, E:0:0, (59.0% identity in 200 aa overlap)
		3320..5007	1670							[Schizosaccharomyces pombe] [Schizosaccharomyces pombe] (AF010145) hexose transporter [Aspergillus parasiticus]	
20077	ENU03871	ANI61C2287:	26-54	1652-	NAP	g4107289	569	237	1.00E-61	35	unknown ; (U50939) amyloid precursor protein-binding protein 1 [Homo sapiens]; (AC004638) amyloid precursor protein-binding protein 1 [APP-B1] [Homo sapiens]
		340..2028	1672							(AB003102) 26S proteasome subunit p44.5 [Homo sapiens]	
20078	ENU03872	ANI61C903:1	23-43	1650-	NAP	g2306977	1793	432	e-176	72	(Z50044) similar to phenylalanyl-tRNA synthetase; cDNA EST EMBL:T01401 comes from this gene; cDNA EST yk303c5.3 comes from this gene; cDNA EST yk452d5.3 comes from this gene; cDNA EST yk452d5.3 comes from this gene; cDNA EST yk...
		894..206	1669								
20079	ENU03873	ANI61C6208:	25-54	1659-	NAP	g4502169	673	189	5.00E-72	35	
		1181..2876	1678								

Seq num	Seq id	Contig Source	Primer 3 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	Score	Score	Blast Prob	% id	% cvrg	Description
20082	ENU03876	ANI61C5447:	3049	1682-	NAP	g2493011	1294	434	e-145	48	33	probable calcium-translocating ATPase	
			2892..1180	1701									8 ; probable membrane protein
20083	ENU03877	ANI61C7051:	34-63	1686-	NAP	g1778093	334	134	4.00E-40	27	89	(U64902) putative sugar transporter;	
			2926..1213	1705									[Beta vulgaris]
20084	ENU03878	ANI61C1717:	55-76	1708-	NAP	g124159	1022	205	e-107			superfamily; integral membrane protein	
			86..183	1728									[Beta vulgaris]
20085	ENU03879	ANI61C5779:	22-54	1677-	NAP	g4127832	513	163	2.00E-51	29	97	"isocitrate dehydrogenase [NAD],	
			1281..2998	1696								mitochondrial subunit 2 precursor	
20086	ENU03880	ANI61C2392:	28-48	1683-	NAP	g417726	667	179	7.00E-71			(isocitric dehydrogenase) (NAD+-	
			100..1817	1702								specific ICDH) ; isocitrate	
												dehydrogenase (NAD <sup>+</sup> ) (EC 1.1.1.41)	
												chain IDH2 precursor - yeast	
												(Saccharomyces cerevisiae); (M74131)	
												isocitrate dehydrogenase	
												kinase/phosphatase [Saccharomyces	
												cerevisiae]; (X94335) YOR3326w	
												[Saccharomyces cerevisiae]; (Z75043)	
												ORF YOR136w [Saccharomyces	
												cerevisiae]"	
												(Y7243) cytochrome P450 [Gibberella	
												fujikuroi]	
												Recessive suppressor of secretory	
												defect ; RSD1 protein - yeast	
												(Saccharomyces cerevisiae); (X75951)	
												RSD1 (SAC1) [Saccharomyces	
												cerevisiae]; (Z28212) ORF YKL212w	
												[Saccharomyces cerevisiae]; (X51672)	
												recessive suppressor of secretory defect	
												[Saccharomyces cerevisiae]; RSD1	
												gene [Saccharomyces cerevisiae]	
												putative transporter YGR260W ;	
												probable membrane protein YGR260w	
												- yeast (Saccharomyces cerevisiae) ;	
												(Z73044) ORF YGR260w	
												[Saccharomyces cerevisiae]; (Y07777)	
												YGR260w ORF [Saccharomyces	
												cerevisiae]	

Seq num	Seq id	Contig Source	Primer 3 pos	Primer 3 pos	Selection Basis	Database	Hit	aat	Blast Score	Blast Prob	% id	% cvrg	Description
20088	ENU03882	ANI61C54:20	22-51	1663-	NAP	g3915154	602	156	1.00E-67	33	99	P450_58'; trichodiene oxygenase (cytochrome P450_58'); trichodiene oxygenase 4 - fungus ( <i>Fusarium sporotrichioides</i> ); (U22462) trichodiene oxygenase [ <i>Fusarium sporotrichioides</i> ]	
20089	ENU03883	ANI50C2738	24-46	1682-	NAP	g114303	300	e-125	47	53	Calcium-transporting ATPase 3 ; Ca2+-transporting ATPase (EC 3.6.1.38) - fission yeast ( <i>Schizosaccharomyces pombe</i> ) ; (J05634) Ca-2+-ATPase (cta3)		
20090	ENU03884	ANI61C6494:	48-67	1706-	NAP	g125349	591	277	2.00E-73	40	46	[ <i>Schizosaccharomyces pombe</i> ] ; (AL021816) calcium-transporting atpase 3 [ <i>Schizosaccharomyces pombe</i> ] ; Carboxypeptidase KEX1 precursor (carboxypeptidase D) ; KEX1 protein precursor - yeast ( <i>Saccharomyces cerevisiae</i> ) ; (M17231) carboxypeptidase B-like peptide [ <i>Saccharomyces cerevisiae</i> ] ; (Z72725) ORF YGL203c [ <i>Saccharomyces cerevisiae</i> ]	
		1725..3		1726									

Seq num	Seq id	Contig Source	Primer 3 pos	Primer 3 pos	Selection Basis	Blast Database Hit	aat ncbi gi	blast Score	blast Score	blast Prob	% id	% cvrg	Description
20091	ENU03885	ANI61C1084	33-52	1689-	NAP	g2914624	152	9.00E-39					"Acid Proteinase (Penicillopepsin) (E.C.3.4.23.20) Complex With Phosphonate Inhibitor: Methyl[cyclo-7(2r)-((N-Valyl)Amino)-2-(Hydroxyl-1s)-1-Methyloxycarbonyl-2-Phenylethoxy] Phosphinyloxy-Ethyl]-1-Naphthaleneacetamide] Sodium Salt ; Acid Proteinase (Penicillopepsin) (E.C.3.4.23.20) Complex With Phosphonate Inhibitor: Methyl (2s)-[1-(((N-Formyl)-L-Valyl)amino-2-(2-Naphthyl)ethyl) Hydroxyporphinyloxy]-3-Phenylpropanoate, Sodium Salt Hydrolase, Penicillopepsin,... ; Acid Proteinase (Penicillopepsin) (E.C.3.4.23.20) Complex With Phosphonate Inhibitor: Methyl (2s)-[1-(((N-1-Naphthaleneacetyl))-L-Valyl)aminomethyl] Hydroxyphosphinyloxy]-3-Phenylpropanoate, Sodium Salt Hydrolase, Penicillopepsin... ; Acid Proteinase (Penicillopepsin) (E.C.3.4.23.20) Complex With Phosphonate Macroyclic Inhibitor: Methyl[cyclo-7(2r)-((N-Valyl)amino)-2-(Hydroxyl-1s)-1-Methoxycarbonyl-2-Phenylethoxy] Phosphinyloxy-Ethyl]-1-Naphthaleneacetamide..."
20092	ENU03886	ANI61C7717: 61-80	1722-3275..4997	1741	NAP	g548494	1662	539	0	61	94		Phosphoglucomutase 2 (glucose phosphomutase 2) (PGM 2); phosphoglucomutase (EC 5.4.2.2) PGM2 - yeast (Saccharomyces cerevisiae); (X74823) phosphoglucomutase [Saccharomyces cerevisiae]; (U09499) phosphoglucomutase [Saccharomyces cerevisiae]; (Z49702) Pgm2p [Saccharomyces cerevisiae]

Seq num	Seq id	Contig Source	Primer 3 pos	Primer Basis	Selection	aat	Blast	Blast	% id	% cvrg	Description	
				NAP	Database Hit	ncbi gi	Score	Prob				
20093	ENU03887	ANI61C6918:	22-49	1683-	g4154078	253	122	7.00E-27	29	55	[AL035161] putative efflux protein [Streptomyces coelicolor]	
20094	ENU03888	ANI61C593:6	71-90	1703-	NAP	g731613	558	196	3.00E-49	32	88	hypothetical 60.6 KD protein in CBP2-SSBR1 intergenic region ; hypothetical protein YHL036w - yeast [Saccharomyces cerevisiae]; (U11583) Small region of weak similarity to ectopic retrovirus receptor [Saccharomyces cerevisiae]
20095	ENU03889	ANI61C1065:	55-79	1718-	NAP	g4218005	95	59	0.000000 1		(AC006135) putative vicilin storage protein (globulin-like) [Arabidopsis thaliana]	
20096	ENU03890	ANI61C3446:	72-92	1730-	NAP	g585356	268	61	1.00E-15	32	40	(2-keto-3-deoxygluconate oxidoreductase); kduD protein - Erwinia chrysanthemi ; (X62073) 2-keto-3-deoxygluconate oxidoreductase [Erwinia chrysanthemi] (AL035218) conserved hypothetical protein [Schizosaccharomyces pombe] (Z69635) cDNA EST yk472e 0.5 comes from this gene; cDNA EST yk473c9.5 comes from this gene; cDNA EST yk473c9.3 comes from this gene; cDNA EST yk472e 0.3 comes from this gene [Caenorhabditis elegans]
20097	ENU03891	ANI61C8444:	22-54	1691-	NAP	g4160583	626	273	2.00E-72	47	58	(AL035218) conserved hypothetical protein [Schizosaccharomyces pombe] (Z69635) cDNA EST yk472e 0.5 comes from this gene; cDNA EST yk473c9.5 comes from this gene; cDNA EST yk472e 0.3 comes from this gene [Caenorhabditis elegans]
20098	ENU03892	ANI61C1118	69-89	1738-	NAP	g3876093	650	148	5.00E-43	40	77	Sugar transporter STL1 ; sugar transport protein STL1 - yeast (Saccharomyces cerevisiae); (U33057) Stlp; plasma membrane sugar transporter; CAI: 0.19 [Saccharomyces cerevisiae]
20100	ENU03894	ANI61C1948:	23-52	1695- 6..1744	NAP	g2250699	289	128	1.00E-28	36	16	(AB001517) PWP2 protein [Homo sapiens]
20101	ENU03895	ANI61C7713:	23-43	1703- 3728..1986	NAP	g2293058	324	94	4.00E-21	33	93	(A1000318) putative RNA-binding protein [Schizosaccharomyces pombe]; (AL022304) putative mta-binding protein. [Schizosaccharomyces pombe] (Z98979) hypothetical protein [Schizosaccharomyces pombe]
20102	ENU03896	ANI61C884:1	50-70	1727- 177..2919	NAP	g2388969	162	76	5.00E-13	30	50	

Seq num	Seq id	Contig Source	Primer 3 pos	Primer Basis	Selection	aat	Blast Score	Blast Prob	% id	% cvrg	Description			
20103	ENU03897	ANI61C6290:	66-85	NAP	g4103070	597	277	2.00E-73	45	37	(AF020705) protein kinase homolog [Schizosaccharomyces pombe] (Z98980) hypothetical protein			
20104	ENU03898	ANI61C8572:	24-44	2282..538	1768	1710-	NAP	g23888980	1225	233	5.00E-84	40	62	[Schizosaccharomyces pombe] hypothetical protein YOR091w - yeast (Saccharomyces cerevisiae); (X94335) YOR360w [Saccharomyces cerevisiae]; (Z74999) ORF YOR091w [Saccharomyces cerevisiae]
20105	ENU03899	ANI61C1026	71-106	1062..2809	1729	1757-	NAP	g2132053	568	237	1.00E-61	46	49	[Saccharomyces cerevisiae]; (Z74999) ORF YOR091w [Saccharomyces cerevisiae] ; (AL032621) similar to Acyl-CoA dehydrogenase; cDNA EST EMBL:D75425 comes from this gene; cDNA EST EMBL:M89392 comes from this gene; cDNA EST EMBL:M89303 comes from this gene; cDNA EST EMBL:D27766 comes from this gene; cDNA EST ... Trichodiene oxygenase (cytochrome P450 58); trichodiene oxygenase 4 - fungus (Fusarium sporotrichioides); (U22462) trichodiene oxygenase [Fusarium sporotrichioides] EMP70 protein precursor - yeast (Saccharomyces cerevisiae); (U53880) Emp70p; P24A protein [Saccharomyces cerevisiae]; (Z73255) ORF YLR083c [Saccharomyces cerevisiae] (AC002328) F22O2.16 [Arabidopsis thaliana]
20106	ENU03900	ANI61C9080:	43-62	5119..3369	1726-	1751	NAP	g2258125	399	87	2.00E-33	27	97	[Amanta muscaria] (Z83828)
20107	ENU03901	ANI61C9442:	39-58	1885..129	1734-	1753	NAP	g3881018	389	210	3.00E-53	34	79	(Z74999) ORF YOR091w [Saccharomyces cerevisiae]; (AL032621) similar to Acyl-CoA dehydrogenase; cDNA EST EMBL:D75425 comes from this gene; cDNA EST EMBL:M89392 comes from this gene; cDNA EST EMBL:M89303 comes from this gene; cDNA EST EMBL:D27766 comes from this gene; cDNA EST ... Trichodiene oxygenase (cytochrome P450 58); trichodiene oxygenase 4 - fungus (Fusarium sporotrichioides); (U22462) trichodiene oxygenase [Fusarium sporotrichioides] EMP70 protein precursor - yeast (Saccharomyces cerevisiae); (U53880) Emp70p; P24A protein [Saccharomyces cerevisiae]; (Z73255) ORF YLR083c [Saccharomyces cerevisiae] (AC002328) F22O2.16 [Arabidopsis thaliana]
20108	ENU03902	ANI61C4984	65-84	226..2469	1751-	1780	NAP	g3915154	868	304	1.00E-81	39	96	probable membrane protein YDL144c - yeast (Saccharomyces cerevisiae); (Z74192) ORF YDL144c [Saccharomyces cerevisiae]
20109	ENU03903	ANI61C382:6	55-74	514..4757	1744-	1770	NAP	g2131246	1035	247	e-119	49	70	probable membrane protein YDL144c - yeast (Saccharomyces cerevisiae); (Z74192) ORF YDL144c [Saccharomyces cerevisiae]
20110	ENU03904	ANI61C2254:	29-48	2069..3837	1736-	1755	NAP	g3953471	288	146	3.00E-34	32	35	probable membrane protein YDL144c - yeast (Saccharomyces cerevisiae); (Z74192) ORF YDL144c [Saccharomyces cerevisiae]
20111	ENU03905	ANI61C9764:	41-60	4110..2337	1745-	1772	NAP	g2132443	124	75	2.00E-12	30	21	

Seq num	Seq id	Contig Source	Primer 3 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat	Blast Score	Blast Prob	% id	% cvrg	Description
20112	ENU03906	ANI61C9185:	45-65	1753-	NAP	g121855	1258	176	2.00E-87				"Exoglucanase II precursor (exocellulobiohydrolase II) (CBHII) (1,4-beta-cellulobiosidase (EC 3.2.1.91) II - fungus beta-cellulobiosidase (EC 3.2.1.91) II precursor - fungus (Trichoderma reesei) ; cellulose 1,4-beta-celllobiosidase (EC 3.2.1.91) II - fungus (Trichoderma viride); (M16190) cellobiohydrolase II [Trichoderma reesei]; cellobiohydrolase II [Trichoderma reesei] ; cellulose 1,4-beta-celllobiosidase-associated protein (CAP); adenylyl cyclase-associated protein cap - fission yeast (Schizosaccharomyces pombe); (L16577) adenylyl cyclase-associated protein [Schizosaccharomyces pombe] formyltetrahydrofolate DEformylase (formyl-FH(4) hydrolase); formyltetrahydrofolate deformylase (EC 3.5.1.10) - Corynebacterium sp; (U23955) 10-formyltetrahydrofolate hydrolase [Corynebacterium sp.] (AF067947) contains similarity to NADH oxidase [Caenorhabditis elegans] (Z50108) esterase [Streptomyces lividans]
20113	ENU03907	ANI61C113	50-71	1763-1:3625..4360	NAP	g543928	697	162	6.00E-59	38	87		
20114	ENU03908	ANI61C9049:	33-52	1743-12..1788	NAP	g2500006	708	289	4.00E-77	52	56		
20115	ENU03909	ANI61C114	71-91	1781-2:3154..2530	NAP	g3193204	256	65	0.000000	36	19		
20116	ENU03910	ANI61C203:	2 46-74	1756-141..365	NAP	g908888	95	55	0.000002	31	27		
20117	ENU03911	ANI61C352:	2 45-64	1759-500..4277	NAP	g731284	1337	475	e-133	47	80		
20118	ENU03912	ANI61C237:	44-71	1755-3593..1814	NAP	g4007753	513	166	2.00E-53	33	81		
20119	ENU03913	ANI61C6098:	72-95	1790-2210..429	NAP	g4557164	805	233	5.00E-83	45	74		
20120	ENU03914	ANI61C1044	44-64	1749-1:1964..182	NAP	g2132659	404	94	4.00E-29	32	77		
												[Saccharomyces cerevisiae]	

Seq num	Seq id	Contig Source	Primer 3 pos	Primer Basis	Selection	aat	Blast Score	Blast Prob	% id	% cvrg	Description		
			5 pos	NAP	Database Hit	ncbi gi	Score	Prob	5	5	(X89442) peptide synthetase [Metarhizium anisopliae]		
20121	ENU03915	ANI61C1119:	69-88	1793-	4762..2977	1812	2120	161	1.00E-38	36	5 repressible alkaline phosphatase precursor ; alkaline phosphatase (EC 3.1.3.1) - yeast (Saccharomyces cerevisiae) ; (U33050) Pho8p: repressible alkaline phosphatase; CAI: 0.16 [Saccharomyces cerevisiae]		
20122	ENU03916	ANI61C9379:	27-47	1751-	2592..804	1770	NAP	g2851586	1085	300	2.00E-84	48	94 [Saccharomyces cerevisiae] ; (U33050) Pho8p: quinate permease (quinate transporter); quinate transport protein - Emericella nidulans ; (X13525) quinate permease [Emericella nidulans] (AC000133) ORF [Emericella nidulans]
20123	ENU03917	ANI61C8749:	70-89	1788-1819	NAP	g131768	118	1.00E-53					
20124	ENU03918	ANI61C1159:	35-68	1751-6201..4408	NAP	g1870209	2185	195	2.00E-77	84	61 hypothetical 45.2 KD GTP-binding protein in TRX1-RTA1 intergenic region ; probable membrane protein YGR210c - yeast (Saccharomyces cerevisiae) ; (Z49133) unknown [Saccharomyces cerevisiae]; (U40843) ORFS7; Method: conceptual translation supplied by author. [Saccharomyces cerevisiae] ; (Z72995) ORF YGR210c [Saccharomyces cerevisiae]		
20126	ENU03920	ANI61C8242:	27-52	1763-2420..623	NAP	g4557575	453	105	2.00E-33	36	87 fatty acid amide hydrolase ; (U82535) fatty acid amide hydrolase [Homo sapiens] ; (AF098019) fatty acid amide hydrolase [Homo sapiens] (AL035216) component of chaperonin-containing T-complex (zeta subunit) [Schizosaccharomyces pombe]		
20127	ENU03921	ANI61C6145:	58-81	1797-2678..878	NAP	g4160347	1694	549	e-180	69	95 SEL-10 protein ; (Z79757) Similarity to Candida CDC4 gene (TR:E234056); cDNA EST EMBL:D27699 comes from this gene; cDNA EST EMBL:D27698 comes from this gene; cDNA EST from this gene; cDNA EST EMBL:D33271 comes from this gene;		
20128	ENU03922	ANI61C8452:	56-75	1790-35..1841	NAP	g3915881	467	210	2.00E-53	38	30 ...		

Seq num	Seq id	Contig Source	Primer 3 pos	Primer Basis	Selection	aat	Blast Score	Blast Prob	% id	% cvrg	Description	
			5 pos	Database Hit	ncbi gi	Score	Prob					
20129	ENU03923	ANI61C1699:	22-47	NAP	g2983324	578	201	9.00E-51	43	52	(AE00705) hypothetical protein [Aequifex aeolicus]	
			1845..35								"endo-beta-1,6-glucanase - fungus (Trichoderma harzianum); (X79197)	
20130	ENU03924	ANI61C1046	23-49	NAP	g1084975	522	130	6.00E-68	38	76	glucan endo-1,6-beta-glucosidase [Trichoderma harzianum]" (AL022244) hypothetical protein	
			8.2683..868								[Schizosaccharomyces pombe]	
20131	ENU03925	ANI61C7744:	60-79	1807-	NAP	g2995342	890	206	3.00E-94	52	69	3-hydroxy-3-methylglutaryl-coenzyme A reductase (HMG-CoA reductase); (X94307) HMG-CoA-reductase [Gibberella fujikuroi]
			2111..295	1834							(AL022104) kinase-binding protein	
20132	ENU03926	ANI61C9735:	61-90	1804-	NAP	g2495263	2565	473	e-177	75	43	[Schizosaccharomyces pombe]
			2573..757	1835							A reductase (HMG-CoA lyase); (X94307) HMG-CoA-reductase	
20133	ENU03927	ANI61C8580:	22-41	1790-	NAP	g2956763	936	300	4.00E-87	46	71	[Schizosaccharomyces pombe]
			752..2581	1809							hydroxymethylglutaryl-CoA lyase (HMG-CoA lyase) (HL) (3-hydroxy-3-methylglutamate-CoA lyase); (EC 4.1.3.4) - Pseudomonas sp ; (M31807)	
20134	ENU03928	ANI61C3143:	28-47	1798-	NAP	g127562	437	152	7.00E-36	43	56	HMG-CoA-lyase (mvaB) [Pseudomonas mevalonii] ; (M24016) HMG-CoA lyase (EC 4.1.3.4)
			6798..4967	1817							[Pseudomonas mevalonii] ; (AF02688) putative transmembrane transporter Liz1p	
20135	ENU03929	ANI61C7424:	52-71	1822-	NAP	g2981103	75	8.00E-25				
			5243..3411	1842							[Schizosaccharomyces pombe]; (AL0223706) transmembrane transporter Liz1p	
20136	ENU03930	ANI61C7315:	22-47	1793-	NAP	g2388904	144	65	2.00E-12	36	14	[Schizosaccharomyces pombe] (Z98974) hypothetical protein
			1047..1914	1812							[Schizosaccharomyces pombe] (Z98597) hypothetical protein	
20137	ENU03931	ANI61C4353:	68-90	1838-	NAP	g2330711	737	282	7.00E-75	43	65	[Schizosaccharomyces pombe] (Z983828) AmMst-1 [Amanita muscaria]
			44..1879	1861							Oligosaccharyl transferase STT3 subunit; STT3 protein - yeast (Saccharomyces cerevisiae); (Z72544) ORF YGL022w [Saccharomyces cerevisiae]	

Seq num	Seq id	Contig Source	Primer 3 pos	Primer 1802-	Selection Basis	Database Hit	ncbi gi	aat	Blast Score	Blast Score	% id	% cvrg	Description
20140	ENU03934	ANI61C1122:	5 pos	5430..3592	NAP	g730721	751	182	9.00E-45	40	99	SCD2	[Schizosaccharomyces pombe]; (Z69730) mating and morphogenesis protein [Schizosaccharomyces pombe] (AJ223327) rA_sp f 9 [Aspergillus fumigatus]
20141	ENU03935	ANI61C3398:	22-49	1794-3680..1842	NAP	g2879890	665	276	3.00E-73	49	97	hypothetical 34.4 KD protein in IDS2-MPI2 intergenic region ; hypothetical protein YJL145w - yeast (Saccharomyces cerevisiae); (X87371) ORF10 [Saccharomyces cerevisiae]; (Z49420) ORF YJL145w	
20142	ENU03936	ANI61C4813:	25-46	1804-4967..6807	NAP	g1353018	177	103	3.00E-21	33	29	[Saccharomyces cerevisiae] Acetamidase ; amdS protein - Emericella nidulans ; (M16371) acetamidase enzyme [Emericella nidulans]	
20143	ENU03937	ANI61C1056	62-85	1839-841..1883	NAP	g113701	469	98	8.00E-26	40	68	(U84350) hypothetical hydroxylase a [Amycolatopsis orientalis] (AL035259) conserved hypothetical protein [Schizosaccharomyces pombe] (D14846) endo alpha-1,4-polygalactosaminidase precursor [Pseudomonas sp.] " (AL031786) putative atp dependent mnhelcase [Schizosaccharomyces pombe] hypothetical 64.5 KD protein in COX4-GTS1 intergenic region ; probable membrane protein YGL186c - yeast (Saccharomyces cerevisiae); (X91489) putative purine-cytosine transport protein [Saccharomyces cerevisiae]; (Z72708) ORF YGL186c [Saccharomyces cerevisiae]	
20144	ENU03938	ANI61C1054	41-60	1807-5:1443..3286	NAP	g1872509	256	98	3.00E-19	31	67	hypothetical 34.4 KD protein in IDS2-MPI2 intergenic region ; hypothetical protein YJL145w - yeast (Saccharomyces cerevisiae); (X87371) ORF10 [Saccharomyces cerevisiae]; (Z49420) ORF YJL145w	
20145	ENU03939	ANI61C7623:	33-52	1809-2597..749	NAP	g4176557	522	132	2.00E-44	30	73	[Amycolatopsis orientalis] (AL035259) conserved hypothetical protein [Schizosaccharomyces pombe] (D14846) endo alpha-1,4-polygalactosaminidase precursor [Pseudomonas sp.] " (AL031786) putative atp dependent mnhelcase [Schizosaccharomyces pombe] hypothetical 64.5 KD protein in COX4-GTS1 intergenic region ; probable membrane protein YGL186c - yeast (Saccharomyces cerevisiae); (X91489) putative purine-cytosine transport protein [Saccharomyces cerevisiae]; (Z72708) ORF YGL186c [Saccharomyces cerevisiae]	
20146	ENU03940	ANI61C61:28	69-91	1834-09..959	NAP	g286165	397	191	1.00E-47	41	41	hypothetical 34.4 KD protein in IDS2-MPI2 intergenic region ; probable membrane protein YGL186c - yeast (Saccharomyces cerevisiae); (X91489) putative purine-cytosine transport protein [Saccharomyces cerevisiae]; (Z72708) ORF YGL186c [Saccharomyces cerevisiae]	
20147	ENU03941	ANI61C7855:	40-59	1833-2315..455	NAP	g3687476	907	161	6.00E-65	42	91	hypothetical 34.4 KD protein in IDS2-MPI2 intergenic region ; probable membrane protein YGL186c - yeast (Saccharomyces cerevisiae); (X91489) putative purine-cytosine transport protein [Saccharomyces cerevisiae]; (Z72708) ORF YGL186c [Saccharomyces cerevisiae]	
20148	ENU03942	ANI61C7388:	46-64	1845-2470..4331	NAP	g1723945	480	144	4.00E-37	32	87	hypothetical 34.4 KD protein in IDS2-MPI2 intergenic region ; probable membrane protein YGL186c - yeast (Saccharomyces cerevisiae); (X91489) putative purine-cytosine transport protein [Saccharomyces cerevisiae]; (Z72708) ORF YGL186c [Saccharomyces cerevisiae]	
20149	ENU03943	ANI61C6750:	22-50	1824-3824..2437	NAP	g2120652	126	5.00E-28	45	42	capacia; (UJ9883) unknown [Burkholderia cepacia]	hypothetical protein 1 - Pseudomonas	

Seq num	Seq id	Contig Source	Primer 3 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat	Blast Score	Blast Score	% id	% evrg	Description
20150	ENU03944	ANI61C5845:	53-72	1853-1879	NAP	g731893	815	286	3.00E-76	38	97	putative transporter YIL166C; probable membrane protein YIL166c - yeast [Saccharomyces cerevisiae]; (Z46921) unknown [Saccharomyces cerevisiae]	
20151	ENU03945	ANI61C1049	22-55	1833-1852	NAP	g1709915	2011	695	0	72	95	phosphoribosylaminoimidazolecarboxamide formyltransferase 2 (AICAR transformylase) / IMP cyclohydrolase (inosicase) /IMP synthetase) (ATIC); hypothetical protein YMR120c - yeast (Saccharomyces cerevisiae); (Z49273) unknown [Saccharomyces cerevisiae] "Y09476" YisK [Bacillus subtilis]; (Z99109) similar to 5-oxo-1,2,5-tricarboxilic-3-penten acid decarboxylase [Bacillus subtilis]" (AL031534) Major facilitator superfamily protein	
20152	ENU03946	ANI61C9731:	32-52	1843-2136..4011	NAP	g2145376	505	218	1.00E-55	47	33	[Schizosaccharomyces pombe] finger [Schizosaccharomyces pombe] (Z98602) hypothetical WW domain-containing protein	
20153	ENU03947	ANI61C916:2	64-82	1866-201..324	NAP	g3560142	669	131	9.00E-60	32	95	[Schizosaccharomyces pombe] (AL034490) putative PHD-type zinc finger [Schizosaccharomyces pombe] (Z98602) hypothetical WW domain-containing protein	
20154	ENU03948	ANI61C1096	41-63	1858-3673..2552	NAP	g4008555	305	104	4.00E-32	28	95	[Schizosaccharomyces pombe] (AL023860) short chain dehydrogenase [Schizosaccharomyces pombe] hypothetical 65.3 KD protein in MAD1-SCY1 intergenic region; probable membrane protein YGL084c - yeast (Saccharomyces cerevisiae); (Z72606) ORF YGL084c	
20155	ENU03949	ANI61C8717:	49-70	198..2079	NAP	g2330816	792	205	3.00E-75	35	64	[Saccharomyces pombe] (AL023860) short chain dehydrogenase [Schizosaccharomyces pombe] hypothetical 65.3 KD protein in MAD1-SCY1 intergenic region; probable membrane protein YGL084c - yeast (Saccharomyces cerevisiae); (Z72606) ORF YGL084c	
20156	ENU03950	ANI61C532:4	32-62	1852-68..1024	NAP	g3218393	261	125	1.00E-27	35	32	[Saccharomyces cerevisiae]	
20157	ENU03951	ANI61C916:7:	22-51	1838-2721..834	NAP	g1723878	1097	374	e-111	47	92	quinate permease (quinate transporter); quinate transport protein - Emericella nidulans ; (X13525) quinate permease [Emericella nidulans]	
20158	ENU03952	ANI61C8749:	22-49	1848-2731..841	NAP	g131768	118	1.00E-53					

Seq num	Seq id	Contig Source	Primer 3 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat	Blast Score	Blast Prob	% id	% cvrg	Description
20159	ENU03953	ANI61C7362:	44-63	1877-	NAP	g140371	516	206	2.00E-56	32	95	"hypothetical 58.8 KD protein in GLK1-SRO9 intergenic region ; hypothetical protein YCL038c - yeast (Saccharomyces cerevisiae); (X59720) YCL038c, len:528 [Saccharomyces cerevisiae]"	
20160	ENU03954	ANI61C1642:	22-48	1848-	NAP	g2822399	320	84	1.00E-33	43	37	(AF016485) ORF H1434 [Halobacterium sp. NRC-1]	
20161	ENU03955	ANI61C1137	40-61	1878-	NAP	g464876	363	82	4.00E-31			transcription factor TAU 131 KD subunit (TFIIC 131 KD subunit); transcription factor IIC chain TFC4 - yeast (Saccharomyces cerevisiae); (L12722) transcription factor IIIB 131kDa subunit [Saccharomyces cerevisiae]; (Z72832) ORF YGR047c [Saccharomyces cerevisiae]	
20162	ENU03956	ANI61C888:2	24-52	1866-60..2163	NAP	g731640	1216	392	e-134	58	49	putative prolyl-tRNA synthetase YHR020W (proline--tRNA ligase) (PRORS); multifunctional amino acid-tRNA ligase homolog - yeast (Saccharomyces cerevisiae); (U10399) Yhr020wp [Saccharomyces cerevisiae] (X05204) arom polypeptide [Emericella nidulans] (AF121000) oxidoreductase protein homolog Oxi [Corynebacterium glutamicum]	
20163	ENU03957	ANI61C4369:	24-45	1866-2546..639	NAP	g3834343	3235	888	0	99	38	(Saccharomyces cerevisiae); (U10399) Yhr020wp [Saccharomyces cerevisiae] (X05204) arom polypeptide [Emericella nidulans]	
20164	ENU03958	ANI61C4856:	45-66	1885-1151..3057	NAP	g4583402	259	55	1.00E-19	32	55	(AF121000) oxidoreductase protein homolog Oxi [Corynebacterium glutamicum]	
20165	ENU03959	ANI61C8873:	23-51	1869-3767..5674	NAP	g2497824	1471	324	e-127	47	72	DNA replication licensing factor MCM6 (P105MCM); (D84557) HsMcM6 [Homo sapiens]	
20166	ENU03960	ANI61C3272:	31-50	1873-10..1919	NAP	g2499479	2644	481	e-135	97	96	NEMPA protein precursor; (U62332) NEMPA [Emericella nidulans] (Z99163) very hypothetical protein [Schizosaccharomyces pombe] (AL031855) putative vacuolar membrane protein	
20167	ENU03961	ANI61C1676:	48-67	1898-2734..824	NAP	g4584706	300	53	4.00E-10	36	25	[Schizosaccharomyces pombe] (AL023518) hypothetical protein [Schizosaccharomyces pombe]	
20168	ENU03962	ANI61C2883:	22-45	1874-2223..310	NAP	g3738200	918	207	4.00E-96	35	65		
20169	ENU03963	ANI61C5338:	69-88	1922-3066..1151	NAP	g3130053	967	277	7.00E-97	45	80		

Seq num	Seq id	Contig Source	Primer 3 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
20170	ENU03964	ANI61C1051	54..79	1908..1927	NAP	g3879809	172	85	1.00E-15				(Z47356) similar to protein kinase C substrate; cDNA EST EMBL:M75788 comes from this gene; cDNA EST EMBL:D71530 comes from this gene; cDNA EST EMBL:C08471 comes from this gene; cDNA EST yk427a3.3 comes from this gene; cDNA EST ... ; (Z47358) similar to protein kinase C substrate; cDNA EST EMBL:M75788 comes from this gene; cDNA EST EMBL:D71530 comes from this gene; cDNA EST EMBL:C08471 comes from this gene; cDNA EST yk427a3.3 comes from this gene; cDNA EST ... ; (AL035085) t-complex protein 1, alpha subunit homolog; chaperonin family [Schizosaccharomyces pombe] " (D45893) acr-2 [Neurospora crassa]
20171	ENU03965	ANI61C8625: 4894..2977	63..82	1919..1938	NAP	g4107478	1900	541	0	73	98		"(AL035085) t-complex protein 1, alpha subunit homolog; chaperonin family [Schizosaccharomyces pombe] " (D45893) acr-2 [Neurospora crassa]
20172	ENU03966	ANI61C1025 8..241..2165	58..78	1910..1940	NAP	g1754596	129	92	1.00E-17	25	72		tubulin alpha-2 chain ; tubulin alpha-2 chain - <i>Emericella nidulans</i> (AL035259) putative utp--glucose-1-phosphate uridylyltransferase [Schizosaccharomyces pombe] (AL009146) alternatively spliced form [Drosophila melanogaster] (AL031786) hypothetical protein
20173	ENU03967	ANI61C3731: 2027..101	62..81	1927..1946	NAP	g135407	1617	592	e-168	97	67		[Schizosaccharomyces pombe] L-amino acid oxidase precursor (LAO) ; L-amino-acid oxidase (EC 1.4.3.2) precursor - <i>Neurospora crassa</i> hypothetical protein YDR425w - yeast (Saccharomyces cerevisiae); (U33007) Ydr425wp; CAI: 0.15 [Saccharomyces cerevisiae]
20174	ENU03968	ANI61C7229: 2862..936	50..69	1912..1934	NAP	g4176544	1741	691	0	68	81		transposon TNT 1..94 [contains: protease ; reverse transcriptase ; endonuclease]; hypothetical protein - common tobacco (X1377) ORF [Nicotiana tabacum]
20175	ENU03969	ANI61C1097 8..9619..11546	22..45	1878..1908	NAP	g2827482	41	0.027					
20176	ENU03970	ANI61C9827: 1002..2933	22..44	1890..1909	NAP	g3687484	193	79	9.00E-14	38	22		
20177	ENU03971	ANI61C1125: 1551..3485	29..48	1902..1921	NAP	g129307	885	126	5.00E-55	52	22		
20178	ENU03972	ANI61C8860: 1235..3176	68..87	1947..1966	NAP	g2131481	271	116	5.00E-25	34	43		
20179	ENU03973	ANI61C3512: 34..159	55..90	1926..1955	NAP	g130582	77	4.00E-13					

Seq num	Seq id	Contig Source	Primer 3 pos	Primer Basis	Selection	aat	Blast Score	Blast Prob	% id	% cvrg	Description
20180	ENU03974	ANI61C9440:	37-58	NAP	g2257503	484	195	1.00E-53	42	52	(AB004335) BEM46 protein
			725..2668								[Schizosaccharomyces pombe]
20181	ENU03975	ANI61C4271:	38-57	NAP	g2896767	656	157	8.00E-78	42	51	(AL021899) hypothetical protein
			17..1960								Rv2030c [Mycobacterium tuberculosis]
20182	ENU03976	ANI61C8421:	68-90	NAP	g2492615	280	68	2.00E-10	35	26	acetate kinase (acetokinase); (X8904)
			190..2133								acetate kinase [Corynebacterium glutamicum]
20183	ENU03977	ANI61C3682:	22-45	NAP	g1408257	222	88	2.00E-16	32	16	(U60989) putative transposase
			2406..3670								[Magnaporthe grisea]
20184	ENU03978	ANI61C4018:	22-51	NAP	g231361	332	167	2.00E-40	38	62	1-aminoacylcopropane-1-carboxylate deaminase (ACC deaminase); (M73488) 1-aminoacylcopropane-1-carboxylate deaminase [Pseudomonas sp.]
			2033..87								(AE000870) conserved protein
20185	ENU03979	ANI61C7081:	22-48	NAP	g2622063	272	99	2.00E-28	32	48	[Methanobacterium thermoautotrophicum] (Z80108) lipi [Mycobacterium tuberculosis]
			1116..3066								putative 60.3 KD transcriptional regulatory protein in PRP5-THI2 intergenic region; probable regulatory protein - yeast (Saccharomyces cerevisiae); (Z35108) ORF YBR239c [Saccharomyces cerevisiae]
20186	ENU03980	ANI61C1105	22-44	NAP	g1542908	96	1.00E-18				(AL031004) RNA lariat debranching enzyme - like protein [Arabidopsis thaliana]
			9..2142..1967								(AF050534) severin kinase
20187	ENU03981	ANI61C9507:	54-73	NAP	g586354	353	136	4.00E-31	28	88	[Dictyostelium discoideum] (U22463) T-2 toxin biosynthesis protein; TRI7 [Fusarium sporotrichioides]
			517..2475								(D85129) bphC [Pseudomonas stutzeri]
20188	ENU03982	ANI61C7071:	56-77	NAP	g3281851	707	94	2.00E-18	43	26	
			2078..119								
20189	ENU03983	ANI61C1040	71-95	NAP	g3075511	968	385	e-106	47	82	
			5..785..2755								
20190	ENU03984	ANI61C9829:	35-67	NAP	g4249357	275	92	2.00E-28	31	40	(U22463) T-2 toxin biosynthesis protein; TRI7 [Fusarium
			50..2024								sporotrichioides]
20191	ENU03985	ANI61C7972:	40-62	NAP	g2116732	277	68	2.00E-10	34	55	(D85129) bphC [Pseudomonas stutzeri]
			4612..2636								

Seq num	Seq id	Contig Source	Primer 3 pos	Primer Basis	Selection Database Hit	aat	Blast Score	Blast Prob	% id	% cvrg	Description
			5 pos	NAP	ncbi gi	500	230	2.00E-59	28	67	
20192	ENU03986	ANI61C6593:	42-61	NAP	g117619						
		5081..3101	1980								
20193	ENU03987	ANI61C6331:	53-82	1981-	NAP	g3130051	1240	311	e-132	52	86
		4568..6163	2001								
20194	ENU03988	ANI61C8122:	45-65	1979-	NAP	g2132851	303	122	1.00E-26	29	52
		491..2486	1998								
20195	ENU03989	ANI61C4157:	70-89	1996-	NAP	g1723584	698	234	1.00E-60	48	60
		3380..1381	2026								
20196	ENU03990	ANI61C6693:	58-77	2001-	NAP	g913016	651	188	1.00E-46	31	19
		6873..4872	2020								
20197	ENU03991	ANI61C7484:	42-61	1989-	NAP	g1709060	437	157	3.00E-37	39	46
		4040..2031	2008								
20198	ENU03992	ANI61C1217:	22-45	1981-	NAP	g4049341	402	74	2.00E-37	38	53
		6456..6123	2003								
20199	ENU03993	ANI61C314:2	22-47	1983-	NAP	g3169059	1605	207	e-140	57	75
		538..514	2004								
20200	ENU03994	ANI61C6921:	24-43	1988-	NAP	g4584703	569	214	1.00E-54	29	63
		2053..28	2007								
20201	ENU03995	ANI61C1070	30-49	1996-	NAP	g2226422	2075	744	0	58	97
		0..2196..4224	2015								

Seq num	Seq id	Contig Source	Primer 3 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat	Blast Score	Blast Prob	% id	% cvrg	Description
20202	ENU03996	ANI61C9941:	22-51	2021	NAP	g401441	1673	263	0	50	85	dolichyl-phosphate-mannose--protein mannosyltransferase 2 ; hypothetical protein YAL023 - yeast (Saccharomyces cerevisiae) ; (L05146) Pmt2p; protein O-D-	
20203	ENU03997	ANI61C1146	48-68	2027-2.56..2097	NAP	g4007778	284	166	5.00E-40	30	38	mannosyltransferase [Saccharomyces cerevisiae] ; (L05027) ORF YAL23 [Saccharomyces cerevisiae]	
20204	ENU03998	ANI61C6137:	45-68	2021-2940..896	NAP	g3766370	698	129	1.00E-67	39	88	[Schizosaccharomyces pombe] (AL031907) lysyl-tRNA synthetase	
20205	ENU03999	ANI61C3240:	32-52	2009-2321..270	NAP	g2507312	402	141	7.00E-39	56	35	60S ribosomal protein L23A (L25); (U44800) ribosomal protein L23a [Puccinia graminis f. sp. avenae] (U89924) protein phosphatase 1 binding protein PTG [Mus musculus] (AL031534) Major facilitator superfamily protein	
20206	ENU04000	ANI61C1068	22-54	2016-4..93..2057	NAP	g1888566	73	5.00E-12					
20207	ENU04001	ANI61C6812:	70-89	2052-2231..4290	NAP	g3560142	479	90	1.00E-37	31	78	[Schizosaccharomyces pombe] (AF015771) putative transcriptional regulator [Magnaporthe grisea] (X97657) serine/threonine kinase [Neurospora crassa]	
20208	ENU04002	ANI50C8879	60-79	2066-1..2468..401	NAP	g2367591	136	5.00E-31	45	71	hypothetical 143.6 KD protein C26A3.09C in chromosome I; (Z69240) hypothetical protein [Schizosaccharomyces pombe]		
20209	ENU04003	ANI61C7903:	36-55	2041-1959..4027	NAP	g1870019	1576	254	e-176	57	97	"hypothetical 143.6 KD protein C26A3.09C in chromosome I; (Z69240) hypothetical protein [Schizosaccharomyces pombe]"	
20210	ENU04004	ANI61C6374:	39-64	2056-1829..3908	NAP	g1723237	319	103	2.00E-34	38	13	"hypothetical zinc metalloproteinase YIL108W ; probable membrane protein YIL108w - yeast (Saccharomyces cerevisiae) ; (Z38125) orf, [len: 696, CAI: 0.15 [Saccharomyces cerevisiae]	
20211	ENU04005	ANI61C6284:	29-55	2047-4146..6226	NAP	g731856	820	348	9.00E-95	37	92	"[Cochliobolus heterostrophus] (AL034490) putative ATP-dependent DNA helicase [Schizosaccharomyces pombe]	
20212	ENU04006	ANI61C195:2	67-87	2080-097..16	NAP	g1546072	364	96	2.00E-28	33	14	(U68040) polyketide synthase	
20213	ENU04007	ANI61C8249:	28-50	2049-1665..3749	NAP	g4008550	656	154	2.00E-36	34	97	DNA helicase [Schizosaccharomyces pombe]	

Seq num	Seq id	Contig Source	Primer 3 pos	Primer Basis	Selection Database Hit	aat	Blast Score	Blast Prob	% id	% cvrg	Description	
20214	ENU04008	ANI61C1046	22-52	NAP	g2648250	73	7.00E-12				(AE000948) 3-hydroxyacyl-CoA dehydrogenase (fbhd-10) [Archaeoglobus fulgidus]	
20215	ENU04009	ANI61C8491:	40-59	2062-	NAP	g1872502	184	83	5.00E-15	35	(U84349) hypothetical hydroxylase a [Amycolatopsis orientalis]	
20216	ENU04010	ANI61C7424:	56-75	2078-	NAP	g2506921	322	66	1.00E-29	42	"probable taurine catabolism dioxygenase (sulfate starvation-induced protein 3) (SS13); (D85613) dioxygenase [Escherichia coli]; (U73857) dioxygenase [Escherichia coli]; (AE000143) taurine dioxygenase, 2-oxoglutarate-dependent [Escherichia coli]" (AC000133) ORF [Emericella nidulans]	
20217	ENU04011	ANI61C1159:	23-44	2036-	NAP	g1870209	2185	353	e-124	84	(AF091042) putative cercosporin transporter [Cercospora kikuchii]	
20218	ENU04012	ANI61C378:6	66-85	2098-	NAP	g2885836	769	258	1.00E-67	33	hypothetical 49.7 KD protein in GIN-STE3 intergenic region ; hypothetical protein YKL172w - yeast (Saccharomyces cerevisiae); (Z26878) unknown [Saccharomyces cerevisiae]; (Z28172) ORF YKL172w [Saccharomyces cerevisiae] ; ORF (PI4-kinase) (PTDINS-4-kinase); probable 1-phosphatidylinositol 4-kinase (EC 2.7.1.67) - yeast (Saccharomyces cerevisiae); (D13717) homologous protein to PI3-kinase (STT4) [Saccharomyces cerevisiae]; (U17247) Stt4p: Phosphatidylinositol-4-kinase [Saccharomyces cerevisiae] alpha-adaptin homolog ; (Y11104) melanogaster [Drosophila sapiens]	
20219	ENU04013	ANI61C5335:	32-52	2077-	NAP	g549736	485	154	2.00E-36	37		
20220	ENU04014	ANI61C257:4	29-50	2073-	NAP	g586048	1636	431	e-148	54		
20221	ENU04015	ANI61C8788:	22-55	65..2177	2092	NAP	g3912968	1229	362	e-128	41	
20222	ENU04016	ANI61C6107:	22-48	2067-	NAP	g3820614	949	231	e-106	43		
			2158..45	2093								

Seq num	Seq id	Contig Source	Primer 3 pos	Primer Basis	Selection	Blast gi	aat Score	Blast Prob	% id	% cvrg	Description
			5 pos	Database Hit	ncbi gi	Score	0.00000	0.00000			
20223	ENU04017	ANI61C9256:	72-94	2119-	g401172	65	0.00000	0.00000			Tetracycline resistance protein (transposon TN4351 / TN4400); NADP-requiring oxidoreductase - Bacteroides fragilis ; (M37699) tetracycline resistance protein [Transposon Th4351]
20224	ENU04018	ANI61C6644:	45-64	2096-4295..2181	NAP	g481285	3041	1143	0	85	98 NADPH--ferrithemoprotein reductase (EC 1.6.2.4) - Aspergillus niger; (Z226938) NADPH cytochrome P450 oxidoreductase [Aspergillus niger]; NADPH cytochrome P450 reductase [Aspergillus niger] (AL02377) hypothetical protein
20225	ENU04019	ANI61C1430:	40-62	2086-5060..2944	NAP	g3184096	1012	263	e-115	40	98 [Schizosaccharomyces pombe] (AF004516) El-like protein [Homo sapiens]
20226	ENU04020	ANI61C6107:	30-59	2105-2162..45	NAP	g3820614	949	231	e-106	43	84 phenylalanine ammonia-lyase; phenylalanine ammonia-lyase (EC 4.3.1.5) - fungus (Rhodosporidium toruloides) (strain CBS14); (X51513) phenylalanine ammonia-lyase [Rhodosporidium toruloides]; (X12702) L-phenylalanine ammonia-lyase [Rhodosporidium toruloides] A-agglutinin attachment subunit precursor ; $\alpha$ -agglutinin core protein AGA1 - yeast (Saccharomyces cerevisiae) ; (M60590) $\alpha$ -agglutinin core subunit [Saccharomyces cerevisiae] ; (Z71659) ORF YNR044w [Saccharomyces cerevisiae]
20227	ENU04021	ANI61C4674	62-81	2135-1..2175	NAP	g129593	1039	270	e-115	43	79 pisatin demethylase (cytochrome P450 57A2) ; pisatin demethylase - fungus (Nectria haematococca) ; (X73145) pisatin demethylase [Nectria haematococca]
20228	ENU04022	ANI61C6214:	43-62	2113-47..2184	NAP	g416592	40	0.052			
20229	ENU04023	ANI61C4312:	24-55	2086-3724..1589	NAP	g585695	208	120	4.00E-26	29	54

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat	Blast Score	Blast Prob	% id	% cvrg	Description
20230	ENU04024	ANI61C1100	22-45	206-	NAP	g731771	453	148	1.00E-47	31	82		"hypothetical 59.7 KD protein in BET1-PAN1 intergenic region ; probable membrane protein YIL001w-yeast (Saccharomyces cerevisiae) ; (Z38062) orf, len: 513, CAI: 0.12
20231	ENU04025	ANI61C5348:	29-48	2115-	NAP	g2501339	2759	813	0	80	99		[Saccharomyces cerevisiae]" Copper amine oxidase 1 ;(UJ31869) copper amine oxidase [Aspergillus niger]
20232	ENU04026	ANI61C9151:	37-59	2129-	NAP	g2959373	297	137	2.00E-32	34	62		(AL022117) hypothetical protein [Schizosaccharomyces pombe]
20233	ENU04027	ANI61C9700:	70-89	2161-	NAP	g2435522	619	164	9.00E-73	38	72		(AF024504) contains similarity to other AMP-binding enzymes [Arabidopsis thaliana]
20234	ENU04028	ANI61C9533:	54-75	2153-	NAP	g2130244	120	46	0.001	39	31		hypothetical protein - fission yeast (Schizosaccharomyces pombe) fragment
20235	ENU04029	ANI61C1143	58-77	2159-	NAP	g4033481	304	148	1.00E-34	33	33		putative tartrate transporter ;(U32375) membrane protein [Agrobacterium vitis]
20236	ENU04030	ANI61C1020	29-52	2127-	NAP	g4007795	1053	407	e-115	34	55		(AL034463) putative nuclear envelope pore membrane protein
20237	ENU04031	ANI61C8814:	22-57	2130-	NAP	g2226427	1130	318	e-120	44	91		[Schizosaccharomyces pombe] (Z97204) hypothetical protein [Schizosaccharomyces pombe] (AJ007840) Clt4 protein
20238	ENU04032	ANI61C5857:	23-43	2139-	NAP	g3334847	392	180	2.00E-44	41	30		[Schizosaccharomyces pombe] (AL034382) mating-type locus and centromeric silencing protein Ch4p [Schizosaccharomyces pombe]
20239	ENU04033	ANI61C466:4	28-47	2142-	NAP	g2501570	395	137	1.00E-36	35	70		hypothetical 51.4 KD protein in RAR1-SCJ1 intergenic region ; hypothetical protein YMIR210w - yeast (Saccharomyces cerevisiae) ; (Z49809)
20240	ENU04034	ANI61C5683:	23-45	2141-	NAP	g729091	1165	418	e-130	48	83		unknown [Saccharomyces cerevisiae] cell division control protein 5 ; probable transcription factor cdc5 - fission yeast (Schizosaccharomyces pombe) ; (L19525) Cdc5 [Schizosaccharomyces pombe]
		2294..114	2161										

Seq num	Seq id	Contig Source	Primer 3 pos	Primer Basis	Selection	Blast gi	aat	Blast Score	Prob	% id	% cvrg	Description
			5 pos	NAP	Database Hit	ncbi gi	Score	Score	Prob	(AL031603)	mRNA cap methyltransferase	
20241	ENU04035	ANI61C5347:	23-58 1539..46	2164- 2183	g3646451	391	158	1.00E-37	41	44	[Schizosaccharomyces pombe] (X00528) URF c-ras (sc-2) [Saccharomyces cerevisiae] (AL023781) N-terminal acetyltransferase 1	
20242	ENU04036	ANI61C1073	32-51 5,536..2746	2174- 2200	NAP	g4291	167	87	6.00E-16	41	22	[Schizosaccharomyces pombe] (X00528) URF c-ras (sc-2) [Saccharomyces cerevisiae]
20243	ENU04037	ANI61C9737:	61-80 2829..5041	2212- 2231	NAP	g3184082	1297	494	e-139	39	95	(Nectria haematococca); (L20976) pisatin demethylase [Nectria haematococca mpVI]
20244	ENU04038	ANI61C4134:	57-76 3666..1450	2209- 2230	NAP	g1709439	951	262	e-102	53	69	2-oxoisovalerate dehydrogenase alpha subunit precursor (branched-chain alpha-keto acid dehydrogenase component alpha chain (E1)) (BCKDH E1-alpha); (L47335) branched chain alpha ketoacid decarboxylase E1a subunit [Mus musculus]
20245	ENU04039	ANI61C4107:	42-61 6895..9114	2202- 2219	NAP	g1703215	400	147	2.00E-34	28	54	general alpha-glucoside permease; alpha-glucoside transport protein - yeast (Saccharomyces cerevisiae); (Z73074) ORF YGR289c [Saccharomyces cerevisiae]
20246	ENU04040	ANI61C1092	29-52 2.63..2287	2185- 2211	NAP	g131761	59	4.00E-28				quinate permease (quinate transporter); quinate transport protein - Neurospora crassa; (X14603) quinate transporter [Neurospora crassa]
20247	ENU04041	ANI61C1113	64-83 0:3895..1642	2256- 2275	NAP	g416866	1065	273	1.00E-92	65	53	Cyanide hydratase (formamide hydrolyase); cyanide hydratase (EC 4.2.1.66) - imperfect fungus (Gloeocercospora sorghi); (M99044) cyanide hydratase [Gloeocercospora sorghi]
20248	ENU04042	ANI61C1109	22-51 9:10158..7892	2227- 2246	NAP	g2276360	848	330	3.00E-89	36	98	(Z97992) N-acetylglucosaminyl-phosphatidylinositol biosynthetic protein [Schizosaccharomyces pombe] 57A1); pisatin demethylase - fungus (Nectria haematococca); (L20976) pisatin demethylase [Nectria haematococca mpVI]
20249	ENU04043	ANI61C1047	41-63 9:2159..4426	2247- 2266	NAP	g3929362	396	113	2.00E-30	32	80	

Seq num	Seq id	Contig	Source	5 pos	3 pos	Primer Basis	Selection	Blast Score	Blast Prob	% id	% cvrg	Description
						Database Hit	ncbi gi					
20250	ENU04044	ANI61C5969:	32-51	3987..1712	2247..2266	NAP	g731746	119	52	0	30	hypothetical 42.4 KD protein in ENO2- STB5 intergenic region ; hypothetical protein YHR176w - yeast
20251	ENU04045	ANI61C6532:	46-65	3329..1053	2260..2281	NAP	g136287	3886	1273	0	99	[Saccharomyces cerevisiae]; (U00027) Yhr176wp [Saccharomyces cerevisiae]
20252	ENU04046	ANI61C2678:	42-62	273..2553	2261..2280	NAP	g2673955	755	192	8.00E-48	67	(IGPS); N-(5'-phosphoribosyl)anthranilate isomerase (PRA1)); anthranilate synthase multifunctional protein - Emericella nidulans
20253	ENU04047	ANI61C2605:	63-89	2520..233	2282..2308	NAP	g1723238	578	193	4.00E-48	31	[Aspergillus fumigatus]; (U62936) multidrug resistance protein 2 [Aspergillus fumigatus]
20254	ENU04048	ANI61C9553:	23-51	2365..4652	2243..2268	NAP	g2506961	640	139	7.00E-50	41	75 hypothetical 104.5 KD protein C26A3.10 in chromosome I; (Z69240) putative zinc finger protein [Schizosaccharomyces pombe]
20255	ENU04049	ANI61C1074	65-84	2297..71744..4039	NAP	g3746533	379	175	1.00E-42	34	46 (AF059202) ACAT 1 related gene product 1 [Homo sapiens]	
20256	ENU04050	ANI61C6708:	58-88	2298..2595..4897	NAP	g1546072	1290	169	9.00E-41	35	10 (U668040) polyketide synthase [Cochliobolus heterostrophus]	
20257	ENU04051	ANI61C8242:	24-55	2272..2932..623	NAP	g4557575	453	105	3.00E-33	35	71 fatty acid amide hydrolase ; (U82535) fatty acid amide hydrolase [Homo sapiens]; (AF098019) fatty acid amide hydrolase [Homo sapiens]	

Seq num	Seq id	Contig Source	Primer 3 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	Score	Score	Blast Prob	% id	% cvrg	Description
20258	ENU04052	ANI61C153:2	39-61	2285-547..236	NAP	g1168266	1199	316	3.00E-85	45	96	alpha-L-arabinofuranosidase (L29005) alpha-L-arabinofuranosidase [Aspergillus niger]	
20259	ENU04053	ANI61C624:8	35-57	2280-8568..6252	NAP	g3023956	1360	344	1.00E-93	38	42	Vegetable incompatibility protein HET-E-1 ; (L28125) beta transducin-like protein [Podospora anserina]	
20260	ENU04054	ANI50C2773	46-66	2308-4_1..2361..39	NAP	g548630	349	e-128	46	92	peptide transporter PTR2 (peptide permease PTR2) ; peptide transport protein PTR2 - yeast (Saccharomyces cerevisiae) ; (X73541) ORF YKR413 [Saccharomyces cerevisiae] ; (Z28318) ORF YKR093w [Saccharomyces cerevisiae]		
20261	ENU04055	ANI61C8136: 61-83	2331-285..2616	2350	NAP	g3123199	953	354	e-102	40	94	CUT9 protein ; anaphase control protein cut9 - fusion yeast (Schizosaccharomyces pombe) ; (Z98533) cut9 protein; possible anaphase control	
20262	ENU04056	ANI61C1097	38-61	2314-6:4140..3035	2337	NAP	g1076205	86	45	0.003	26	26	[Schizosaccharomyces pombe] ; cut9 gene [Schizosaccharomyces pombe] "hypothetical protein WP6 - Chlamydomonas eugametos ; (L29028) amino acid feature: N-glycosylation sites, aa 41..43, 46..48, 51..53, 72..74, 107..109, 128..130, 132..134, 158..160, 163..165; amino acid feature: Rod protein domain, aa 169..340; amino acid feature: globular pro..."
20263	ENU04057	ANI61C498:3	35-55	2313-824..5910	2334	NAP	g3915154	868	115	1.00E-24	43	16	Trichodiene oxygenase (cytochrome P450 58) ; trichodiene oxygenase 4 - fungus (Fusarium sporotrichioides) ; (U22462) trichodiene oxygenase [Fusarium sporotrichioides]

Seq num	Seq id	Contig Source	Primer 3 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	Score	Score Prob	% id	% cvrg	Description
20264	ENU04058	ANI61C9423:	64-84	2343-2368	NAP	g4506957	412	152	1.00E-35	57	30	unknown ; clathrin coat assembly protein AP19 (clathrin coat associated protein AP19) (GOLGI adaptor AP-19 KD adaptin) (HA1 19 KD subunit) (clathrin assembly protein complex 1 small chain) ; (AB015320) sigma1B subunit of AP-1 clathrin adaptor complex [Homo sapiens]
20265	ENU04059	ANI61C3730:	34-53	2306-4255..1906	NAP	g2498971	725	173	3.00E-65	39	75	putative sterigmatocystin biosynthesis monooxygenase STCW ; (U34740) putative FAD-containing
20266	ENU04060	ANI61C753:4	22-51	2313-859..2507	NAP	g1352945	188	63	2.00E-19	28	49	hypothetical 39.0 KD protein in DAL5-THI11 intergenic region ; hypothetical protein YJR154w - yeast (Saccharomyces cerevisiae) ; (Z49654) ORF YJR154w [Saccharomyces cerevisiae]
20267	ENU04061	ANI61C9176:	27-53	2320-4403..4737	NAP	g1711561	261	62	7.00E-22	29	67	SUGAR transporter STL1 ; sugar transport protein STL1 - yeast (Saccharomyces cerevisiae) ; (U33057) Stl1p; plasma membrane sugar transporter; CAI: 0.19 [Saccharomyces cerevisiae]
20268	ENU04062	ANI61C5315:	70-89	2370-697...3059	NAP	g1351637	581	168	5.00E-57	39	74	"hypothetical 58.5 KD protein C12G12.14 in chromosome 1; hypothetical protein SPAC12G12.14- fission yeast (Schizosaccharomyces pombe) ; (Z66568) SPAC12G12.14, unknown, len: 510, some similarity to PIR-A24907 hypothetical protein 1 (chromosome 4 centromere) - yeast [Schizosaccharomyces pombe]" (D73369) pyranose oxidase [Coriolus versicolor]
20269	ENU04063	ANI61C9185:	24-49	2323-10946..7334	NAP	g1845549	555	192	8.00E-48	38	57	"(AF05035) alpha 1,2-mannosidase [Spodoptera frugiperda]" hypothetical 38.5 KD protein C3H8.04 in chromosome 1 ; (Z69086) unknown [Schizosaccharomyces pombe]
20270	ENU04064	ANI61C1046	63-81	2365-1..3851..6221	NAP	g2245570	437	89	2.00E-36	33	43	
20271	ENU04065	ANI61C1113	22-57	2333-1..6189..8561	NAP	g1723215	162	94	4.00E-18	36	24	

Seq num	Seq id	Contig Source	Primer 3 pos	Primer Basis	Selection	aat	Blast Score	Blast Prob	% id	% cvrg	Description
			5 pos	NAP	Database Hit	ncbi gi	Score	5.00E-37	26	75	
20272	ENU04066	ANI61C9602:	22-50	2345-	g3915154	334	156				Trichodiene oxygenase (cytochrome P450 58); trichodiene oxygenase 4 - fungus ( <i>Fusarium sporotrichioides</i> ); (U22462) trichodiene oxygenase [ <i>Fusarium sporotrichioides</i> ]
20273	ENU04067	ANI61C4610:	47-66	2366-	NAP	g2104963	2260	330	e-177	68	98 ( <i>U96568</i> ) alcohol oxidase [ <i>Pichia pastoris</i> ] (Y15277) cytochrome P450
20274	ENU04068	ANI61C1053	49-84	2377-	NAP	g3549879	649	256	5.00E-67	46	27 monoxygenase [ <i>Gibberella fujikuroi</i> ] (AF092565) splicing factor Prp8
20275	ENU04069	ANI61C1031	42-62	2362-	NAP	g3661610	9138	1158	0	73	33 [Homo sapiens] probable serine/threonine-protein kinase YJL057C; probable membrane protein YJL057c - yeast ( <i>Saccharomyces cerevisiae</i> ); (Z49332) ORF YJL057c [ <i>Saccharomyces cerevisiae</i> ]
20276	ENU04070	ANI61C7390:	28-49	2356-	NAP	g1346384	293	166	6.00E-40	30	32 kinase YJL057C; probable membrane protein YJL057c - yeast ( <i>Saccharomyces cerevisiae</i> ); (Z49332) ORF YJL057c [ <i>Saccharomyces cerevisiae</i> ]
20277	ENU04071	ANI61C1117	36-55	2384-	NAP	g3641350	132	63	0.000000		[ <i>Bos taurus</i> ] putative ATP-dependent RNA helicase C12C2.06 ; (Z54140) probable ATP-dependent RNA helicase
20278	ENU04072	ANI61C8270:	22-47	2372-	NAP	g1175426	889	150	2.00E-66	56	39 [Schizosaccharomyces pombe] Nucleoporin NUP100(NSP100) (nuclear pore protein NUP100(NSP100); nuclear pore complex protein NUP100 -yeast ( <i>Saccharomyces cerevisiae</i> ); (Z15035) nuclear pore complex protein NUP100 [ <i>Saccharomyces cerevisiae</i> ]; (X75780) B959 [ <i>Saccharomyces cerevisiae</i> ]; (Z228068) ORF YKL068w [ <i>Saccharomyces cerevisiae</i> ]; nuclear pore complex protein NUP100 [ <i>Saccharomyces cerevisiae</i> ]
20279	ENU04073	ANI61C6479:	22-56	2413-1,2453	NAP	g400320	296	85	2.00E-15		

Seq num	Seq id	Contig Source	Primer 3 pos	Primer Basis	Selection	Blast ncbi gi	aat Score	Blast Prob Score	% id	% cvrg	Description
						g400320	296	85	2.00E-15		
20280	ENU04074	ANI61C6479:	22-56	NAP							Nucleoporin NUP100/NSP100 (nuclear pore protein NUP100/NSP100); nuclear pore complex protein NUP100 - yeast ( <i>Saccharomyces cerevisiae</i> ); (Z15035) nuclear pore complex protein NUP100 [ <i>Saccharomyces cerevisiae</i> ]; (X75180) B959 [ <i>Saccharomyces cerevisiae</i> ]; (Z28068) ORF YKL068w [ <i>Saccharomyces cerevisiae</i> ]; nuclear pore complex protein NUP100 [probable membrane protein NUP100 [ <i>Saccharomyces cerevisiae</i> ]]
20281	ENU04075	ANI61C1047	22-54	2426-2445	NAP	g2132942	206	122	5.00E-27	25	50 probable membrane protein YOR306c - yeast ( <i>Saccharomyces cerevisiae</i> ); (Z75214) ORF YOR306c [ <i>Saccharomyces cerevisiae</i> ] (U51927) SpiR [ <i>Salmonella typhimurium</i> ]
20282	ENU04076	ANI61C1016	26-45	2434-2453	NAP	g1498305	233	96	8.00E-19	26	43 Sugar transporter STL1 ; sugar transport protein STP1 - yeast ( <i>Saccharomyces cerevisiae</i> ) ; (U33057) Stlp; plasma membrane sugar transporter; CAI: 0.19 [ <i>Saccharomyces cerevisiae</i> ]
20283	ENU04077	ANI61C9107:	72-95	2486-51..2531	NAP	g1711561	718	180	8.00E-54	38	46 (Saccharomyces cerevisiae); (Z46833) unknown [ <i>Saccharomyces cerevisiae</i> ] hypothetical 61.8 KD protein in KGD1-SIM1 intergenic region; probable membrane protein YIL120w-yeast ( <i>Saccharomyces cerevisiae</i> ); (Z46833) unknown [ <i>Saccharomyces cerevisiae</i> ] "L76169" reverse transcriptase, RNaseH [ <i>Glomerella cingulata</i> ] "hypothetical 90.6 KD protein C1D4.10 in chromosome I ; (Z69239) unknown [ <i>Schizosaccharomyces pombe</i> ] (Z99296) 60s ribosomal protein L32 [ <i>Schizosaccharomyces pombe</i> ] pisatin demethylase (cytochrome P450 57A1) ; pisatin demethylase - fungus ( <i>Nectria haematococca</i> ) ; (L20976) pisatin demethylase [ <i>Nectria haematococca mpVI</i> ]
20284	ENU04078	ANI61C9639:	27-52	2438-2469	NAP	g731864	383	176	4.00E-43	25	67 hypothetical 61.8 KD protein in KGD1-SIM1 intergenic region; probable membrane protein YIL120w-yeast ( <i>Saccharomyces cerevisiae</i> ); (Z46833) unknown [ <i>Saccharomyces cerevisiae</i> ] "L76169" reverse transcriptase, RNaseH [ <i>Glomerella cingulata</i> ] "hypothetical 90.6 KD protein C1D4.10 in chromosome I ; (Z69239) unknown [ <i>Schizosaccharomyces pombe</i> ] (Z99296) 60s ribosomal protein L32 [ <i>Schizosaccharomyces pombe</i> ] pisatin demethylase (cytochrome P450 57A1) ; pisatin demethylase - fungus ( <i>Nectria haematococca</i> ) ; (L20976) pisatin demethylase [ <i>Nectria haematococca mpVI</i> ]

Seq num	Seq id	Contig Source	Primer 3 pos	Primer Basis	Selection	Blast aat	Blast Score	Blast Prob	% id	% cvrg	Description
			5 pos	NAP	Database Hit	ncbi gi	Score	Prob			
20289	ENU04083	ANI61C6741:	22-50	2532-	g115642	412	134	1.00E-36	37	85	acid protease precursor ; acid proteinase (EC 3.4.23.-) PEP1 precursor - yeast ( <i>Saccharomyces fibuligera</i> ) ; (D00313) open reading frame of PEP1 (putative secretable acid protease)
	2948..5519		2551								[ <i>Saccharomyces fibuligera</i> ] ; acid protease PEP1 [ <i>Saccharomyces fibuligera</i> ]
20290	ENU04084	ANI61C7542:	72-93	2530-	NAP	g2293233	159	6.00E-38			(AF008220) YicJ [ <i>Bacillus subtilis</i> ] ; (Z99119) similar to hypothetical proteins [ <i>Bacillus subtilis</i> ]
	3960..1378		2610								[ <i>Schizosaccharomyces pombe</i> ] (Z98979) putative oxidoreductase [Schizosaccharomyces pombe] (Z98979) putative phosphatidylserine decarboxylase proenzyme
20291	ENU04085	ANI50C1102	52-71	2566-	NAP	g1175420	386	e-106	43	64	hypothetical 63.9 KD protein C12C2.03C in chromosome II ; (Z54140) putative oxidoreductase
	5..1..441..3023		2592								[ <i>Schizosaccharomyces pombe</i> ] (Z98979) putative phosphatidylserine decarboxylase proenzyme
20292	ENU04086	ANI61C1043	67-86	2576-	NAP	g2388966	188	105	1.00E-21	32	15
	9..2596..13		2608								[ <i>Schizosaccharomyces pombe</i> ] hypothetical 112.2 KD protein in TIF5-NPL3 intergenic region (ORF1) ; hypothetical protein YDR430c - yeast ( <i>Saccharomyces cerevisiae</i> ) ; (U33007) Ydr430cp ; CAI: 0.15 [ <i>Saccharomyces cerevisiae</i> ]
20293	ENU04087	ANI61C9480:	23-49	2550-	NAP	g3915964	1332	319	e-145	37	84
	57..2646		2569								[ <i>Saccharomyces cerevisiae</i> ] ; (J05603) choline transport protein
20294	ENU04088	ANI61C9498:	22-47	2554-	NAP	g117619	371	90	5.00E-33	27	81
	3043..442		2581								choline transport protein ; choline transport protein - yeast ( <i>Saccharomyces cerevisiae</i> ) ; (J05603) choline transport protein
20295	ENU04089	ANI61C9516:	23-42	2571-	NAP	g2330659	2225	816	0	53	67
	3271..656		2596								[ <i>Schizosaccharomyces pombe</i> ] (Z98595) putative snf2 family helicase

Seq num	Seq id	Contig Source	Primer 3 pos	Primer Basis	Selection	aat	Blast Score	Blast Prob	% id	% cvrg	Description
				NAP	Database Hit	ncbi gi	Score	Score			
20296	ENU04090	ANI61C5840:	2648	2618-	g115208	2843	555	0			"C-1-tetrahydrofolate synthase, cytoplasmic (C1-THF synthase) (methylENETetrahydrofolate dehydrogenase / methenyltetrahydrofolate cyclohydrolase / formyltetrahydrofolate synthetase ; methylenetetrahydrofolate dehydrogenase (NADP+) (EC 1.5.1.5) - yeast (Saccharomyces cerevisiae); (M12878) C-1-tetrahydrofolate synthase [Saccharomyces cerevisiae]; (Z49133) C-1-tetrahydrofolate synthase [Saccharomyces cerevisiae]; (Z72989) ORF YGR204w [Saccharomyces cerevisiae]"
20297	ENU04091	ANI61C8143:	23-43	2617- 98..2760	NAP	g125935	553	138	1.00E-60	33	54 lactose permease ; lactose permease - yeast ([Kluyveromyces marxianus var. lactis) ; (X06997) lactose permease (AA 1-587) [Kluyveromyces lactis] DHP1 protein ; dhp1 protein - fission yeast (Schizosaccharomyces pombe); (D17752) Dhp1 protein
20298	ENU04092	ANI61C1129:	45-64	2666- 443..3125	NAP	g729332	1949	350	0	47	82 [Schizosaccharomyces pombe]; (Z69240) dna exoribonuclease [Schizosaccharomyces pombe] mitotic control protein DIS3 ; mitotic control protein dis3+ - fission yeast (Schizosaccharomyces pombe); (M74094) mitotic control protein [Schizosaccharomyces pombe]; (AL031743) mitotic control protein dis3. [Schizosaccharomyces pombe] Sugar transporter STL1 ; sugar transport protein STL1 - yeast (Saccharomyces cerevisiae); (U33057) Stlp; plasma membrane sugar transporter; CAI: 0.19 [Saccharomyces cerevisiae] (U5846) transposase [Aspergillus awamori]
20300	ENU04094	ANI61C9176:	40-58	2680- 1414..4115	NAP	g1711561	261	62	9.00E-22	29	58
20301	ENU04095	ANI61C9979:	24-45	2671- 1144..1080	NAP	g1805251	367	188	1.00E-46	30	60

Seq num	Seq id	Contig Source	Primer 3 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat	Blast Score	Blast Prob	% id	% cvrg	Description
20302	ENU04096	ANI61C6593:	41-62	2708-	NAP	g117619	500	230	3.00E-59	26	75	choline transport protein ; choline transport protein - yeast (Saccharomyces cerevisiae) ; (J05603)	
		3013..2451		2732									[Saccharomyces cerevisiae] ; (Z72599) ORF YGL077c [Saccharomyces cerevisiae]
20303	ENU04097	ANI61C3011:	22-55	2744-	NAP	g131761	449	163	5.00E-49	28	71	quinate permease (quinate transporter); quinate transport protein - Neurospora crassa ; (X14603) quinate transporter [Neurospora crassa]	
		670..3453		2763									Carboxypeptidase S precursor (YSCS) (GLY-X carboxypeptidase) ; Gly-X carboxypeptidase (EC 3.4.17.4) precursor - yeast (Saccharomyces cerevisiae) ; (X63068) carboxypeptidase yscS [Saccharomyces cerevisiae] ; (Z49447) ORF YJL172w [Saccharomyces cerevisiae]
20304	ENU04098	ANI61C1560:	31-53	2751-	NAP	g1168802	578	275	1.00E-72	37	56	(AC004793) Strong similarity to g13600044 T12H20.12 protease homolog from Arabidopsis thaliana BAC gb AF080119 and is a member of the reverse transcriptase family PF00078.	
		2550..5335		2774									Sugar transporter STL1 ; sugar transport protein STP1 - yeast (Saccharomyces cerevisiae) ; (U33305) Stlp1; plasma membrane sugar transporter; CAI: 0.19 [Saccharomyces cerevisiae]
20305	ENU04099	ANI61C3679:	29-50	2749-	NAP	g4512618	665	252	2.00E-93	28	63	(D83125) secretory component [Sarcophaga peregrina]	
		5645..2857		2775									"Ca2+-transporting ATPase (EC 3.6.1.38), fast skeletal muscle - edible frog ; (X63009) fast skeletal muscle Ca-ATPase [Rana esculenta] ; Ca ATPase [Rana esculenta]" hypothetical protein C56F8.17C in chromosome 1 ; (Z69728) unknown [Schizosaccharomyces pombe]
20306	ENU04100	ANI61C1146	71-91	2802-	NAP	g1711561	592	282	8.00E-75	37	57		
		4.4675..1884		2820									
20307	ENU04101	ANI61C9791:	32-58	2776-	NAP	g1402634	288	155	1.00E-36	32	29		
		10551..7746		2795									
20308	ENU04102	ANI61C8214:	56-77	2824-	NAP	g104311	2172	541	0	54	87	"Ca2+-transporting ATPase (EC 3.6.1.38), fast skeletal muscle - edible frog ; (X63009) fast skeletal muscle Ca-ATPase [Rana esculenta] ; Ca ATPase [Rana esculenta]" hypothetical protein C56F8.17C in chromosome 1 ; (Z69728) unknown [Schizosaccharomyces pombe]	
		2948..121		2843									
20309	ENU04103	ANI61C241:3	67-85	2836-	NAP	g1723448	37	0.0003					
		468..636		2857									

Seq num	Seq id	Contig Source	Primer 3 pos	Primer Basis	Selection Database Hit	aat	Blast Score	Blast Prob	% id	% cvrg	Description	
20310	ENU04104	ANI61C230:1	39-58	NAP	g1166378	924	442	e-123	33	84	"(L76169) reverse transcriptase, RNaseH [Glomerella cingulata]"	
20311	ENU04105	ANI61C7266:	46-65	2830-	2834	277	125	1.00E-27	21	26	"myosin heavy chain form B, nonmuscle - African clawed frog ; (L09740) nonmuscle myosin heavy chain b [Xenopus laevis]"	
20312	ENU04106	ANI61C716:3	68-97	2867-	NAP	g4580007	3063	1016	0	61	91	(D87259) poly(A)+ RNA transport protein Ptr3p [Schizosaccharomyces pombe]
20313	ENU04107	ANI61C8701:	22-52	2834-	NAP	g3150139	720	131	6.00E-78	36	57	[Schizosaccharomyces pombe] (AL023594) amino-acid permease
20314	ENU04108	ANI61C7618:	22-45	2832-	NAP	g1710803	714	145	2.00E-33	42	21	Retrograde regulation protein 2 ; RTG2 protein - yeast (Saccharomyces cerevisiae) ; (X94357) ORF NRF588; EMBL:SCRTG2X;M97691; PIR:B44344;B44344 [Saccharomyces cerevisiae]; (M97691) Rtg2p [Saccharomyces cerevisiae]; (Z72774) ORF YGL252c [Saccharomyces cerevisiae]
20315	ENU04109	ANI61C9-204	45-65	2919-	NAP	g125935	459	108	8.00E-43	30	45	lactose permease ; lactose permease - yeast (Kluyveromyces marxianus var. lactis) ; (X06997) lactose permease (AA_1-587) [Kluyveromyces lactis] "YAC060608" putative acyl coenzyme A oxidase, peroxisomal component [Arabidopsis thaliana]" (AJ001909) transcriptional activator [Aspergillus niger] "Exoglucanase I precursor (exocellobiohydrolase I) (1,4-beta-cellulobiohydrolase I) (beta-glucancellobiohydrolase I); (AB002821) cellobiohydrolase I [Aspergillus aculeatus]" "hypothetical 75.4 KD protein in HAP2-ADE5,6 intergenic region ; hypothetical protein YGL236c - yeast (Saccharomyces cerevisiae) ; (Z72758) ORF YGL236c [Saccharomyces cerevisiae]" "
20319	ENU04113	ANI61C7699:	22-45	2923-	NAP	g1723974	1511	564	e-160	50	74	"hypothetical 75.4 KD protein in HAP2-ADE5,6 intergenic region ; hypothetical protein YGL236c - yeast (Saccharomyces cerevisiae) ; (Z72758) ORF YGL236c [Saccharomyces cerevisiae]" "
			3947..974	2953								

Seq num	Seq id	Contig Source	Primer 3 pos	Primer Basis	Selection	Blast at	Blast at	% id	% cvrg	Description	
			5 pos	NAP	Database Hit	ncbi gi	Score	Prob	e-171	CAMP-dependent protein kinase SCH9 ; probable protein kinase SCH9 (EC 2.7.1.-) - yeast (Saccharomyces cerevisiae) ; (U00029) Sch9p: cAMP-dependent protein kinase	
20321	ENU04115	ANI61C9768:	28-61	2936-2971	NAP	g118901	2303	426	0	45	63 [Saccharomyces cerevisiae] DNA polymerase zeta catalytic subunit ; DNA-directed DNA polymerase (EC 2.7.7.7) REV3 - yeast (Saccharomyces cerevisiae) ; (M29683) DNA polymerase (pot.) ; putative [Saccharomyces cerevisiae] ; (Z73523) ORF YPL167c [Saccharomyces cerevisiae] ; (X96770) P2535 protein [Saccharomyces cerevisiae] "Carboxylic acid transporter protein homolog" ; hypothetical protein YKL217w - yeast (Saccharomyces cerevisiae) ; (X75951) ORF3, A616 [Saccharomyces cerevisiae] ; (Z228217) ORF YKL217w [Saccharomyces cerevisiae] ; (U24155) carboxylic acid transporter protein homolog
20322	ENU04116	ANI61C8537:	45-64	2973-5851..8841	NAP	g549755	360	89	2.00E-26	27	50 [Saccharomyces cerevisiae] "Carboxylic acid transporter protein homolog" ; hypothetical protein YKL217w - yeast (Saccharomyces cerevisiae) ; (X75951) ORF3, A616 [Saccharomyces cerevisiae] ; (Z228217) ORF YKL217w [Saccharomyces cerevisiae] ; (U24155) carboxylic acid transporter protein homolog
20323	ENU04117	ANI61C6226:	33-64	2970-4891..7889	NAP	g728850	43	0.009			"glucoamylase S1/S2 precursor (glucan 1,4-alpha glucosidase) (1,4-alpha-D-glucan glucohydrolase) ; glucan 1,4-alpha glucosidase (EC 3.2.1.3) - yeast (Saccharomyces cerevisiae) ; (Z38061) mal5, stal, len: 1367, CAI: 0.3, AMYH_yeast_P08640 glucoamylase S1 (EC 3.2.1.3) [Saccharomyces cerevisiae] ; (U30626) glucoamylase [Saccharomyces cerevisiae var. diastaticus]"
20324	ENU04118	ANI61C7076:	62-81	944-963	NAP	g2132846	495	156	2.00E-37	29	58 probable membrane protein YOL119c - yeast (Saccharomyces cerevisiae) ; (Z74861) ORF YOL119c [Saccharomyces cerevisiae] ; (X95258) unknown protein [Saccharomyces cerevisiae]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database	Hit	ncbi gi	aat Score	Blast Score	Prob	% id	% cvrg	Description
20325	ENU04119	ANI61C1070	63..86	944..965	NAP		g120777	1144	373	e-103	57	64	"Succinate-semialdehyde dehydrogenase (NADP+)-SSDH"; (M88334) succinic semialdehyde dehydrogenase [Escherichia coli]; (AE000351) succinate-semialdehyde dehydrogenase, NADP-dependent activity [Escherichia coli]"	
20326	ENU04120	ANI61C4798:	41..62	924..944	NAP		g2388907	606	65	6.00E-10	29	22	(Z98974) hypothetical protein [Schizosaccharomyces pombe]	
20327	ENU04121	ANI61C1948:	25..46	908..928	NAP		g4127832	475	171	6.00E-42	37	57	(Y17243) cytochrome P450 [Gibberella fujikuroi]	
20328	ENU04122	ANI61C681:2	58..80	946..965	NAP		g119216	1224	322	3.00E-87	65	63	"Elongation factor TU, mitochondrial precursor; translation elongation factor Tu precursor, mitochondrial - yeast (Saccharomyces cerevisiae); (Z75095) ORF YOR187w [Saccharomyces cerevisiae]"	
20329	ENU04123	ANI61C6816:	48..70	938..957	NAP		g4079649	162	63	7.00E-18	32	21	((U78168)cAMP-regulated guanine nucleotide exchange factor 1 [Homo sapiens])	
20330	ENU04124	ANI61C1101	66..85	957..979	NAP		g1351683	341	139	2.00E-32	35	55	hypothetical 53.9 KD protein C1F5.08C in chromosome 1; (Z68136) unknown [Schizosaccharomyces pombe]	
20331	ENU04125	ANI61C1047:	38..57	934..954	NAP		g3122248	669	233	1.00E-60	40	67	D-hydantoinase (dihydropyrimidinase) (DHPASE); (X91070) D-hydantoinase [Agrobacterium radiobacter] (AL031644) hypothetical protein [Schizosaccharomyces pombe] hypothetical 154.9 KD protein in CPR7-PET191 intergenic region; hypothetical protein YJR033c - yeast (Saccharomyces cerevisiae); (Z49533) ORF YJR033c [Saccharomyces cerevisiae]	
20332	ENU04126	ANI61C6326:	22..49	917..943	NAP		g3647336	439	102	3.00E-44	52	46	[Schizosaccharomyces pombe] hypothetical 154.9 KD protein in CPR7-PET191 intergenic region; hypothetical protein YJR033c - yeast (Saccharomyces cerevisiae); (Z49533) ORF YJR033c [Saccharomyces cerevisiae]	
20333	ENU04127	ANI61C1037	36..66	938..957	NAP		g1352875	801	66	1.00E-22	33	19	[Schizosaccharomyces pombe] "chitinase, 33k, precursor - fungus (Trichoderma harzianum); (X80006) chitinase [Trichoderma harzianum]"	
20334	ENU04128	ANI61C9715:	42..61	946..965	NAP		g1794292	1171	353	1.00E-96	55	65	(U77983) WD-domain protein [Schizosaccharomyces pombe]	
20335	ENU04129	ANI61C627:4	69..93	981..1001	NAP		g2133298	552	233	1.00E-60	49	82	"chitinase, 33k, precursor - fungus (Trichoderma harzianum); (X80006) chitinase [Trichoderma harzianum]"	

Seq num	Seq id	Contig Source	Primer 3 pos	Primer 3 pos Basis	Selection	Database Hit	ncbi gi	aat	Blast Score	Blast Prob	% id	% cvrg	Description
20336	ENU04130	ANI61C9947:	43-62	942-977	NAP	g3915154	647	154	1.00E-36	34	57	Trichodiene oxygenase (cytochrome P450 58); trichodiene oxygenase 4 - fungus (Fusarium sporotrichioides); (U22462) trichodiene oxygenase [Fusarium sporotrichioides]	
20337	ENU04131	ANI61C942:4	22-40	942-964	NAP	g22228233	336	130	1.00E-29	40	27	(U24215) p-cumic aldehyde dehydrogenase [Pseudomonas putida] hypothetical 42.9 KD protein in ILV2-ADE17 intergenic region; hypothetical protein YMR114c - yeast (Saccharomyces cerevisiae); (Z49702) unknown [Saccharomyces cerevisiae] (Y16399) multidrug resistance protein [Candida albicans] (Y16399) multidrug resistance protein [Candida albicans]	
20338	ENU04132	ANI61C7124:	56-74	980-1001	NAP	g2497154	337	133	2.00E-30	35	73	hypothetical 42.9 KD protein in ILV2-ADE17 intergenic region; hypothetical protein YMR114c - yeast (Saccharomyces cerevisiae); (Z49702) unknown [Saccharomyces cerevisiae] (Y16399) multidrug resistance protein [Candida albicans] (Y16399) multidrug resistance protein [Candida albicans]	
20339	ENU04133	ANI61C8753:	72-94	997-1020	NAP	g3378550	84	1.00E-15					
20340	ENU04134	ANI61C8753:	72-94	997-1020	NAP	g3378550	84	1.00E-15					
20341	ENU04135	ANI61C1583:	42-61	974-999	NAP	g1730576	316	90	3.00E-17	35	58	Proline iminopeptidase (prolyl aminopeptidase); prolyl aminopeptidase (EC 3.4.11.5) - Aeromonas sobria; (D30714) prolyl aminopeptidase [Aeromonas sobria] (AC006570) putative polyprotein [Arabidopsis thaliana]	
20342	ENU04136	ANI61C8605:	63-90	997-1023	NAP	g4432807	477	89	5.00E-36	32	20	"Exopolygalacturonase precursor (EXOPG) (galacturan 1,4-alpha-galacturonidase) (poly(1,4-alpha-D-galacturonide)galacturonohydrolase); (L48982) exo-alpha 1,4-polygalacturonase [Cochliobolus carbonum]" (AL021841) amib [Mycobacterium tuberculosis]	
20343	ENU04137	ANI61C1048	50-69	989-1012	NAP	g2499717	430	86	3.00E-16	34	25	"Exopolygalacturonase precursor (EXOPG) (galacturan 1,4-alpha-galacturonidase) (poly(1,4-alpha-D-galacturonide)galacturonohydrolase); (L48982) exo-alpha 1,4-polygalacturonase [Cochliobolus carbonum]" (AL021841) amib [Mycobacterium tuberculosis]	
20344	ENU04138	ANI61C7225:	28-47	976-996	NAP	g2894215	427	139	4.00E-34	37	71	[Schizosaccharomyces pombe] hypothetical 58.0 KD protein C2C6.08 in chromosome 1; (AL031324) hypothetical protein [Schizosaccharomyces pombe] (AL031154) putative transmembrane transporter [Schizosaccharomyces pombe]	
20345	ENU04139	ANI61C3186:	23-43	961-992	NAP	g3650407	435	115	7.00E-25	43	59	[Schizosaccharomyces pombe] hypothetical 58.0 KD protein C2C6.08 in chromosome 1; (AL031324) hypothetical protein [Schizosaccharomyces pombe] (AL031154) putative transmembrane transporter [Schizosaccharomyces pombe]	
20346	ENU04140	ANI61C5164:	41-59	989-1010	NAP	g3183406	846	274	6.00E-73	49	57		
20347	ENU04141	ANI61C9636:	22-50	971-993	NAP	g3367790	723	100	1.00E-31	49	60		

Seq num	Seq id	Contig Source	Primer 3 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	Score	Score	Blast Prob	% id	% cvrg	Description
20348	ENU04142	ANI61C9116:	45-67	997-1017	NAP	g1293655	778	109	4.00E-46	40	47	(U51327) versicolorin B synthase [Aspergillus parasiticus]; (U51328) versicolorin B synthase [Aspergillus parasiticus]	
20349	ENU04143	ANI61C6687:	24-46	977-996	NAP	g2226429	826	260	2.00E-78	47	53	(Z97204) putative vacuolar protein sorting-associated protein.	
20350	ENU04144	ANI61S2225:	56-75	1010-1029	NAP	g3810866	108	6.00E-30	50	94	[Schizosaccharomyces pombe] (AL032681) putative hydroxyacylglycerol thione hydrolase [Schizosaccharomyces pombe]		
20351	ENU04145	ANI61C9501:	34-53	987-1009	NAP	g2132474	1332	518	e-146	74	55	probable membrane protein YDR091c - yeast [Saccharomyces cerevisiae]; (Z5011) unknown [Saccharomyces cerevisiae]	
20352	ENU04146	ANI61C164:3	42-64	998-1018	NAP	g114971	1677	276	2.00E-73	45	37	beta-glucosidase precursor (gentiobiose) (cellobiose) (beta-D-glucoside glucohydrolase); beta-glucosidase (EC 3.2.1.21) precursor - yeast [Kluyveromyces marxianus var. marxianus]; (X05918) beta-glucosidase (AA 1 - 845)	
20353	ENU04147	ANI61C9646:	30-50	990-1011	NAP	g4538856	247	111	6.00E-24	35	49	[Kluyveromyces marxianus] (A1223758) 54 kDa vacuolar H(+)-ATPase subunit [Saccharomyces cerevisiae] hypothetical 81.2 KD protein C3D6.13C in chromosome II; (Z95620) putative thioredoxin [Schizosaccharomyces pombe]	
20354	ENU04148	ANI61C8673:	23-47	980-1011	NAP	g3183238	529	181	7.00E-54	36	46	hypothetical protein YPR021c - yeast (Saccharomyces cerevisiae); (Z49274) unknown [Saccharomyces cerevisiae]; (Z71255) unknown [Saccharomyces cerevisiae]	
20355	ENU04149	ANI61C8886:	71-90	1037-1060	NAP	g1084944	742	319	3.00E-86	59	32		

Seq num	Seq id	Contig Source	Primer 3 pos	Primer Basis	Selection	Blast gi	aat	Blast Score	Blast Prob	% id	% cvrg	Description
				NAP	Database Hit	ncbi gi	Score	Score	Prob			
20356	ENU04150	ANI61C7428:	62-81	1030-1051	g125401	163	94	2.00E-18				choline kinase ; choline kinase (EC 2.7.1.32) ; yeast [Saccharomyces cerevisiae] ; (I04454) choline kinase [Saccharomyces cerevisiae] ; (X91258) choline kinase [Saccharomyces cerevisiae] ; (U53881) Ck1lp; choline kinase [Saccharomyces cerevisiae] ; (Z73305) ORF YLR133w [Saccharomyces cerevisiae]
20357	ENU04151	ANI61C1035	47-67	1016-1041	NAP	g3334221	1166	203	3.00E-90	60	74	4-hydroxyphenylpyruvate dioxygenase (4HPPD) (HPPD) ; (AF038152) 4-hydroxyphenylpyruvate dioxygenase [Mycosphaerella graminicola] "Isocitrate dehydrogenase (NADP), mitochondrial precursor (oxalosuccinate decarboxylase) (IDH) (NADP+-specific ICDH) (IDP) ; (AB000261) NADP-dependent isocitrate dehydrogenase precursor [Aspergillus niger] ; (AB000262) NADP-dependent isocitrate dehydrogenase precursor [Aspergillus niger]" (AF079317) unknown [Sphingomonas aromaticivorans]
20358	ENU04152	ANI61C3101:	22-54	g3023999	999-1018	NAP	1801	210	e-108	85	55	(Z99164) hypothetical protein [Schizosaccharomyces pombe] (U62931) multidrug resistance protein 1 [Aspergillus flavus] ; (U62932) multidrug resistance protein 1 [Aspergillus flavus] "ubiquitin fusion degradation protein 4 (UB fusion protein 4) ; hypothetical protein YKL010c - yeast (Saccharomyces cerevisiae) ; (S53418) orf YKL162 [Saccharomyces cerevisiae=yeast, Peptide, 1483 aa] [Saccharomyces cerevisiae] ; (Z28010) ORF YKL010c [Saccharomyces cerevisiae]"
20359	ENU04153	ANI61C7048:	70-89	1055-1076	NAP	g3378447	462	153	6.00E-48	39	73	"ubiquitin fusion degradation protein 4 (UB fusion protein 4) ; hypothetical protein YKL010c - yeast (Saccharomyces cerevisiae) ; (S53418) orf YKL162 [Saccharomyces cerevisiae=yeast, Peptide, 1483 aa] [Saccharomyces cerevisiae] ; (Z28010) ORF YKL010c [Saccharomyces cerevisiae]"
20360	ENU04154	ANI61C299:1	40-59	1020-1046	NAP	g2408044	108	56	0.000000	22	43	"ubiquitin fusion degradation protein 4 (UB fusion protein 4) ; hypothetical protein YKL010c - yeast (Saccharomyces cerevisiae) ; (S53418) orf YKL162 [Saccharomyces cerevisiae=yeast, Peptide, 1483 aa] [Saccharomyces cerevisiae] ; (Z28010) ORF YKL010c [Saccharomyces cerevisiae]"
20361	ENU04155	ANI61C1017	22-50	1014-1035	NAP	g2673947	994	346	1.00E-98	67	23	"ubiquitin fusion degradation protein 4 (UB fusion protein 4) ; hypothetical protein YKL010c - yeast (Saccharomyces cerevisiae) ; (S53418) orf YKL162 [Saccharomyces cerevisiae=yeast, Peptide, 1483 aa] [Saccharomyces cerevisiae] ; (Z28010) ORF YKL010c [Saccharomyces cerevisiae]"
20362	ENU04156	ANI61C9779:	70-97	1062-1086	NAP	g465668	930	235	3.00E-61	42	22	"ubiquitin fusion degradation protein 4 (UB fusion protein 4) ; hypothetical protein YKL010c - yeast (Saccharomyces cerevisiae) ; (S53418) orf YKL162 [Saccharomyces cerevisiae=yeast, Peptide, 1483 aa] [Saccharomyces cerevisiae] ; (Z28010) ORF YKL010c [Saccharomyces cerevisiae]"

Seq num	Seq id	Contig Source	Primer 3 pos	Primer Basis	Selection	Blast ncbi gi	aat Score	Blast Score	Prob %	% id	% cvrg	Description
20363	ENU04157	ANI61C4566:	33..58	NAP	g3041656	717	110	1.00E-43	43	62	NADPH:adrenodoxin oxidoreductase precursor (adrenodoxin reductase) (ferredoxin-NADP(+) reductase); (J03826) adrenodoxin reductase	
20364	ENU04158	ANI61C269..9	22..47	1017-	NAP	g113600	99	41	0.000000	29	89	alcohol dehydrogenase (NADP(+)) (aldehyde reductase); alcohol dehydrogenase (NADP(+)) (EC 1.1.1.2) - human ; (I04794) aldehyde reductase (EC 1.1.1.2) [Homo sapiens] ; (AF036683) aldehyde reductase [Homo sapiens]
20365	ENU04159	ANI61C7606:	60..79	1065-2390..1323	NAP	g3411013	450	175	6.00E-43	33	35	(AF000232) protein mannosyltransferase 1 [Candida albicans]
20366	ENU04160	ANI61C1879:	29..54	1037-1257..2325	NAP	g3702635	532	184	1.00E-45	35	79	(AL031825) hypothetical protein [Schizosaccharomyces pombe] (AB002530) mus-23 [Neurospora crassa]
20367	ENU04161	ANI61C4366:	23..44	1032-1466..396	NAP	g3434965	1013	316	2.00E-85	54	66	(AL033396) hypothetical protein [Candida albicans] hypothetical protein YLR410w - yeast (Saccharomyces cerevisiae); (U20162) Ylr410wp [Saccharomyces cerevisiae] (AF028783) proteasome regulatory subunit 12 [Hypocrea jecorina] (AL034381) conserved hypothetical PFAM UPF0031 containing protein [Schizosaccharomyces pombe] (Y16834) hexose transporter [Candida albicans]
20368	ENU04162	ANI61C1061	71..90	1083-3..3032..1957	NAP	g3850152	564	184	3.00E-54	36	76	(AL033396) hypothetical protein [Candida albicans] hypothetical protein YLR410w - yeast (Saccharomyces cerevisiae); (U20162) Ylr410wp [Saccharomyces cerevisiae] (AF028783) proteasome regulatory subunit 12 [Hypocrea jecorina] (AL034381) conserved hypothetical PFAM UPF0031 containing protein [Schizosaccharomyces pombe] (Y16834) hexose transporter [Candida albicans]
20369	ENU04163	ANI61C7489:	22..46	1035-2110..1036	NAP	g1363755	931	244	7.00E-64	50	26	(Y15278) cytochrome P450 monooxygenase [Gibberella fujikuroi] gamma-Butyrobetaine Hydroxylase; (AF082868) gamma butyrobetaine hydroxylase [Homo sapiens]
20370	ENU04164	ANI61C2606:	31..50	1042-2026..951	NAP	g2599117	1269	189	e-125	80	93	(Y15278) cytochrome P450 monooxygenase [Gibberella fujikuroi] gamma-Butyrobetaine Hydroxylase; (AF082868) gamma butyrobetaine hydroxylase [Homo sapiens]
20371	ENU04165	ANI61C8172:	64..83	1077-1317..243	NAP	g3947854	481	148	2.00E-38	50	76	(Y15278) cytochrome P450 monooxygenase [Gibberella fujikuroi] gamma-Butyrobetaine Hydroxylase; (AF082868) gamma butyrobetaine hydroxylase [Homo sapiens]
20372	ENU04166	ANI61C4401:	67..86	1081-135..1211	NAP	g33336839	290	81	3.00E-28	30	57	(Y15278) cytochrome P450 monooxygenase [Gibberella fujikuroi] gamma-Butyrobetaine Hydroxylase; (AF082868) gamma butyrobetaine hydroxylase [Homo sapiens]
20373	ENU04167	ANI61C2761:	54..73	1067-1270..194	NAP	g35349891	364	102	7.00E-42	32	61	(Y15278) cytochrome P450 monooxygenase [Gibberella fujikuroi] gamma-Butyrobetaine Hydroxylase; (AF082868) gamma butyrobetaine hydroxylase [Homo sapiens]
20374	ENU04168	ANI61C1042	22..51	1040-5..576..1655	NAP	g4502369	324	156	3.00E-37	30	89	(Y15278) cytochrome P450 monooxygenase [Gibberella fujikuroi] gamma-Butyrobetaine Hydroxylase; (AF082868) gamma butyrobetaine hydroxylase [Homo sapiens]

ફોર્મ ડાયાગ્નોસ્ટિક રીપોર્ટ " લાંબા સુધી વિશેર્પેડ રીપોર્ટ "

Seq num	Seq id	Contig Source	Primer 3 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat	Blast Score	Blast Prob	% id	% cvrg	Description
20375	ENU04169	ANI61C7010:	42-61	1052-	NAP	g1176483	500	129	2.00E-33	45	45	CHS6 intergenic region ; hypothetical protein YIL100w - yeast	
		21..1103		1080								(Saccharomyces cerevisiae) ; (X85021)	
												orf12 [Saccharomyces cerevisiae] ; (Z49375) ORF YIL100w	
20376	ENU04170	ANI61C1082	25-48	1033-7:471..1551	NAP	g4539596	179	102	2.00E-22	28	44	[Saccharomyces cerevisiae]	
				1063								(AL049522) hypothetical DNAJ domain protein [Schizosaccharomyces pombe]	
20377	ENU04171	ANI61C5138:	25-43	1041-172..1252	NAP	g2132490	228	100	3.00E-24	41	29	probable membrane protein YDR282c - yeast (Saccharomyces cerevisiae); (U51030) Ydr282cp [Saccharomyces cerevisiae]	
						g3850081	987	294	7.00E-79	50	67	(AL033389) aminotransferase [Schizosaccharomyces pombe]	
20378	ENU04172	ANI61C22:30	69-92	1096-60..4145	NAP	g2499716	564	97	2.00E-52	38	68	"Exopolygalacturonase precursor (EXOPG) (galacturan 1,4-alpha-galacturonidase) (poly(1,4-alpha-D-galacturonide)galacturonohydrolase); (X99795) exopolygalacturonase [Aspergillus tubingensis]"	
				1115								probable membrane protein YOR306c - yeast (Saccharomyces cerevisiae); (Z75214) ORF YOR306c	
20379	ENU04173	ANI61C9101:	60-78	1090-1688..597	NAP	g2132942	348	145	7.00E-34	29	66	[Saccharomyces cerevisiae]	
				1109								(AL023554) dna topoisomerase iii. [Schizosaccharomyces pombe] (Y12819) putative RNA helicase (DEAD box) [Danio rerio]	
20380	ENU04174	ANI61C5379:	22-49	1051-58..1149	NAP	g4388617	1412	259	7.00E-80	49	52		
				1071									
20381	ENU04175	ANI61C2460:	25-51	1053-2020..3114	NAP	g2558533	596	94	2.00E-29	39	42		
				1103-2:1354..2459	NAP								
				1122									

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat	Blast Score	Blast Prob	% id	% cvrg	Description
20383	ENU04177	ANI61C9581:	49..1156	61-80	NAP	g3876562	194	88	1.00E-16	28	37	(Z81074) Similarity to Soybean 3-methylcrotonyl-CoA carboxylase (TR:Q42777); cDNA EST; EMBL:M75819 comes from this gene; cDNA EST EMBL:M89099 comes from this gene; cDNA EST EMBL:D32737 comes from this gene; cDNA EST EMBL:D32763 ...	
20384	ENU04178	ANI61C9305:	47-68	3996..5103	NAP	g1020413	363	59	0.000000	22	68	(D63703) isobutene-forming enzyme and benzoate 4-hydroxylase [Rhodotorula minuta] (AL031854) hypothetical protein [Schizosaccharomyces pombe]	
20385	ENU04179	ANI61C5766:	65-88	383..1490	NAP	g3738180	216	52	0.000000	002	46	hypothetical 70.5 KD protein in AGP3-DAK3 intergenic region ; probable membrane protein YFL054c - yeast (Saccharomyces cerevisiae); (D50617) YFL054C [Saccharomyces cerevisiae]; (D44603) unknown [Saccharomyces cerevisiae]	
20387	ENU04181	ANI61C2930:	43-62	888..1997	NAP	g2190550	420	182	3.00E-51	42	95	"(AC001229) ESTs gbt T45673.gbt N37512 come from this gene. [Arabidopsis thaliana]"	
20388	ENU04182	ANI61C1100	53-78	4:1280..171	NAP	g127286	1673	316	4.00E-93	62	63	mitochondrial processing peptidase alpha subunit precursor (alpha-MPP); mitochondrial processing peptidase (EC 3.4.99.41) alpha chain precursor - Neurospora crassa (U26160) 43 kDa secreted glycoprotein precursor [Paracoccidioides brasiliensis] ; glycoprotein gp43 [Paracoccidioides brasiliensis] (AL022070) yeast mic1 homolog [Schizosaccharomyces pombe] "D89136) similar to Saccharomyces cerevisiae BCS1 protein, SWISS-PROT Accession Number P32839 [Schizosaccharomyces pombe]"	

Seq num	Seq id	Contig source	Primer Basis	Primer Selection	aat	Blast Score	Blast Prob	% id	% cvrg	Description		
		5 pos	NAP	Database Hit	ncbi gi	Score	Prob					
20392	ENU04186	ANI61C1135	22.57	1086-	g4008554	53	0.00003	(AL034490) putative tyrosine kinase [Schizosaccharomyces pombe]				
20393	ENU04187	ANI61C5254:	59-78	1105				hypothetical 104.0 KD protein in HXT5-NRK1 intergenic region ; hypothetical protein YHR098c - yeast (Saccharomyces cerevisiae); (U00060) Yhr098cp [Saccharomyces cerevisiae]; (AJ009784) Sfb3 [Saccharomyces cerevisiae]				
20394	ENU04188	ANI61C2574:	23-42	1091-	NAP	g2894293	380	93	3.00E-18	32	62 (AL021837) hypothetical protein [Schizosaccharomyces pombe]	
20395	ENU04189	ANI61C7640:	37-56	1109-	NAP	g1711561	495	165	3.00E-47	34	57 sugar transporter STL1 ; sugar transport protein STP1 - yeast (Saccharomyces cerevisiae); (U33057) Stlp; plasma membrane sugar transporter; CAI: 0.19 [Saccharomyces cerevisiae]	
20396	ENU04190	ANI61C1134:	63-82	1131-	NAP	g3256111	38	0.13	(AL024456) 1-evidence=predicted by motif: 1- match_accession=PROSITE:PS00017; 1-match_description=ATP/GTP-binding site motif A (P-loop); 1-method=ppsearch;; 1-evidence_end; 2-evidence=predicted by match; 2-match_accession=SWISS...			
20397	ENU04191	ANI61C8073:	46-74	1122-	NAP	g2842688	558	77	2.00E-13	26	21 hypothetical 70.6 KD protein C1F8.03C in chromosome I; (Z81312) unknown [Schizosaccharomyces pombe]	
20398	ENU04192	ANI61C6332:	29-56	3210..2068	1102-	NAP	g549755	690	156	2.00E-37	39	27 "carboxylic acid transporter protein homolog ; hypothetical protein YKL217w - yeast (Saccharomyces cerevisiae); (X75951) ORF3_A616 [Saccharomyces cerevisiae]; (Z28217) ORF YKL217w [Saccharomyces cerevisiae]; (U24155) carboxylic acid transporter protein homolog [Saccharomyces cerevisiae]"

Seq num	Seq id	Contig source	Primer 3 pos	Primer Basis	Selection Database Hit	atc	Blast Score	Blast Prob	% id	% cvrg	Description
20399	ENU04193	ANI61C4155:	22-42	NAP	g2497126	96	64	0.000000	26	54	actin-like protein ARP9 ; probable membrane protein YMR033w - yeast (Saccharomyces cerevisiae) ; (Z49213)
20400	ENU04194	ANI61C2929:	27-47	1110-1129	NAP	g140489	735	142	2.00E-68		"GNS1 protein ; probable membrane protein YCR034w - yeast (Saccharomyces cerevisiae) ; (X56909) YCR521 [Saccharomyces cerevisiae] (S78624) YCR521 [Saccharomyces cerevisiae=yeast; Peptide, 347 aa] [Saccharomyces cerevisiae] ; (X59720) YCR034w, len:347 [Saccharomyces cerevisiae] ; (AF012655) v-snare bypass mutant [Saccharomyces cerevisiae]" (AL023634) protein kinase dskl1 [Schizosaccharomyces pombe]
20401	ENU04195	ANI61C7783:	22-52	1105-496...1642	NAP	g3150261	85	1.00E-15			sexual differentiation process protein ISP7 ; isp7 protein - fission yeast (Schizosaccharomyces pombe) ; (D14064) ORF [Schizosaccharomyces pombe]
20402	ENU04196	ANI61C6885:	72-91	1154-1175..24	NAP	g729862	157	72	4.00E-16	32	ISP7 ; isp7 protein - fission yeast (Schizosaccharomyces pombe) ; (D14064) ORF [Schizosaccharomyces pombe]
20403	ENU04197	ANI61C4087:	25-44	1099-316..1468	NAP	g2506349	449	109	8.00E-46	33	potassium-activated aldehyde dehydrogenase precursor ; probable aldehyde dehydrogenase (NAD+) (EC 1.2.1.3) YOR374w - yeast (Saccharomyces cerevisiae) ; (Z75822) ORF YOR374w [Saccharomyces cerevisiae]
20404	ENU04198	ANI50C1851	46-65	1128-1:10..1152	NAP	g3850128	120	2.00E-26	34	76	(AL033391) COQ3 homologue [Candida albicans]
20405	ENU04199	ANI61C1123	25-44	1110-1:3476..4627	NAP	g2950465	216	85	7.00E-16		(AL022071) fructosyl amine [Schizosaccharomyces pombe]
20406	ENU04200	ANI61C1724:	39-60	1136-554..1712	NAP	g3183342	350	109	2.00E-41	33	hypothetical 44.5 KD protein C14C4.09 in chromosome I ; (Z98596) hypothetical protein [Schizosaccharomyces pombe]

Seq num	Seq id	Contig source	5 pos	Primer Basis	Selection	aat	Blast Score	Blast Prob	% id	% cvrg	Description
				NAP	Database Hit	ncbi gi	Score	Prob	99	67	
20407	ENU04201	ANI61C5929:	56-75	1153-							proline-specific permease (proline transport protein) ; (X79797) proline permease [Emericella nidulans] (AB011173) KIAA0601 protein [Homo sapiens]
20408	ENU04202	ANI61C9268:	22-52	1124-	NAP	g3043726	505	176	2.00E-43	45	22
		4133..2971		1142							
20409	ENU04203	ANI61C6430:	22-43	1115-	NAP	g3560143	77	55	0.000000	35	10
		8426..7264		1142							
20410	ENU04204	ANI61C9220:	22-49	1123-	NAP	g2500937	1219	221	5.00E-96	48	62
		2429..1263		1146							
20411	ENU04205	ANI61C9825:	44-63	1139-	NAP	g3367585	164	90	3.00E-17	33	44
		23..1190		1169							
20412	ENU04206	ANI61C3276:	28-47	1141-	NAP	g3687231	208	114	1.00E-24	31	51
		3347..2173		1160							
20413	ENU04207	ANI61C2648:	54-73	1166-	NAP	g1077378	522	179	2.00E-44	35	39
		1339..165		1186							
20414	ENU04208	ANI61C5015:	24-43	1124-	NAP	g517205	261	134	1.00E-30	31	59
		1300..122		1159							
20415	ENU04209	ANI61C7035:	59-78	1167-	NAP	g2808776	242	125	6.00E-28	33	62
		40..1217		1194							
20416	ENU04210	ANI61C5367:	22-47	1131-	NAP	g3560020	520	210	1.00E-53	38	40
		1331..151		1160							
20417	ENU04211	ANI61C3671:	55-74	1177-	NAP	g2498968	112	50	0.000000	30	57
		1222..34		1200							
20418	ENU04212	ANI61C1123	47-67	1173-	NAP	g1174727	199	52	7.00E-14	38	37
		2:1473..284		1193							

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95, 781–792

Seq num	Seq id	Contig source	5 pos	Primer Basis	Primer Selection	aat	Blast Score	Blast Prob	% id	% cvg	Description
20419	ENU04213	ANI61C1041	22-48	NAP	g2384693	91	48	5.00E-10	28	51	(AF013216) unknown [Myxococcus xanthus]
20420	ENU04214	ANI61C3678:	22-43	NAP	g3819705	726	187	6.00E-62	37	53	(AL032824) syntaxin binding protein 1; sec1 family secretor y protein [Schizosaccharomyces pombe] (U97107) membrane glycoprotein CIG30 [Mus musculus]
20421	ENU04215	ANI61C2667:	54-76	NAP	g2289244	37	0.00005				
		1302..91		1204-							
20422	ENU04216	ANI61C1041	56-75	NAP	g4490992	312	122	4.00E-27	37	76	(AL035707) putative salicylate hydroxylase [Streptomyces coelicolor]
20423	ENU04217	ANI61C1191:	22-54	NAP	g417358	260	113	5.00E-37	30	56	ADA3 protein (NGG1 protein) ; NGG1 protein - yeast (Saccharomyces cerevisiae) ; (L12137) NGG1 [Saccharomyces cerevisiae] ; (Z46727) Ngg1p [Saccharomyces cerevisiae] (L35487) mannanase [Aspergillus aculeatus]
20424	ENU04218	ANI61C1120	31-51	NAP	g558311	1277	332	e-121	66	93	
		0-2052..833		1207							
20425	ENU04219	ANI61C6026:	22-55	NAP	g731415	1049	317	7.00E-86	56	29	probable calcium-transferring ATPase 6 ; hypothetical protein YEL031w - yeast [Saccharomyces cerevisiae] ; (U18530) P-type ATPase; YEL031w [Saccharomyces cerevisiae]
		2826..1607		1199							
20426	ENU04220	ANI61C433:3	22-45	NAP	g731893	922	217	2.00E-62	39	67	putative transporter YIL166C ; probable membrane protein YIL166c - yeast (Saccharomyces cerevisiae) ; (Z46921) unknown [Saccharomyces cerevisiae]
		174..1949		1205							
20427	ENU04221	ANI61C9916:	59-87	NAP	g2388995	159	66	7.00E-13	27	30	(Z98981) hypothetical protein [Schizosaccharomyces pombe]
20428	ENU04222	ANI61C5847:	28-52	NAP	g2497199	514	152	5.00E-48	33	77	hypothetical 50.5 KD protein in RNA1-RNT1 intergenic region ; probable membrane protein YMR238W - yeast (Saccharomyces cerevisiae) ; (Z49939) unknown [Saccharomyces cerevisiae] (AF039534) salicylate hydroxylase [Pseudomonas stutzeri] (AJ001261) NIPSNAP2 protein [Mus musculus]
20429	ENU04223	ANI61C8210:	22-40	NAP	g4104775	46	0.0005				
		1498..256		1222							
20430	ENU04224	ANI61C6527:	59-79	NAP	g2769258	367	53	3.00E-12	26	55	
		5092..6335		1240-							
		1260									

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database	nebi gi	aat	Blast Score	Blast Prob	% id	% cvrg	Description
20431	ENU04225	ANI61C9146:	31-52	1219-	NAP	g4585875	169	48	0.000000	32	89	2	(AC005850) Unknown protein [Arabidopsis thaliana]
20432	ENU04226	ANI61C8955:	33-52	1225-	NAP	g1175374	1122	433	e-120	57	75		hypothetical 57.8 KD protein C2F7.11 in chromosome I ; hypothetical protein SPAC2F7.11 - fission yeast (Schizosaccharomyces pombe); (Z50142) unknown
			198..1453	1246									[Schizosaccharomyces pombe] ; (AF079876) Nrd1p [Schizosaccharomyces pombe] (AF014950) chitinase A
20433	ENU04227	ANI61C5197:	22-50	1222-	NAP	g2429326	89	62	2.00E-15	30	36		[Stenotrophomonas maltophilia] (AL031534) Major facilitator superfamily protein
20434	ENU04228	ANI61C1024	32-55	1241	NAP	g3560142	716	173	2.00E-42	33	64		[Schizosaccharomyces pombe] proline-specific permease (proline transport protein); (X79797) proline permease [Emericella nidulans] (AL022244) hypothetical protein [Schizosaccharomyces pombe] (M82963) hexose transporter [Saccharomyces cerevisiae]
20435	ENU04229	ANI61C1120	61-80	1263-	NAP	g3929399	1125	380	e-104	48	76		hypothetical protein YHR016c - yeast (Saccharomyces cerevisiae); (U10400) Ysc84p [Saccharomyces cerevisiae] (AJ235272) SCO2 protein precursor (SCO2) [Rickettsia prowazekii]
			3:1271..2534	1282									"(AF031228) D-arabinono-1,4-lactone oxidase; L-galactono-gamma-lactone oxidase [Candida albicans]" "transcription factor btf3 homolog ; (U29488) similar to human transcription factor BTF3 and to S. cerevisiae GAL4 DNA-binding enhancer protein [Caenorhabditis elegans]
20436	ENU04230	ANI61C9721:	42-61	1245-	NAP	g2995339	1134	337	e-109	56	46		
20437	ENU04231	ANI61C7513:	41-61	1266	NAP	g171741	395	164	1.00E-39	25	74		
20438	ENU04232	ANI61C352:1	72-92	1248-	NAP	g626598	707	247	7.00E-72	43	83		
			358..78	1309									
20439	ENU04233	ANI61C1051	26-49	1248-	NAP	g3861132	225	97	3.00E-19	29	60		
20440	ENU04234	ANI61C6078:	23-47	1267	NAP	g4090945	619	307	1.00E-82	38	76		"(AF031228) D-arabinono-1,4-lactone oxidase; L-galactono-gamma-lactone oxidase [Candida albicans]" "transcription factor btf3 homolog ; (U29488) similar to human transcription factor BTF3 and to S. cerevisiae GAL4 DNA-binding enhancer protein [Caenorhabditis elegans]
			3729..5017	1269									
20441	ENU04235	ANI61C3595:	60-79	1284-	NAP	g2493356	309	125	5.00E-28	47	39		
			1111..2400	1307									

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	aat	Blast Score	Blast Prob	% id	% cvrg	Description
20442	ENU04236	ANI61C1023	23-48	1252-	NAP	g1352621	1338	303	e-115	64	83	dihydrodilipoamide acetyltransferase component of pyruvate dehydrogenase complex precursor (E2) (PDC-E2) (MRP3); dihydrodilipoamide acetyltransferase homolog -
20443	ENU04237	ANI61C5788:	22-46	1247-	NAP	g3581917	200	86	6.00E-16	40	65	Neurospora crassa ; (J04432) ribosomal protein [Neurospora crassa] (AL031545) hypothetical protein [Schizosaccharomyces pombe]
20444	ENU04238	ANI61C8008:	22-48	1268-	NAP	g3885836	584	113	5.00E-62	37	62	(AFD91042) putative cercosporin transporter [Cercospora kikuchii]
20445	ENU04239	ANI61C132:1	38-61	1284-	NAP	g2645229	430	163	3.00E-39	37	40	(UT8597) kinesin light chain [Plectonema boryanum]
20446	ENU04240	ANI61C7007:	23-52	1257-	NAP	g2213548	432	181	8.00E-45	33	70	(Z97052) hypothetical protein [Schizosaccharomyces pombe]
20447	ENU04241	ANI61C7007:	23-52	94..1402	NAP	g2213548	432	181	8.00E-45	33	70	[Schizosaccharomyces pombe] ("S80872) putative Tc1-mariner class transposase/IS630-Tc1 homolog [Aspergillus niger, chlorate-resistant mutant 46, transposon Ant1, Peptide Transposon, 325 aa] [Aspergillus niger]" "3',5'-cyclic-nucleotide phosphodiesterase (PDEASE); probable 3',5'-cyclic-nucleotide phosphodiesterase (EC 3.1.4.17) pde1-fission yeast (Schizosaccharomyces pombe) ; (S64907) Dictyostelium discoideum phosphodiesterase homolog [Schizosaccharomyces pombe=fission yeast, Peptid, 346 aa] [Schizosaccharomyces pombe] ; (AL031545) 3',5'-cyclic-nucleotide phosphodiesterase [Schizosaccharomyces pombe] ; pde1 gene [Schizosaccharomyces pombe]"
20448	ENU04242	ANI61C194:2	53-76	1317-	NAP	g1911486	269	81	1.00E-14	41	47	
			083..757	1337								
20449	ENU04243	ANI61C756:1	71-91	1336-1358	NAP	g544049	263	78	1.00E-13			
			778..449									

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvg	%	Description
20450	ENU04244	ANI61C2416:	22-45	1293-	NAP	g3400276	531	142	2.00E-53					"mitochondrial peptide chain release factor 1 precursor (MRFF-1) ; translation releasing factor RF-1, mitochondrial - yeast ( <i>Saccharomyces cerevisiae</i> ) ; (X60381) mitochondrial release factor 1 [ <i>Saccharomyces cerevisiae</i> ] ; (Z72665) ORF YGL143c [Saccharomyces cerevisiae] ; (X99960) YGL143c [ <i>Saccharomyces cerevisiae</i> ] ; (X99960) high-affinity glucose transporter ; (U22525) high affinity glucose transporter [ <i>Kuyveromyces lactis</i> ] (Saccharomyces cerevisiae) (Z95397) unknown [Schizosaccharomyces pombe]
20451	ENU04245	ANI61C1065	22-43	1290-	NAP	g1346290	339	87	2.00E-35	29	63			(U22525) high affinity glucose transporter [ <i>Kuyveromyces lactis</i> ] (Saccharomyces cerevisiae) (Z95397) unknown [Schizosaccharomyces pombe]
20452	ENU04246	ANI61C5171:	68-90	1345-	NAP	g1072485	442	166	4.00E-40	31	79			cycloheximide resistance protein ; (M64932) cyclohexamide resistance protein [ <i>Candida maltosa</i> ] hypothetical 44.9 KD protein in ERG7- NMD2 intergenic region ; hypothetical protein YHR075c - yeast ( <i>Saccharomyces cerevisiae</i> ) ; (U10556) Yhr075cp [ <i>Saccharomyces cerevisiae</i> ] Peroxisomal targeting signal receptor (peroxisomal protein PAY32) (peroxin-5) (PTS1 receptor) ; (U28155) Pay32p [ <i>Yarrowia lipolytica</i> ] ; Pay32 gene [ <i>Yarrowia lipolytica</i> ]
20453	ENU04247	ANI61C3347:	42-64	1326-	NAP	g2104457	666	244	1.00E-68	46	92			Hypothetical 55.6 KD protein C13F4.15C in chromosome I; hypothetical protein - fission yeast ( <i>Schizosaccharomyces pombe</i> ) ; (AL031322) putative diphthamide biosynthesis protein [Schizosaccharomyces pombe]
20454	ENU04248	ANI61C1024	72-96	1351-	NAP	g416864	103	3.00E-21						
20455	ENU04249	ANI61C2921:	38-57	1321-	NAP	g731676	349	85	8.00E-16	38	84			
			1350..1	1345										
20456	ENU04250	ANI61C6844:	68-89	1345-	NAP	g2501342	1085	409	e-113	54	68			
			1816..464	1378										
20457	ENU04251	ANI61C2078:	44-63	1333-	NAP	g1723275	544	189	4.00E-47	35	80			
			2042..688	1356										

Seq num	Seq id	Contig source	Primer 3 pos	Primer Basis	Selection	aat	Blast Score	Blast Prob	% id	% cvrg	Description	
				NAP	Database Hit	ncbi gi	Score	Prob				
20458	ENU04252	ANI61C2445:	48-71	1348-1367	g3915154	523	198	6.00E-50	34	76	P450 58) ; trichodiene oxygenase 4 - fungus (Fusarium sporotrichioides); (U22462) trichodiene oxygenase [Fusarium sporotrichioides]	
20459	ENU04253	ANI61C6612:	56-73	1361-1380	NAP	g3560246	806	327	9.00E-89	45	90	(AL031532) putative acetylornithine aminotransferase precursor [Schizosaccharomyces pombe]
20460	ENU04254	ANI61C6742:	22-47	1325-1351	NAP	g729376	787	201	1.00E-50	31	61	urea active transporter ; urea transport protein - yeast (Saccharomyces cerevisiae); (U11582) No definition line found [Saccharomyces cerevisiae]
20461	ENU04255	ANI61C211:3	25-46	1336-1357	NAP	g2132005	271	59	4.00E-11	29	49	hypothetical protein YOL057w - yeast (Saccharomyces cerevisiae); (Z74799) ORF YOL057w [Saccharomyces cerevisiae]
20462	ENU04256	ANI61C1019	36-56	1347-1371	NAP	g2132942	525	189	4.00E-47	33	79	probable membrane protein YOR306c-yeast (Saccharomyces cerevisiae); (Z75214) ORF YOR306c [Saccharomyces cerevisiae]
20463	ENU04257	ANI61C3867:	24-44	1341-1363	NAP	g3287945	447	140	1.00E-34	36	22	hypothetical 123.7 KD protein C14C4.02 in chromosome I
20464	ENU04258	ANI61C6734:	26-48	1348-2085..3468	NAP	g3560227	558	158	2.00E-65	39	83	(AL031530) hypothetical protein [Schizosaccharomyces pombe] (AF014950) chitinase A
20465	ENU04259	ANI61C5197:	22-50	1347-1366	NAP	g2429326	89	69	1.00E-17	31	38	[Stenotrophomonas maltophilia]
20466	ENU04260	ANI61C9460:	22-54	1347-1368	NAP	g4185142	795	314	9.00E-85	41	37	(AC005724) putative DNA repair and recombination protein of the SNF2 family [Arabidopsis thaliana] (Z29098) transposase (putative)
20467	ENU04261	ANI61C9182:	22-56	1337-1368	NAP	g436464	179	71	2.00E-11	24	89	[Drosophila hydei]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat	Blast Score	Blast Prob	% id	% cvrg	Description
20468	ENU04262	ANI61C1082	22..51	1356-	NAP	g1351640	1327	354	6.00E-97	55	78	hypothetical	62.7 KD protein C8A4.06 in chromosome I ; hypothetical protein SPAC8A4.06 - fission yeast
		7.1859..3253		1374									(Schizosaccharomyces pombe) ; (Z66569) unknown
20469	ENU04263	ANI61C5930:	22..51	1356-	NAP	g1805251	1103	150	2.00E-35	40	29	[Schizosaccharomyces pombe] ; (AL032824) putative chromatin binding snw family nuclear pr otein.	
		8907..8658		1375									(U58946) transposase [Aspergillus awamori]
20470	ENU04264	ANI50C2449	48..68	1383-	NAP	g140464		195	2.00E-88	48	48	"hypothetical	107.9 KD protein in POL4-SRD1 intergenic region ; probable membrane protein YCR017c - yeast (Saccharomyces cerevisiae) ; (X59720) YCR017c, len:953
		7..146..1451		1411									[Saccharomyces cerevisiae] ; (U78597) kinesin light chain [Plectonema boryanum]
20471	ENU04265	ANI61C3644:	54..73	1396-	NAP	g2645229	494	153	2.00E-36	37	57	dynamin-related protein DNM1 ;	
		5962..6753		1418									(Saccharomyces cerevisiae) ; (Z73106) ORF YLL001w [Saccharomyces cerevisiae] ; (X9488) L1381/DNM1 protein [Saccharomyces cerevisiae] (AF052515) eburicol 14alpha demethylase; CYP51; cytochrome P450 sterol 14-demethylase [Erysiphe graminis f. sp. hordei]
20473	ENU04267	ANI61C1059	22..43	1371-2..83..1499	NAP	g4049645	1538	484	e-136	64	82	"putative leucyl-tRNA synthetase, cytoplasmic (leucine--tRNA ligase) (LEURS) ; (Z73100) unknown [Schizosaccharomyces pombe]"	
20474	ENU04268	ANI61C7107:	53..83	1408-373..1797	NAP	g1711638	1372	128	e-105	51	39		
				1434									

Seq num	Seq id	Contig source	Primer 3 pos	Primer Basis	Selection Database Hit	atc	Blast Score	Blast Prob	% id	% cvrg	Description	
20475	ENU04269	ANI61C8415:	72-91	1445-							geranylgeranyl pyrophosphate synthetase (GGPP synthetase) (dimethylallyltransferase / geranyltransferase / farnesyltransferase ; geranylgeranyl pyrophosphate synthetase - <i>Neurospora crassa</i> ; (U20940) geranylgeranyl pyrophosphate synthetase [Neurospora crassa]	
20476	ENU04270	ANI61C2838:	44-64	1411-	NAP	g3182996	539	78	1.00E-30	42	92	translation initiation factor EIF-2B beta subunit (EIF-2B GDP-GTP exchange factor) (S20115) ; (U040756) S20115 [Fugu rubripes] lignostilbene dioxygenase [Sphingomonas paucimobilis]
20477	ENU04271	ANI61C7391:	38-59	1416-	NAP	g448379	681	155	5.00E-52	41	82	alpha-amylase (EC 3.2.1.1) precursor - <i>Aspergillus oryzae</i>
20478	ENU04272	ANI61C1048	44-63	1423-	NAP	g422215	825	290	8.00E-94	43	89	probable peptidyl-prolyl cis-trans isomerase C21E11.05C ; hypothetical protein SPAC21E11.05c - fission yeast ( <i>Schizosaccharomyces pombe</i> ) ; (Z67999) peptidyl-prolyl cis-trans isomerase [Schizosaccharomyces pombe]
20479	ENU04273	ANI61C1029	52-71	1441-	NAP	g1351676	992	330	e-101	52	87	(Y14317) catalase/peroxidase [Streptomyces reticuli]
20480	ENU04274	ANI61C8002:	69-88	1463-	NAP	g3758890	2466	656	0	65	65	putative dolichyl-diphosphooligosaccharide-protein glycosyltransferase alpha subunit precursor (oligosaccharyl transferase alpha subunit) ; (Z69368) unknown [Schizosaccharomyces pombe] (AL021816) hypothetical protein [Schizosaccharomyces pombe] (AF076848) tritydroxytoluene oxygenase [Burkholderia cepacia]
20481	ENU04275	ANI61C6047:	52-71	1447-	NAP	g1709501	414	181	1.00E-44	30	97	
20482	ENU04276	ANI61C1060:	23-42	1417-	NAP	g2879870	59	0.000000				
20483	ENU04277	ANI61C5186:	23-51	1420-	NAP	g3746666	281	101	3.00E-23	36	98	
			843..2305	1443								

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat	Blast Score	Blast Prob	% id	cvrg	%	Description
20484	ENU04278	ANI61C9834:	72-93	1480-1499	NAP	g2621739	892	308	6.00E-83	46	74	(AE000845) long-chain-fatty-acid-CoA ligase [Methanobacterium thermoautotrophicum]		
20485	ENU04279	ANI61C5211:	65-85	1474-1493	NAP	g4007751	485	125	6.00E-28	36	62	(Z99126) putative chromatin assembly factor subunit [Schizosaccharomyces pombe]		
20486	ENU04280	ANI61C8457:	48-68	1458-1485	NAP	g731422	724	110	4.00E-30	43	33	hypothetical 70.6 KD protein in HXT8-CAN1 intergenic region ; hypothetical protein YEL065w - yeast (Saccharomyces cerevisiae) ; (U18795) Yel065wp [Saccharomyces cerevisiae]		
20487	ENU04281	ANI61C1136	22-41	1440-1459	NAP	g731864	438	154	1.00E-36	29	79	hypothetical 61.8 KD protein in KGD1-SIM1 intergenic region ; probable membrane protein YIL120w - yeast (Saccharomyces cerevisiae) ; (Z46833) unknown [Saccharomyces cerevisiae] "aldehyde dehydrogenase, dimeric nadp-prefering (class 3) (tumor-associated aldehyde dehydrogenase) (HTC-ALDH) ; aldehyde dehydrogenase (NADP+) (EC 1.2.1.4) 3, tumor-associated - rat ; (J03637) aldehyde dehydrogenase [Rattus norvegicus]"		
20488	ENU04282	ANI61C1015	36-55	1455-1474	NAP	g118507	771	236	2.00E-79	41	96	"aldehyde dehydrogenase, dimeric nadp-prefering (class 3) (tumor-associated aldehyde dehydrogenase) (HTC-ALDH) ; aldehyde dehydrogenase (NADP+) (EC 1.2.1.4) 3, tumor-associated - rat ; (J03637) aldehyde dehydrogenase [Rattus norvegicus]"		
20489	ENU04283	ANI61C6871:	22-47	1442-1462	NAP	g112800	524	130	3.00E-55	39	73	4-coumarate--COA ligase 1 (4CL) ; 4-coumarate--CoA ligase (EC 6.2.1.12) (clone pc4CL-1) - parsley ; (X13324) 4-coumarate:CoA ligase Pc4CL-1 (AA 1-544) [Petroselinum crispum] (AF029885) putative homoserine O-acetyltransferase [Emericella nidulans]		
20490	ENU04284	ANI61C3461:	30-49	1442-1476	NAP	g2605934	2542	914	0	98	94	(U09580) beta-D-glucoside glucohydrolase [Trichoderma reesei] (AB004535) hypothetical 105.9 KD protein in AAC3-RFC5 intergenic region. [Schizosaccharomyces pombe] (AB004535) hypothetical 105.9 KD protein in AAC3-RFC5 intergenic region. [Schizosaccharomyces pombe]		
20491	ENU04285	ANI61C7333:	71-90	1500-1519	NAP	g493580	1781	287	e-111	58	57			
20492	ENU04286	ANI50C7209	23-47	1453-1472	NAP	g2257513	147	4.00E-52	31	66				
20493	ENU04287	ANI50C7209	23-47	1453-1472	NAP	g2257513	147	4.00E-52	31	66				

શ્રી રામ કૃત્તિમાન પાઠ્ય માલા

Seq num	Seq id	Contig source	Primer Basis	Primer NAP	Selection	Database	Hit gi	aat	Blast Score	Blast Prob	% id	% cvrg	Description
20494	ENU04288	ANI61C1125	5 pos	3 pos	g730942	744	134	1.00E-47					probable thiamin biosynthetic bifunctional enzyme [contains: thiamin-phosphate pyrophosphorylase (TMP pyrophosphorylase) (TMP-PASE); hydroxethylthiazole kinase (4-methyl-5-beta-hydroxyethylthiazole kinase) (THZ kinase) ... ; thi4 protein - fission yeast (Schizosaccharomyces pombe); (X78824) thi4 [Schizosaccharomyces pombe]; (Z98977) thiamin biosynthetic bifunctional enzyme
20495	ENU04289	ANI61C1139:	22-44	1450-	NAP	g1723423	602	92	2.00E-33	27	70		[Schizosaccharomyces pombe] hypothetical 70.4 KD protein C4G9.04C in chromosome I; (Z69727) hypothetical protein
20496	ENU04290	ANI61C1055	27-46	1468-	NAP	g2924503	979	306	3.00E-82	44	84		[Schizosaccharomyces pombe] (AL022019) glucosyltransferase [Schizosaccharomyces pombe]
20497	ENU04291	ANI61C5108:	36-56	1481-	NAP	g3417417	357	116	1.00E-34	36	59		(AL031261) hypothetical protein [Schizosaccharomyces pombe]
20498	ENU04292	ANI61C901:4	22-41	1477-	NAP	g3915154	728	173	2.00E-73	39	84		trichodiene oxygenase (cytochrome P450 58); trichodiene oxygenase 4 - fungus ( <i>Fusarium sporotrichioides</i> ); (U22462) trichodiene oxygenase [Fusarium sporotrichioides] (D38414) ORF2 [ <i>Bombyx mori</i> ]
20499	ENU04293	ANI61C9197:	25-46	1481-	NAP	g1549144	70	3.00E-11					
		1602..84	1501	1504-	NAP	g3929337	271	114	1.00E-24	25	44		amino acid permease 2; (AL053231) amino acid permease [Neurospora crassa]
20500	ENU04294	ANI61C1903:	60-79	1538		g2127851	616	136	6.00E-44	34	82		dihydroxy-acid dehydratase (EC 4.2.1.9) - <i>Methanococcus jannaschii</i> ; (U67568) dihydroxy-acid dehydratase (ilvD) [ <i>Methanococcus jannaschii</i> ] (M16076) low temperature essential protein [ <i>Saccharomyces cerevisiae</i> ]
20502	ENU04296	ANI61C1103	44-68	1508-	NAP	g171850	350	152	5.00E-36	31	65		
		3..3840..5366	1527										

Seq num	Seq id	Contig source	Primer 3 pos	Primer Basis	Selection	aat	Blast Score	Blast Prob	% id	% cvrg	Description	
				NAP	Database Hit	ncbi gi	Score	Prob				
20503	ENU04297	ANI61C3982:	37-57	1500-	g544017	624	268	7.00E-71	35	90	protein kinase CHK1 (checkpoint kinase CHK1) ; protein kinase chk1 (EC 2.7.1.-) - fission yeast	
	1171..2702			1525							(Schizosaccharomyces pombe) ; (L13742) protein kinase [Schizosaccharomyces pombe] ; (U37421) protein kinase [Schizosaccharomyces pombe] ; (AL024564) protein kinase chk1 [Schizosaccharomyces pombe] (AF027687) GTPase activating protein homolog [Cochliobolus heterostrophus] (AL033389) aminotransferase	
20504	ENU04298	ANI61C8369:	48-67	1518-1620..81	NAP	g2598189	899	123	1.00E-39	47	60	[Schizosaccharomyces pombe] ; (U37421) protein kinase [Schizosaccharomyces pombe] ; (Pichia pastoris) ; (Z36987) PAS1 [Pichia pastoris]
				1544							[Schizosaccharomyces pombe] peroxisome biosynthesis protein PAS1 (peroxin-1) ; PAS1 protein - yeast (Pichia pastoris) ; (Z36987) PAS1 [Pichia pastoris]	
20505	ENU04299	ANI61C2578:	22-57	1507-4121..5669	NAP	g3850081	962	293	6.00E-84	45	97	[Schizosaccharomyces pombe]
				1526							[Schizosaccharomyces pombe] peroxisome biosynthesis protein PAS1 (peroxin-1) ; PAS1 protein - yeast (Pichia pastoris) ; (Z36987) PAS1 [Pichia pastoris]	
20506	ENU04300	ANI61C1144	63-86	1551-4:1677..128	NAP	g1172019	1098	345	4.00E-94	50	37	[Schizosaccharomyces pombe] ; (U15645) serine palmitoyltransferase [Schizosaccharomyces pombe] ; (U15645) serine palmitoyltransferase [Schizosaccharomyces pombe] ; (Z99259) serine palmitoyltransferase 2 [Schizosaccharomyces pombe] (AL023704) putative translocation elongation factor-Tu family
				1570							[Schizosaccharomyces pombe] ; (D89136) similar to Saccharomyces cerevisiae BCS1 protein, SWISS-PROT Accession Number P32839 [Schizosaccharomyces pombe]" (AB018331) KIAA0788 protein [Homo sapiens]	
20510	ENU04304	ANI61C4319:	63-82	1582-4290..5870	NAP	g3882297	2494	460	e-128	48	37	(AF042379) spindle pole body protein spc97 homolog GCP2 [Homo sapiens]
				1601							[Homo sapiens]	
20511	ENU04305	ANI61C8432:	67-95	1577-2298..709	NAP	g2801701	575	134	2.00E-48	32	49	(AF042379) spindle pole body protein spc97 homolog GCP2 [Homo sapiens]
				1612							[Homo sapiens]	

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat	Blast Score	Blast Prob	% id	% cvrg	Description
20512	ENU04306	ANI61C3797:	31-54	1549-	NAP	g2132851	204	82	1.00E-14	24	87	probable membrane protein YOL137w	-yeast ( <i>Saccharomyces cerevisiae</i> ) ; (Z74879) ORF YOL137w
237..1828				1580									[ <i>Saccharomyces cerevisiae</i> ] ; (X95465) ORF [ <i>Saccharomyces cerevisiae</i> ] ; (U33057) St1p; plasma membrane sugar transporter; CAI: 0.19 [ <i>Saccharomyces cerevisiae</i> ] (AL034463) hypothetical protein [Schizosaccharomyces pombe]
20513	ENU04307	ANI61C9558:	22-47	1555-	NAP	g1711561	506	199	5.00E-50	30	85	sugar transporter STP1 ; yeast transport protein STP1 - yeast ( <i>Saccharomyces cerevisiae</i> ) ; (U33057) St1p; plasma membrane sugar transporter; CAI: 0.19 [ <i>Saccharomyces cerevisiae</i> ] (AL034463) hypothetical protein [Schizosaccharomyces pombe]	
4822..3228			4822..3228	1574									
20514	ENU04308	ANI61C8986:	23-44	1556-	NAP	g4007794	111	69	1.00E-10	28	41	"translation initiation factor IF-2, mitochondrial precursor (IF-2MT) ; mitochondrial initiation factor IF-2, mitochondrial - yeast ( <i>Saccharomyces cerevisiae</i> ) ; (Z74765) ORF YOL023w [Saccharomyces cerevisiae]" putative transporter YGR260W ; probable membrane protein YGR260w - yeast ( <i>Saccharomyces cerevisiae</i> ) ; (Z73044) ORF YGR260w [ <i>Saccharomyces cerevisiae</i> ] ; (Y07777) YGR260w ORF [ <i>Saccharomyces cerevisiae</i> ] (AL031528) pseudouridine synthase [Schizosaccharomyces pombe] (Z99164) hypothetical protein [Schizosaccharomyces pombe]	
99..1693			99..1693	1579									
20515	ENU04309	ANI61C5894:	26-46	1565-	NAP	g1351684	1064	314	e-109	43	13	C1F5.11C in chromosome I ; (Z68136) unknown [ <i>Schizosaccharomyces pombe</i> ] "translation initiation factor IF-2, mitochondrial precursor (IF-2MT) ; mitochondrial initiation factor IF-2, mitochondrial - yeast ( <i>Saccharomyces cerevisiae</i> ) ; (Z74765) ORF YOL023w [Saccharomyces cerevisiae]" putative transporter YGR260W ; probable membrane protein YGR260w - yeast ( <i>Saccharomyces cerevisiae</i> ) ; (Z73044) ORF YGR260w [ <i>Saccharomyces cerevisiae</i> ] ; (Y07777) YGR260w ORF [ <i>Saccharomyces cerevisiae</i> ] (AL031528) pseudouridine synthase [Schizosaccharomyces pombe] (Z99164) hypothetical protein [Schizosaccharomyces pombe]	
1725..125			1725..125	1584									
20516	ENU04310	ANI61C1677:	40-59	1589-	NAP	g2506776	993	410	e-113	42	79		
1762..1704			1762..1704	1609									
20517	ENU04311	ANI61C8887:	70-90	1642-	NAP	g1723769	177	61	0.000000	27	41		
227..1875			227..1875	1676				03					
20518	ENU04312	ANI61C1038	26-45	1608-	NAP	g3560201	423	153	2.00E-36	34	45		
7.2377..735			7.2377..735	1635									
20519	ENU04313	ANI61C9601:	48-70	1642-	NAP	g2408051	1465	271	e-119	45	57		
4936..3281			4936..3281	1661									

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	atn	Blast Score	Blast Prob	% id	cvg	Description
20520	ENU04314	ANI61C6953:	22..44	1625-	NAP	g1175369	331	126	4.00E-28	32	83 hypothetical DNA polymerase beta-like protein C2F7.06C ; hypothetical
			1015..2681	1645							protein SPAC2F7.06c - fission yeast (Schizosaccharomyces pombe) ; (Z50142) unknown [Schizosaccharomyces pombe] (L25310) beta-mannase [Trichoderma reesei]
20521	ENU04315	ANI61C2457:	68..86	1669-	NAP	g506848	771	327	2.00E-88	47	66
		611..2271		1692							"5-aminolevulinic acid synthase, mitochondrial precursor (delta-aminolevulinate synthase) (delta-Ala synthetase) ; 5-aminolevulinate synthase (EC 2.3.1.37) precursor - Emericella nidulans ; (X64170) 5-aminolevulinic acid synthase [Emericella nidulans]"
20522	ENU04316	ANI50C4730	33..52	1641..1..12..1681	NAP	g585244	1033	0	99	82	
				1660							mitochondrial precursor (delta-aminolevulinate synthase) (delta-Ala synthetase) ; 5-aminolevulinate synthase (EC 2.3.1.37) precursor - Emericella nidulans ; (X64170) 5-aminolevulinic acid synthase [Emericella nidulans]"
20523	ENU04317	ANI61C1190:	33..54	1645..15284..13607	NAP	g3023933	1040	73	8.00E-31	42	55
				1667							hypothetical 76.8 KD protein in chromosome II ; (AF064207) putative histone deacetylase [Schizosaccharomyces pombe] (AL035065) putative urea active transporter [Schizosaccharomyces pombe]
20524	ENU04318	ANI61C8043:	70..93	1678..4994..3314	NAP	g4106690	758	220	3.00E-56	41	48
				1708							(AL021816) hypothetical protein [Schizosaccharomyces pombe]
20525	ENU04319	ANI61C7218:	69..93	1699..6352..8047	NAP	g2879870	1686	182	5.00E-45	35	48
				1722							(AE000703) N-methylhydantoinase A [Aquifex aeolicus]
20526	ENU04320	ANI61C8090:	40..61	1670..3206..1509	NAP	g2983296	794	309	4.00E-83	36	82
				1695							(Y15277) cytochrome P450 monooxygenase [Gibberella fujikuroi]
20527	ENU04321	ANI61C1567:	39..70	1682..99..1803	NAP	g3549879	742	292	4.00E-78	39	91
				1701							pisatin demethylase (cytochrome P450 57A1) ; pisatin demethylase - fungus (Nectria haematococca) ; (L20976) pisatin demethylase [Nectria haematococca mpV]
20528	ENU04322	ANI61C3019:	22..55	1663..4317..2609	NAP	g3929362	432	197	3.00E-49	32	72
				1688							
20529	ENU04323	ANI61C8724:	22..47	1677..3953..5671	NAP	g2688966	537	139	2.00E-55	26	90
				1698							[Magnaporthe grisea]

Seq num	Seq id	Contig source	Primer Basis	Primer Database	Selection	aat	Blast	Blast	% id	% cvrg	Description
		5 pos	3 pos	Hit	ncbi gi	Score	Prob				
20530	ENU04324	ANI61C379:2	38..57	1700-	NAP	g3497193	785	170	2.00E-60	36	69
		693..966	1721								
20531	ENU04325	ANI61C1536:	35..55	1708-	NAP	g3650401	278	137	2.00E-31	27	52
		15..1749	1727								
20532	ENU04326	ANI61C8724:	22..51	1707-	NAP	g3688966	537	139	2.00E-55	26	90
		3923..5671	1728								
20533	ENU04327	ANI61C1070:	63..83	1776-	NAP	g4033486	274	82	5.00E-23	31	40
		530..2304	1795								
20534	ENU04328	ANI61C8868:	22..52	1725-	NAP	g2144167	1713	362	e-143	55	71
		6159..4379	1756								
20535	ENU04329	ANI61C9692:	58..77	1836-	NAP	g3924850	252	109	8.00E-23	32	27
		4164..2329	1855								
20536	ENU04330	ANI61C7957:	67..87	1853-	NAP	g4502497	149	69	2.00E-19	32	59
		4466..2619	1872								
20537	ENU04331	ANI61C7791:	23..46	1819-	NAP	g1169823	61	0.000000			
		716..2576	1841			03					
20538	ENU04332	ANI61C1004	70..92	1867-	NAP	g1872514	513	120	3.00E-26	37	33
		0..1927..66	1889								

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat	Blast Score	Blast Prob	% id	cvg	%	Description
20539	ENU04333	ANI61C7032:	22-54	1823-	NAP	g466152	446	173	9.00E-48	35	44			hypothetical 76.2 KD protein ZK632.7 in chromosome III ; hypothetical protein ZK632.7 - Caenorhabditis elegans ; (Z22181) cDNA EST CEESN66F comes from this gene; cDNA EST yk395c9.5 comes from this gene [Caenorhabditis elegans]
20540	ENU04334	ANI61C7032:	22-54	1823-	NAP	g466152	446	173	9.00E-48	35	44			hypothetical 76.2 KD protein ZK632.7 in chromosome III ; hypothetical protein ZK632.7 - Caenorhabditis elegans ; (Z22181) cDNA EST CEESN66F comes from this gene; cDNA EST yk395c9.5 comes from this gene [Caenorhabditis elegans]
		1524..3386		1842										hypothetical 76.2 KD protein ZK632.7 in chromosome III ; hypothetical protein ZK632.7 - Caenorhabditis elegans ; (Z22181) cDNA EST CEESN66F comes from this gene; cDNA EST yk395c9.5 comes from this gene [Caenorhabditis elegans]
20541	ENU04335	ANI61C6610:	28-47	1847-	NAP	g3929362	555	147	2.00E-70	36	98			[Schiossaccharomyces pombe] "D83967" YfkN [Bacillus subtilis]; (Z99108) similar to 2',3'-cyclic-nucleotide 2'-phosphodiesterase [Bacillus subtilis]"
		3603..3426		1880										(AL023781) hypothetical protein [Schiossaccharomyces pombe] "D83967" YfkN [Bacillus subtilis]; (Z99108) similar to 2',3'-cyclic-nucleotide 2'-phosphodiesterase [Bacillus subtilis]"
20542	ENU04336	ANI61C9614:	68-86	1915-	NAP	g3184088	392	160	8.00E-44	29	76			[Emericella nidulans] (L28810) regulatory protein [Emericella nidulans]
		47..1956		1934										[Emericella nidulans] (L28810) regulatory protein [Emericella nidulans]
20543	ENU04337	ANI61C7030:	22-48	1873-	NAP	g2626826	98	3.00E-19						[Schiossaccharomyces pombe] "D83967" YfkN [Bacillus subtilis]; (Z99108) similar to 2',3'-cyclic-nucleotide 2'-phosphodiesterase [Bacillus subtilis]"
		3655..1743		1892										[Schiossaccharomyces pombe] "D83967" YfkN [Bacillus subtilis]; (Z99108) similar to 2',3'-cyclic-nucleotide 2'-phosphodiesterase [Bacillus subtilis]"
20544	ENU04338	ANI61C7115:	71-90	1931-	NAP	g2133268	97	85	2.00E-15	25	52			[Emericella nidulans] (L28810) regulatory protein [Emericella nidulans]
		130..2055		1954										[Emericella nidulans] (L28810) regulatory protein [Emericella nidulans]
20545	ENU04339	ANI61C3433:	22-41	1890-	NAP	g3925758	182	84	3.00E-15	26	76			[Schizosaccharomyces pombe] "AE001146" sensory transduction histidine kinase, putative [Borrelia burgdorferi]"
		1237..3168		1909										[Schizosaccharomyces pombe] "AE001146" sensory transduction histidine kinase, putative [Borrelia burgdorferi]"
20546	ENU04340	ANI61C7725:	22-51	1900-	NAP	g2688313	59	0.000000						[AB023911] chitin synthase [Emericella nidulans]
		2046..107		1919										[AB023911] chitin synthase [Emericella nidulans]
20547	ENU04341	ANI61C680:3	43-70	1932-	NAP	g4519181	3365	1236	0	99	63			[U68040] polyketide synthase [Cochliobolus heterostrophus]
20548	ENU04342	ANI61C6259:	51-72	1955-	NAP	g1546072	1439	149	7.00E-35	30	22			[U68040] polyketide synthase [Cochliobolus heterostrophus]
		5140..7105		1974										[U68040] polyketide synthase [Cochliobolus heterostrophus]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database	Hit ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
20549	ENU04343	ANI61C2341:	54-74	1979-	NAP	g2104457	246	104	8.00E-29	31	45	(Z95397) unknown	
20550	ENU04344	ANI61C9697:	45-67	1967-	NAP	g399198	603	183	8.00E-73	38	35	[Schizosaccharomyces pombe] cell division control protein 25; SKCDC25 protein - yeast (Saccharomyces kluyveri) (fragment); (M82964) CDC25 [Saccharomyces kluyveri]	
20551	ENU04345	ANI61C4603:	24-44	1965-	NAP	g3915154	353	83	2.00E-24	33	91	trichodiene oxygenase (cytochrome P450 58); trichodiene oxygenase 4-fungus (Fusarium sporotrichioides); (U22462) trichodiene oxygenase [Fusarium sporotrichioides]; (U78320) chitinase [Entamoeba invadens]	
20552	ENU04346	ANI61C1932:	35-54	1983-	NAP	g1685364	337	113	1.00E-41	33	44	[Schizosaccharomyces pombe] phosphatidylinositol "probable taurine catabolism protein 3" (SS13); (D85613) dioxygenase [Escherichia coli]; (U73857) dioxygenase [Escherichia coli]; (AE000143) taurine dioxygenase, 2-oxoglutarate-dependent [Escherichia coli]" auxin-induced protein PCNT115; auxin-induced protein - common tobacco · (X56267) auxin-induced protein [Nicotiana tabacum] (AL049628) putative exporter [Streptomyces coelicolor]	
20553	ENU04347	ANI61C9831:	41-60	2004-	NAP	g2117303	1418	346	e-155	66	90	"probable taurine catabolism dioxygenase (sulfate starvation-induced protein 3)" (SS13); (D85613) dioxygenase [Escherichia coli]; (U73857) dioxygenase [Escherichia coli]; (AE000143) taurine dioxygenase, 2-oxoglutarate-dependent [Escherichia coli]" auxin-induced protein PCNT115; auxin-induced protein - common tobacco · (X56267) auxin-induced protein [Nicotiana tabacum] (AL049628) putative exporter [Streptomyces coelicolor]	
20554	ENU04348	ANI61C6656:	54-73	2018-	NAP	g2506921	161	55	0.000001	32	43	"probable taurine catabolism dioxygenase (sulfate starvation-induced protein 3)" (SS13); (D85613) dioxygenase [Escherichia coli]; (U73857) dioxygenase [Escherichia coli]; (AE000143) taurine dioxygenase, 2-oxoglutarate-dependent [Escherichia coli]" auxin-induced protein PCNT115; auxin-induced protein - common tobacco · (X56267) auxin-induced protein [Nicotiana tabacum] (AL049628) putative exporter [Streptomyces coelicolor]	
20555	ENU04349	ANI61C5227:	22-52	1984-	NAP	g728744	53	0.000007					
20556	ENU04350	ANI61C1039	56-77	2022-	NAP	g4585598	65	2.00E-35					
20557	ENU04351	ANI61C1023	45-64	2036-	NAP	g549758	157	119	6.00E-26	28	36	"feric reductase transmembrane component 2 precursor ; feric reductase FRE2 precursor - yeast (Saccharomyces cerevisiae); (X75950) ORF5, F711 [Saccharomyces cerevisiae]; (Z28220) ORF YKL220c [Saccharomyces cerevisiae]; ORF5 [Saccharomyces cerevisiae]"	

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
20558	ENU04352	ANI61C9133:	54..73	2053..393..2453	NAP	g2650375	586	254	2.00E-66	37	55	(AL031740) putative mitochondrial translation system component	
20559	ENU04353	ANI61C2779:	68..89	2079..2099	NAP	g4528	360	0	58	88	[Schizosaccharomyces pombe] (X54316) GTP-binding protein [Saccharomyces cerevisiae]		
20560	ENU04354	ANI61C1106	40..59	2054..7..3274..1719	NAP	g2182972	794	217	e-127	47	68	probable coatomer gamma subunit (gamma-coat protein) (gamma-COP); (Z95396) putative coatomer gamma subunit [Schizosaccharomyces pombe] (U78597) kinesin light chain [Plectonema boryanum]	
20561	ENU04355	ANI61C1103	26..49	2041..1..2700..5209	NAP	g2645229	442	195	8.00E-49	36	39	DNA repair protein RAD50 (153 KD protein); RAD50 protein - yeast (Saccharomyces cerevisiae); (X14814) 153 kD protein (AA 1 - 1312) [Saccharomyces cerevisiae]; (X96722) ORF N0872 [Saccharomyces cerevisiae]; (Z71526) ORF YNL250w [Saccharomyces cerevisiae] (Z83828) AmMst-1 [Amanita muscaria]	
20562	ENU04356	ANI61C9409:	23..45	2031..480..2560	NAP	g131782	956	239	9.00E-89	32	52	(AL021746) phosphatidylserine decarboxylase [Schizosaccharomyces pombe]	
20563	ENU04357	ANI61C439..5	70..89	2092..373..5887	NAP	g2258125	520	209	1.00E-59	33	95	trichodiene oxygenase (cytochrome P450 58); trichodiene oxygenase 4 - fungus (Fusarium sporotrichioides); (U22462) trichodiene oxygenase [Fusarium sporotrichioides]	
20564	ENU04358	ANI61C8264:	46..67	2074..1449..3554	NAP	g2842521	730	322	6.00E-87	50	100	(AL021816) hypothetical protein [Schizosaccharomyces pombe]	
20565	ENU04359	ANI61C4603:	26..61	2108..2881..737	NAP	g3915154	353	83	2.00E-24	33	87	SpoC1-C1C protein - Emericella nidulans ; (M83571) SpoC1-C1C [Emericella nidulans]	
20566	ENU04360	ANI61C1060:	23..42	2143..2378..196	NAP	g2879870	59	0.000000	09				
20567	ENU04361	ANI61C9302:	68..92	2183..2590..1817	NAP	g283343	304	80	1.00E-17	58	16	SpoC1-C1C protein - Emericella nidulans ; (M83571) SpoC1-C1C [Emericella nidulans]	

Seq num	Seq id	Contig source	Primer 3 pos	Primer Basis	Selection Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description	
20568	ENU04362	ANI61C1076	9:1972..4306	61-80	2318-	NAP	g1174987	1186	166	3.00E-61	45	20	vacuolar protein sorting-associated protein VPS35 ; vacuolar protein-sorting protein VPS35 - yeast (Saccharomyces cerevisiae) ; (Z49429)
20569	ENU04363	ANI61C216:3	35-55	2322-	NAP	g1352937	48	45	0.002	25	28	cerevisiae]	[Saccharomyces cerevisiae]
			135..785	2343								hypothetical 39.9 KD protein in HOM6-PMT4 intergenic region ; probable membrane protein YJR141w - yeast (Saccharomyces cerevisiae) ; (Z49641) ORF YJR141w	
20570	ENU04364	ANI61C5788:	49-68	2330-	NAP	g3618207	721	320	3.00E-86	33	88	(AL031579) conserved hypothetical protein [Schizosaccharomyces pombe]	[Schizosaccharomyces pombe]
			2376..22	2361								DNA repair protein RAD9 ; rad9 protein - fission yeast	
20571	ENU04365	ANI61C1001	66-87	2359-	NAP	g131816	189	64	6.00E-16			(Schizosaccharomyces pombe) ; rad9 protein - fission yeast	(Schizosaccharomyces pombe) ; (X58331) rad9 protein
			4:243..2606	2385								[Schizosaccharomyces pombe] ; (X64648) rad9 [Schizosaccharomyces pombe] ; (X77276) rad9	
20572	ENU04366	ANI61C9256:	60-80	2362-	NAP	g3915154	75	2.00E-31				[Schizosaccharomyces pombe] trichodiene oxygenase (cytochrome P450 58) ; trichodiene oxygenase 4 - fungus (Fusarium sporotrichioides) ; (U22462) trichodiene oxygenase [Fusarium sporotrichioides]	[Fusarium sporotrichioides]
			4444..4770	2381								6-phosphofructokinase (phosphohexokinase) ; (Z79690) phosphofructokinase [Aspergillus niger]	
20574	ENU04368	ANI61C1048	47-72	2372-	NAP	g1175379	541	111	2.00E-44	44	27	hypothetical 88.2 KD protein C2F7.18C in chromosome 1	(U13644) F56D2.5 gene product [Caenorhabditis elegans]
20575	ENU04369	ANI61C3090:	22-48	2413-	NAP	g1945502	98	82	2.00E-14	34	6		
			650..3116	2445									

Seq num	Seq id	Contig source	Primer Basis	Primer Selection	aat	Blast Score	Blast Prob	% id	% cvrg	Description	
			NAP	Database Hit	ncbi gi	Score	Prob				
20576	ENU04370	ANI61C9380:	70-89	2490-	g1175371	138	80	5.00E-14	31	22 hypothetical 71.9 KD protein C2F7.08C in chromosome I;	
		3693..1211	2510							hypothetical protein SPAC2F7.08c - fission yeast (Schizosaccharomyces pombe); (Z50142) unknown [Schizosaccharomyces pombe]	
20577	ENU04371	ANI61C9639:	44-75	2490-	NAP	g731864	383	176	4.00E-43	25	65 hypothetical 61.8 KD protein in KGD1-SIM1 intergenic region ; probable membrane protein YIL120w - yeast (Saccharomyces cerevisiae); (Z46833) unknown [Saccharomyces cerevisiae] (Z99753) hypothetical protein [Schizosaccharomyces pombe]
		8574..6059	2516							(AF059906) ubiquitin fusion degradation protein-2 [Schizosaccharomyces pombe]	
20578	ENU04372	ANI61C3273:	34-53	2497-	NAP	g2465152	240	95	2.00E-18	40	13 2-oxoglutarate dehydrogenase EI component precursor (alpha-ketoglutarate dehydrogenase); oxoglutarate dehydrogenase (lipoamide) (EC 1.2.4.2) precursor - yeast (Saccharomyces cerevisiae); (Z46833) 2-oxoglutarate dehydrogenase E1 component [Saccharomyces cerevisiae]
		2642..118	2517							"transcription initiation factor IIIE, alpha subunit (TFIIE-alpha) (transcription factor A large subunit) (factor A 66 KD subunit); transcription initiation factor IIIE chain TFA1 - yeast (Saccharomyces cerevisiae); (Z28028) ORF YKL028w [Saccharomyces cerevisiae]; (U12825) transcription factor TFIIE, large subunit [Saccharomyces cerevisiae]" (AB018297) KIAA0754 protein [Homo sapiens]	
20580	ENU04374	ANI61C9792:	24-45	2547-	NAP	g730221	3335	788	0	67	81 2-oxoglutarate dehydrogenase EI component precursor (alpha-ketoglutarate dehydrogenase); oxoglutarate dehydrogenase (lipoamide) (EC 1.2.4.2) precursor - yeast (Saccharomyces cerevisiae); (Z46833) 2-oxoglutarate dehydrogenase E1 component [Saccharomyces cerevisiae]
		5406..2821	2566								
20581	ENU04375	ANI61C1144	64-85	2639-	NAP	g549038	133	71	1.00E-13		
		2..2530..2683	2658								
20582	ENU04376	ANI61C8159:	70-89	2659-	NAP	g3882229	85	46	0.001	26	21
		4169..1515	2682								

Seq num	Seq id	Contig source	Primer 3 pos	Primer Basis	Selection Database Hit	atc ncbi gi	blast Score	blast Score Prob	% id	% cvrg	Description	
20583	ENU04377	ANI61C4130:	22-41	NAP	g3005592	548	166	7.00E-40	34	27	(AF051911) telomerase reverse transcriptase; mTERT [Mus musculus]; (AF073311) telomerase catalytic subunit [Mus musculus]	
20584	ENU04378	ANI61C9698:	56-75	2651-	NAP	g1723845	377	171	3.00E-41	34	45	putative ATP-dependent RNA helicase YGL064C; hypothetical protein [Saccharomyces cerevisiae]; (Z72586) ORF YGL064c (AL023592) putative helicase [Schizosaccharomyces pombe]
20585	ENU04379	ANI61C1132:	72-94	2676-155..2820	NAP	g3136048	2024	362	5.00E-99	50	64	"SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 3 ; HIP116 protein - human ; (L34673) ATPase [Homo sapiens]", (AC006068) putative acyl coenzyme A oxidase, peroxisomal component [Arabidopsis thaliana]"
20586	ENU04380	ANI61C8590:	22-55	2689-1848..4579	NAP	g4507071	509	229	5.00E-59	33	43	"chloride channel 3 ; chloride channel protein 3, long form - human ; (X78520) chloride channel 3 [Homo sapiens]" (AL023290) putative ATP-dependent RNA helicase [Schizosaccharomyces pombe]
20587	ENU04381	ANI61C8661:	71-90	2828-50..2869	NAP	g4263786	850	225	e-100	37	86	cytochrome P450 [Papilio polyxenes (X94399) cAMP-dependent protein kinase catalytic subunit [Aspergillus niger] (L42454) EF-hand protein [Schizosaccharomyces pombe] (AL023288) hypothetical protein [Schizosaccharomyces pombe] gamma-adaptin - smut fungus (Ustilago maydis) [Ustilago maydis] (Z95334) putative helicase [Schizosaccharomyces pombe]
20588	ENU04382	ANI61C3919:	51-70	2813-554..3384	NAP	g4502869	1191	176	e-105	43	64	
20589	ENU04383	ANI61C9577:	38-57	2971-3062..68	NAP	g3116148	1166	196	e-133	37	62	
20590	ENU04384	ANI61C3260:	26-46	631-655	NAP	g1513174	66	87	9.00E-17	22	43	
20591	ENU04385	ANI61C1511:	378..1307		NAP	g2113796	807	196	1.00E-57	59	54	
20592	ENU04386	ANI61C6899:	222-240	531-552	NAP	g832882	351	116	1.00E-25	57	100	
20593	ENU04387	ANI61C9048:	1..1497		NAP	g3116134	882	219	2.00E-56	42	10	
20594	ENU04388	ANI61C2436:	35-54	632-651	NAP	g1078673	545	83	3.00E-34	60	22	
20595	ENU04389	ANI61C4421:	34-60	539-561	NAP	g2094863	306	171	3.00E-42	43	19	
			583..1									

Seq num	Seq id	Contig source	5 pos	3 pos	Primer Basis	Selection Database Hit	ncbi gi	aat	Blast Score	Blast Prob	% id	% cvrg	Description
20596	ENU04390	ANI61C291:7	42..61	578..603	NAP		g2501165	134	79	2.00E-14	32	28	hypothetical 59.6 KD protein in DSK2-CAT8 intergenic region
20597	ENU04391	ANI61C1032	70..88	516..536	NAP		g2498702	86	70	1.00E-11	37	31	[Saccharomyces cerevisiae] sterigmatocystin 7-O-methyltransferase precursor [Aspergillus parasiticus]
20598	ENU04392	ANI61C1073:	71..90	579..598	NAP		g3879319	431	177	5.00E-44	44	29	(Z8319) similar to ABC transporters; cDNA EST EMBL:D67233 comes from this gene; cDNA EST EMBL:D67486 comes from this gene; cDNA EST yk385dl.5 comes from this gene; cDNA EST yk398a5.5 comes from this gene; cDNA EST yk398a5.3 co... [ ]
20599	ENU04393	ANI61C5507:	122..139	442..461	NAP.		g2408049	136	46	0.0001	29	8	(Z99164) hypothetical protein [Schizosaccharomyces pombe]
20600	ENU04394	ANI61C3342:	114..133	372..391	NAP	1..470	g731024	295	145	2.00E-34	46	38	"branched-chain amino acid aminotransferase, mitochondrial precursor (BCAT) (TWT1 protein) [Saccharomyces cerevisiae]"
20601	ENU04395	ANI61C8781:	23..43	728..747	NAP	1035..1	g729397	616	260	8.00E-69	41	64	elongation factor 1-alpha (EF-1-alpha) (elongation factor TU) (EF-TU) [Sulfolobus solfataricus]
20602	ENU04396	ANI61C5009:	114..133	331..358	NAP	1..392	g3116140	276	124	2.00E-28	48	38	(AL023288) hypothetical dolichyl-phosphate beta-glucosyltransferase protein [Schizosaccharomyces pombe]
20603	ENU04397	ANI61S1051:	22..44	261..280	NAP	298..604	g1175960	223	97	9.00E-20	53	43	hypothetical 23.9 KD protein in TH15-AGP3 intergenic region [Saccharomyces cerevisiae]
20604	ENU04398	ANI61C8380:	22..47	394..414	NAP	2017..1526	g1173537	285	140	5.00E-33	42	28	(U30376) Lipomyces kononenkoae subsp. spencermartiniat alpha-amylase [Lipomyces kononenkoae] C14C4.11 in chromosome I
20605	ENU04399	ANI61C5287:	59..86	454..479	NAP	84..543	g3183344	276	105	2.00E-22	37	22	[Schizosaccharomyces pombe] (L41834) nuclear protein [Ensis minor]
20606	ENU04400	ANI61S1675:			NAP		g786117	180	51	0.00001	24	55	hypothetical 54.9 KD protein in CBR5- NOT3 intergenic region [Saccharomyces cerevisiae]
20607	ENU04401	ANI61C6597:	52..71	805..829	NAP	1..835	g731799	405	129	2.00E-29	38	48	NOT3 intergenic region [Saccharomyces cerevisiae]
			10548..9385										

Seq num	Seq id	Contig source	5 pos	3 pos	Primer Basis	Primer Selection	Database	Hit	ncbi gi	aat	Blast Score	Blast Prob	% id	cvg	%	Description
20608	ENU04402	ANI61C9383:	97-116	709-730	NAP			g586521	303	143	2.00E-33	36	29			hypothetical 86.4 KD protein in PHO5-VP15 intergenic region
20609	ENU04403	ANI61C1091	24-51	801-828	NAP		g32261632	498	116	3.00E-28	46	42				[Saccharomyces cerevisiae] (Z79700) accD2 [Mycobacterium tuberculosis]
20610	ENU04404	ANI61C4623:	27-46	660-679	NAP		g2499460	1545	267	9.00E-76	54	33				"phosphoenolpyruvate synthase (pyruvate:water dikinase) (PEP synthase) [Synechocystis sp.]"
20611	ENU04405	ANI61C1654:	25-52	726-744	NAP		g3172113	1585	522	e-148	97	16				(AB014886) typeII DNA topoisomerase [Entericella nidulans]
20612	ENU04406	ANI61C1070	35-54	790-811	NAP		g3121791	701	162	2.00E-63	53	23			sodium transport ATPase 5 [Saccharomyces cerevisiae]	
20613	ENU04407	ANI61S1450:	7.639..1826		NAP		g3037018	302		36	97				(AF041330) NADH dehydrogenase subunit 5 [Bodo saltans]	
20614	ENU04408	ANI61C5938:	850..174		NAP		g2624272	56	69	3.00E-11	27	89			(AL008967) hypothetical protein Rv2750 [Mycobacterium tuberculosis]	
20615	ENU04409	ANI61C1002	22-48	808-829	NAP		g1706177	754	111	6.00E-24	29	27			cutinase transcription factor 1 beta [Fusarium solani f. sp. pisi]	
20616	ENU04410	ANI61C3739:	29-48	756-781	NAP	1..1223	g3766365	756	155	3.00E-37	39	23			(AL031907) putative cystine-rich transcriptional regulator [Schizosaccharomyces pombe]	
20617	ENU04411	ANI61S974:9			NAP	2..551	g1709793	151	60	0.000000	29	69			salivary proline-rich protein PO (allele M) (contains: peptide P-D) [Homo sapiens]	
20618	ENU04412	ANI61C8633:	25-52	802-829	NAP	1..2156	g3929388	3438	221	e-140	99	35			"neutral trehalase (alpha,alpha-trehalase) (alpha,alpha-trehalose glucohydrolase) [Emericella nidulans] abaA protein - Emericella nidulans [Emericella nidulans]"	
20619	ENU04413	ANI61C7207:	2146..1628		NAP		g482275	661	266	5.00E-71	79	21			hypothetical 433.2 KD protein in HXT5-NRK1 intergenic region [Saccharomyces cerevisiae]	
20620	ENU04414	ANI61C3378:	28-49	723-749	NAP	1304..1	g731689	578	164	7.00E-40	30	7			(AF036707) RAD6 [Candida albicans]	
20621	ENU04415	ANI61C1036	39-58	390-413	NAP	0:514..1	g3273562	425	145	3.00E-34	81	59			PET117-CEM1 intergenic region [Saccharomyces cerevisiae]	
20622	ENU04416	ANI61C7198:	1588..1082		NAP		g1723597	318	136	1.00E-31	42	32			41-2 protein antigen precursor [Plasmodium falciparum]	
20623	ENU04417	ANI61C7472:	26-53	310-329	NAP	1962..1577	g112925	127	71	7.00E-12	30	88				

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvg	%	Description
20624	ENU04418	ANI61S4602:	90-108	530-547	NAP	g465511	359	136	2.00E-31	41	33	hypothetical	73.8 KD protein in SAS3-SEC17 intergenic region	
			665..1											[Saccharomyces cerevisiae]
20625	ENU04419	ANI61C3410:	110-137	804-827	NAP	g728828	496	219	3.00E-56	52	49	(Z99163) putative threonine aldolase		
		2232..1354				g2408036	291	117	7.00E-26	35	50	[Schizosaccharomyces pombe]		
20626	ENU04420	ANI61C2027:	171-190	347-366	NAP	g423793	75	58	0.000000	35	45	carboxylesterase (EC 3.1.1.1) -		
		1..578				05						Pseudomonas sp. (strain KWL-56)		
20627	ENU04421	ANI61C7678:	22-47	429-448	NAP	g1321944	224	54	0.000001	26	47	(X97346) FCYX [Saccharomyces cerevisiae]		
		7628..7174				g4218005	263	46	0.0002	27	36	(AC006135) putative vicilin storage protein (globulin-like) [Arabidopsis thaliana]		
20628	ENU04422	ANI61C5312:	22-48	804-823	NAP	g3980554	227	110	6.00E-24	34	63	"(AC004849) similar to several hypothetical proteins: U70849 (PID:g1572765), U00043 (PID:g470341), Z50070 (PID:g899462), AL033127 (PID:g3821335), and P40034 (PID:g731464) [Homo sapiens]" (AL034490) similar to yeast ngl-interacting factor 3		
		1..1093				g4008560	215	88	5.00E-17	57	45	[Schizosaccharomyces pombe]		
20629	ENU04423	ANI61S2268:	1..784		NAP	g1705828	2423	530	e-150	99	26	chitin synthase 2 (chitin-UDP acetyl-glucosaminyl transferase 2)		
			1459..1			g549725	520	189	2.00E-47			[Emericella nidulans]		
20630	ENU04424	ANI61S3044:	98-117	412-435	NAP							NADH-cytochrome B5 reductase precursor (P34/P32) [Saccharomyces cerevisiae]		
		1..528				g3493539	1740	431	e-120	99	69	(AF056182) G-protein beta subunit		
20631	ENU04425	ANI61C3082:	22-46	459-477	NAP	g476807	365	87	8.00E-34	38	51	[Emericella nidulans]		
		366..833				g2131329	388	87	8.00E-35	32	98	rad4/cu5+ product - fission yeast (Schizosaccharomyces pombe) []		
20632	ENU04426	ANI61C5001:	90-109	717-736	NAP							hypothetical protein YDL087c - yeast (Saccharomyces cerevisiae)		
		1020..2041										[Saccharomyces cerevisiae]		
20633	ENU04427	ANI61C8508:	23-50	804-829	NAP									
		1020..2041												
20634	ENU04428	ANI61C1064	22-41	805-829	NAP									
		4..1..1254												
20635	ENU04429	ANI61C7169:	43-62	626-653	NAP									
		75..1												
20636	ENU04430	ANI61C7108:	29-56	806-828	NAP									
		2551..3462												

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database	Hit	ncbi gi	aat	Blast Score	Blast Prob	% id	cvrg	%	Description
20637	ENU04431	ANI61C1554:			NAP	g1351183	806	136	2.00E-44	43	38				"tyrosyl-tRNA synthetase, mitochondrial precursor (tyrosine-tRNA ligase) (TYRS) [Neurospora crassa]"
20638	ENU04432	ANI61C9626:	22-41	792-814	NAP	g3702631	2007	406	e-113	68	36	(AL031824) protein transport protein sec23 homolog [Schizosaccharomyces pombe]			
20639	ENU04433	ANI61S953:6	182-204	567-593	NAP	g3647341	556	237	6.00E-62	58	21	(AL031644) RAD16 nucleotide excision repair protein homolog [Schizosaccharomyces pombe] (AT034260) protein kinase NRC-2 [Neurospora crassa]			
20640	ENU04434	ANI61C2676:	22-47	712-739	NAP	g2654106	1074	201	4.00E-51	74	39	(U47540) TamA [Emericella nidulans]			
20641	ENU04435	ANI61C4833:	1204..1		NAP	g4027860	1541	242	e-125	92	38				
20642	ENU04436	ANI61C5942:	38-57	778-797	NAP	g3183172	874	124	2.00E-52	41	56	"probable threonyl-tRNA synthetase, mitochondrial precursor (threonine-tRNA ligase) (THRS) [Schizosaccharomyces pombe]" hypothetical protein YLR002c - yeast (Saccharomyces cerevisiae)			
20643	ENU04437	ANI61C528:6	22-49	809-828	NAP	g2131739	572	107	1.00E-22	38	36	[Saccharomyces cerevisiae]			
20644	ENU04438	ANI61C7264:	22-43	802-829	NAP	g3318897	725	158	4.00E-38	39	36	"Chain A, Phenol Hydroxylase From Trichosporon Cutaneum [" (X05204) arom polypeptide [Emericella nidulans]			
20645	ENU04439	ANI61C1397:	80-100	719-738	NAP	g3834343	1429	468	e-131	95	17	(D87956) protein involved in sexual development [Schizosaccharomyces pombe]			
20646	ENU04440	ANI61C5143:	44-70	513-532	NAP	g1620896	620	251	2.00E-66	76	59	Succinic semialdehyde dehydrogenase [Homo sapiens]			
20647	ENU04441	ANI61C3620:	144-164	280-301	NAP	g4507229	238	104	2.00E-22	44	20	6-hydroxy-D-nicotine oxidase [Arthrobacter oxidans]			
20648	ENU04442	ANI61C6334:	22-44	722-749	NAP	g448109	216	101	7.00E-21	34	51	(X52633) GAP1 protein (AA 1-601) [Saccharomyces cerevisiae]			
20649	ENU04443	ANI61C3534:	3454..1931	4081..4982	NAP	g3722	498	69	3.00E-19	31	39	kinesin-like protein BIMC [Emericella nidulans]			
20650	ENU04444	ANI61C9310:	22-47	726-749	NAP	g114988	2453	480	e-135	95	22	hypothetical 60.1 KD protein C23C11.06C in chromosome I [Schizosaccharomyces pombe]			
20651	ENU04445	ANI61C5922:	1086..2744		NAP	g3183348	408	136	2.00E-31	35	52				
			1467..1												

Seq num	Seq id	Contig source	5 pos	3 pos	Basis	Primer	Primer	Selection	aat	Blast Score	Blast Prob	% id	% cvrg	Description
						Database	Hit	.ncbi gi	Score					
20652	ENU04446	ANI61C6611:	121-140	409-428	NAP	g3451071	247	80	2.00E-16	45	20	(AL031326) beta adaptin - like protein		
			1..516									[Arabidopsis thaliana]		
20653	ENU04447	ANI61C6297:	26-49	711-730	NAP	g3451463	344	113	2.00E-32	34	57	(AL031349) hypothetical protein		
			2531..3687									[Schizosaccharomyces pombe]		
20654	ENU04448	ANI61C1107	185-204	617-641	NAP	g3914212	470	188	5.00E-47	49	19	5-oxoprolinase (5-oxo-L-prolinase) (pyroglutamase) (5-opase)	[Rattus norvegicus]	
			1..831									(U58946) transposase [Aspergillus awamori]		
20655	ENU04449	ANI61C181:2	22-49	705-730	NAP	g1805251	198	104	1.00E-21	27	41	(L07545) A 'c' was inserted after nt 369 (=nt 10459 in genomic sequence (M10126)) to correct -1 frameshift probably due to gel compression		
			89..1636									[Leishmania tarentolae]		
20656	ENU04450	ANI61C5884:			NAP	g340613	183	38	0.092	27	78	(Z98601) zinc finger protein		
			3718..4724									[Schizosaccharomyces pombe]		
20657	ENU04451	ANI61C4283:	27-54	450-469	NAP	g2330797	199	71	1.00E-17	37	62	(AB018352) KIAA0809 protein		
			2133..2763									[Homo sapiens]		
20658	ENU04452	ANI61C1138:	22-49	804-829	NAP	g3882339	82	139	2.00E-32	33	18	(AL035394) putative receptor kinase		
			12005..10799									[Arabidopsis thaliana]		
20659	ENU04453	ANI61S3751:	36-59	467-486	NAP	g4454043	916	333	7.00E-91	97	28	SYG1 protein	[Saccharomyces cerevisiae]	
			542..1									(U79250) glycerol-3-phosphate dehydrogenase	[Homo sapiens]	
20660	ENU04454	ANI61C2071:	106-127	671-690	NAP	g731805	463	192	2.00E-48	45	26	"2,5-dichloro-2,5-cyclohexadiene-1,4-diol dehydrogenase (2,5-DDOL dehydrogenase) [Sphingomonas paucimobilis]"		
			781..1									(AE000557) cyclopropane fatty acid synthase (cfa)	[Helicobacter pylori]	
20661	ENU04455	ANI61C2856:	118-138	628-655	NAP	g1806628	488	115	1.00E-51	49	50	(Z98602) purine nucleotide binding protein fets5	[Schizosaccharomyces pombe]	
			684..1									hypothetical 63.4 KD protein in SMY2-RPS101 intergenic region	[Saccharomyces cerevisiae]	
20662	ENU04456	ANI61C6770:	102-122	392-413	NAP	g1708835	188	71	3.00E-12	40	48			
			1..434											
20663	ENU04457	ANI61C2510:	43-62	416-437	NAP	g2313520	165	85	5.00E-16	30	45			
			557..1											
20664	ENU04458	ANI61C910:2			NAP	g2330815	137	73	7.00E-13	41	36			
			458..2116											
20665	ENU04459	ANI61C8051:	44-63	803-826	NAP	g586312	641	80	3.00E-21	33	43			
			1749..197											

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat	Blast Score	Blast Prob	% id	cvrg	Description
20666	ENU04460	ANI61C2836: 653..1378		NAP		g1175939	331	86	1.00E-32	40	58		hypothetical 41.9 KD protein in HAC1-CAK1 intergenic region
20667	ENU04461	ANI61C2759: 115-134 581-608	1..716	NAP		g2492763	395	141	8.00E-38	48	67		[Saccharomyces cerevisiae] hypothetical oxidoreductase in MRPL44-MTF1 intergenic region
20668	ENU04462	ANI61C1083 5:3653..3984	30-49	282-301	NAP	g1483145	93	36	0.002	29	97		[Saccharomyces cerevisiae] (D64008) Cytochrome b5 [Ascaris suum]
20669	ENU04463	ANI61C1020 8:1..3278	29-56	804-829	NAP	g1723687	754	129	2.00E-29				hypothetical 140.5 KD protein in CTT1-PRP31 intergenic region
20670	ENU04464	ANI61C4296: 203-222 465-484	1465..856	NAP		g3242972	416	109	1.00E-23	54	25		(AF069523) heat shock protein Hsp88 [Neurospora crassa]
20671	ENU04465	ANI61C6540: 45-64 1520..2718	778-797	NAP		g3218400	425	145	2.00E-40	38	75		(AL023860) ser-thr protein kinase [Schizosaccharomyces pombe]
20672	ENU04466	ANI61C4932: 22-46 720..3626	801-828	NAP		g731882	293	101	9.00E-21				hypothetical 195.1 KD protein in DNA43-UBI1 intergenic region
20673	ENU04467	ANI61C1926: 105-132 1987..1581	366-386	NAP		g3687497	168	66	2.00E-12	44	67		[Saccharomyces cerevisiae] (AL031788) putative mitochondrial inner membrane protease subunit 2
20674	ENU04468	ANI61C8052: 22-48 755..2503	720-744	NAP		g4502323	585	168	6.00E-41	40	17		[Schizosaccharomyces pombe] "ATPase, Cu++ transporting, beta polypeptide (Wilson disease) [Homo sapiens]"
20675	ENU04469	ANI61S1734: 1..854		NAP		g100687	405	37	0.16	41	74		hydroxyproline-rich glycoprotein - rice [Oryza sativa]
20676	ENU04470	ANI61C724: 2 882..1	22-45	807-826	NAP	g2493965	2089	317	5.00E-86	58	20		xanthine dehydrogenase (purine hydroxylase I) [Emericella nidulans] (U62929) multidrug resistance protein 1 [Filobasidiella neoformans]
20677	ENU04471	ANI61C1117 1:1..795	110-129	683-706	NAP	g2668553	311	89	5.00E-26	33	18		(X89442) peptide synthetase [Metarhizium anisopliae] (AJ005258) amyR [Aspergillus oryzae]
20678	ENU04472	ANI61C1823: 1..1738	22-48	748-767	NAP	g2342601	738	137	9.00E-32	29	5		
20679	ENU04473	ANI61C5324: 43-62 1589..1	722-741	NAP		g3043376	1653	240	e-100	75	42		

Seq num	Seq id	Contig source	Primer pos	Primer pos	Selection Basis	Database Hit	atn	Blast Score	Blast Prob	% id	% vrg	Description
20680	ENU04474	ANI61C6771:	5	3	5	gb 879362	341	116	1.00E-25	33	52	"(Z81113) similar to Dnal, prokaryotic heat shock protein, Zinc finger, C2H2 type; cDNA EST yk290e12.5 comes from this gene; cDNA EST yk290e12.3 comes from this gene; cDNA EST yk447h4.5 comes from this gene; cDNA EST yk474e4.5 c... [ ]"
1090..1			24..44	675-697	NAP							(AF063864) essential nuclear protein Mcm3p [Schizosaccharomyces pombe]
20681	ENU04475	ANI61C1089	215-234	464-484	NAP	g3139137	800	308	7.00E-85	84	22	"(AC007296) Similar to gb JU90212 DNA binding protein ACBF from Nicotiana tabacum and contains 3 PF 00076 RNA recognition motif domains. ESTs gb T44278, gb R65195, gb N65904, gb H37499, gb R90487, gb N95952, gb T4427... [ ]"
			9.586..1			g4835793	148	77	8.00E-14			(D87686) KIAA0017 protein [Homo sapiens]
20682	ENU04476	ANI61S4441:	554..1		NAP	g2135765	221	44	0.00002	35	8	"mucin 2 precursor, intestinal - human fragments [ ]"
			1.775			g1711467	277	122	2.00E-27	34	43	dibenzothiophene desulfurization enzyme A [Rhodococcus sp.] (U97002) similar to acyl-CoA dehydrogenases and epoxide hydrolases [Caenorhabditis elegans] (AL008967) ltp1 [Mycobacterium tuberculosis] (AFI31877) amino-deoxyarabinohexitulosonate-7-phosphate synthase [Streptomyces collinus]
20683	ENU04477	ANI61C9025:	37-56	792-812	NAP	g2540219	1169	130	6.00E-59	49	22	PF 00076 RNA recognition motif domains. ESTs gb T44278, gb R65195, gb N65904, gb H37499, gb R90487, gb N95952, gb T4427... [ ]"
			1337..1									(D87686) KIAA0017 protein [Homo sapiens]
20684	ENU04478	ANI61S1996:			NAP	g1938424	285	122	1.00E-27	51	13	enzyme A [Rhodococcus sp.] (U97002) similar to acyl-CoA dehydrogenases and epoxide hydrolases [Caenorhabditis elegans] (AL008967) ltp1 [Mycobacterium tuberculosis] (AFI31877) amino-deoxyarabinohexitulosonate-7-phosphate synthase [Streptomyces collinus]
			1..775			g2624312	413	105	1.00E-40	53	40	UDP-glucose dehydrogenase [Homo sapiens]
20685	ENU04479	ANI61C2726:	102-121	466-486	NAP	g2132651	309	84	2.00E-26	32	35	probable membrane protein YLL028w
			601..1									- yeast (Saccharomyces cerevisiae) [Saccharomyces cerevisiae]
20686	ENU04480	ANI61S2694:	38-65	403-429	NAP	g501027	147	31	4.6	33	99	(U01849) ORF2 [Trypanosoma brucei]
			450..1									
20687	ENU04481	ANI61C7219:	2951-2457		NAP	g4884833	322	103	7.00E-27			
20688	ENU04482	ANI61S4608:	209-228	362-386	NAP							
			431..1									
20689	ENU04483	ANI61C9107:	22-45	807-829	NAP							
			8199..9462									
20690	ENU04484	ANI61C4377:	30-51	583-610	NAP							
			1961..1330									
20691	ENU04485	ANI61S591:3			NAP							
			41..767									

Seq num	Seq id	Contig source	5 pos	3 pos	Primer Basis	Selection Database Hit	ncbi gi	aat	Blast Score	Blast Prob	% id	% cvrg	Description
20692	ENU04486	ANI61C7389:	22..45	636..663	NAP	g2133317	1829	407	e-113	67	38	NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) 78K chain precursor - Neurospora crassa [Neurospora crassa]	
20693	ENU04487	ANI61C2578:	26..45	809..829	NAP	g2909569	118	40	0.000003			(AL021925) hypothetical protein Rv2263 [Mycobacterium tuberculosis]	
20694	ENU04488	ANI61C8776:	26..45	795..815	NAP	g1346422	1459	317	8.00E-86	60	46	serine palmitoyltransferase 2 (long chain base biosynthesis protein 2) (SPT2) [Schizosaccharomyces pombe] actin-like protein ARP5 [Saccharomyces cerevisiae]	
20695	ENU04489	ANI61C510:1	24..46	777..796	NAP	g1730738	805	85	2.00E-19	38	35	(Z97210) hypothetical protein [Schizosaccharomyces pombe]	
20696	ENU04490	ANI61C1122	9..3734..2965		NAP	g2239223	347	77	2.00E-13	40	98	beta-glucosidase precursor (gentiobiase) (cellobiase) (beta-D-glucoside glucohydrolase) [Kluyveromyces marxianus]	
20697	ENU04491	ANI61C3235:	33..52	755..780	NAP	g114971	983	96	1.00E-36	34	32	cutinase transcription factor 1 beta [Fusarium solani f. sp. pisi]	
20698	ENU04492	ANI61C415:2	22..49	615..642	NAP	g1706177	186	62	1.00E-13	34	21	(Z99112) chromosome segregation SMC protein homolog [Bacillus subtilis]	
20699	ENU04493	ANI61S851:7	19..1		NAP	g2633966	304	102	3.00E-21	35	20	hypothetical 81.8 KD protein in YPT52-DBP7 intergenic region [Saccharomyces cerevisiae]	
20700	ENU04494	ANI61C3482:	22..45	648..669	NAP	g549770	377	79	3.00E-22			translation initiation factor EIF-2B alpha subunit (EIF-2B GDP-GTP exchange factor) (guanine nucleotide exchange factor subunit GCN3) (GCD complex subunit GCN3) (transcriptional activator GCN3) [Saccharomyces cerevisiae]	
20701	ENU04495	ANI61C7:378	54..73	804..829	NAP	g121065	548	196	2.00E-49			(AJ007564) Sls2 [Yarrowia lipolytica]	
20702	ENU04496	ANI61C8363:	41..61	712..735	NAP	g2820457	817	214	7.00E-55	47	27	(AF091042) putative cercosporin transporter [Cercospora kikuchii]	
20703	ENU04497	ANI61S1437:	47..66	307..326	NAP	g2885836	265	96	2.00E-19	39	28	"Chain A, Phenol Hydroxylase From Trichosporon Cutaneum [" (AC000133) ORF [Emericella nidulans]	
20704	ENU04498	ANI61C4370:	37..56	655..679	NAP	g3318897	362	138	7.00E-32	44	31		
20705	ENU04499	ANI61C1120	25..51	510..529	NAP	g1870215	1027	291	2.00E-78	95	53		
			61..578										

Seq num	Seq id	Contig source	5 pos	3 pos	Basis	Primer	Primer	Selection	aat	Blast	Blast	%	
								Database Hit	.ncbi gi	Score	Score	id	cvg
									g2342601	827	286	2.00E-76	53
20706	ENU04500	ANI61C1014	37..56	718..739	NAP							5	
			21..5159										[Metarhizium anisopliae] (X05204) arom polypeptide
20707	ENU04501	ANI61C443:1	..651	26..50	567..586	NAP			g2834343	1013	394	e-109	98
			614..1100									13	[Emecicella nidulans]
20708	ENU04502	ANI61C5958:	59..78	457..479	NAP				g1293655	410	178	3.00E-44	55
			1814..2650									25	(US1327) versicolorin B synthase [Aspergillus parasiticus]
20709	ENU04503	ANI61C7613:	32..51	706..725	NAP				g730506	101	95	7.00E-19	22
			13..658									63	nuclear division RFT1 protein [Kluyveromyces lactis]
20710	ENU04504	ANI61C1839:	24..47	592..612	NAP				g3608397	83	68	5.00E-11	32
												52	(AF071085) putative dTDP-4-keto-L-rhamnose reductase [Enterococcus faecalis] (U51327) versicolorin B synthase [Aspergillus parasiticus]
20711	ENU04505	ANI61C5791:	58..84	531..550	NAP				g1293655	292	125	3.00E-28	41
			587..1									29	(L40632) ankyrin 3 [Mus musculus]
20712	ENU04506	ANI61C262:4	54..73	798..820	NAP				g710551	282	76	6.00E-18	29
			131..2626									15	"2,5-dichloro-2,5-cyclohexadiene-1,4-diol dehydrogenase (2,5-DDOL dehydrogenase) [Sphingomonas paucimobilis]"
20713	ENU04507	ANI61C7276:	3527..4344		NAP				g1708836	255	136	2.00E-31	35
												98	"2,5-dichloro-2,5-cyclohexadiene-1,4-diol dehydrogenase (2,5-DDOL dehydrogenase) [Sphingomonas paucimobilis]"
20714	ENU04508	ANI61C1144	61..80	514..538	NAP				g2811058	369	139	1.00E-32	42
			5..672..1255									51	hypothetical 39.5 KD protein in SIGZ-CSN intergenic region [Bacillus subtilis]
20715	ENU04509	ANI61C1164:	22..45	803..829	NAP				g131769	1624	320	7.00E-87	97
			493..1695									70	QUTG protein []
20716	ENU04510	ANI61C1065	30..51	719..738	NAP				g3810843	2437	274	5.00E-73	65
			4..5634..8953									25	"(AL032684) putative yeast cell division control protein 68 homolog, putative transcriptional activator [Schizosaccharomyces pombe]" (AF077409) similar to reverse transcriptases (PFam: rvthmm, score: 60.13) [Arabidopsis thaliana]"
20717	ENU04511	ANI61S3760:	26..45	515..534	NAP				g3319372	547	133	1.00E-30	52
			1..597									17	
20718	ENU04512	ANI61C7330:	69..88	791..810	NAP				g114967	1244	227	7.00E-59	45
			1..2372									33	beta-glucosidase (gentiobiose) (cellobiose) (beta-D-glucoside glucohydrolase) [Agrobacterium tumefaciens] (AL031179) similarity to phosphomannomutases [Schizosaccharomyces pombe]
20719	ENU04513	ANI61C8930:	26..45	483..502	NAP				g3395586	234	113	1.00E-24	42
			1243..1956									29	

Seq num	Seq id	Contig source	5 pos	Primer 3 pos	Primer Basis	Selection Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
20720	ENU04514	ANI61C1385:	22-42	704-731	NAP		g2467275	484	143	1.00E-33	32	56	(Z99759) serine/threonine-protein kinase [Schizosaccharomyces pombe]
20721	ENU04515	ANI61C1019	25-52	792-816	NAP		g3850093	138	48	0.00006	30	42	(AL033389) putative allantoin permease [Schizosaccharomyces pombe]
20722	ENU04516	ANI61C1039	70-89	618-637	NAP		g1711561	582	126	2.00E-28	39	45	sugar transporter STL1 [Saccharomyces cerevisiae]
20723	ENU04517	ANI61C7331:	24-43	764-783	NAP		g127568	298	124	9.00E-28	31	86	interferon-induced GTP-binding protein MX [Perca fluviatilis] hypothetical 433.2 KD protein in HXT5-NRK1 intergenic region [Saccharomyces cerevisiae]
20724	ENU04518	ANI61C8161:	22-46	721-740	NAP		g731689	1445	313	9.00E-85	51	7	
20725	ENU04519	ANI61C1040	5-4687..4196		NAP		g12688	626	182	1.00E-58	89	46	(Y00650) URF 1 [Emericella nidulans]
20726	ENU04520	ANI61C9790:	29-56	802-829	NAP		g731871	1132	153	1.00E-36	32	11	hypothetical 269.9 KD protein in FKH1-MET18 intergenic region [Saccharomyces cerevisiae]
20727	ENU04521	ANI61C1128	23-43	725-747	NAP		g3738194	664	153	1.00E-46	42	40	(AL031854) hypothetical protein [Schizosaccharomyces pombe] (X892442) peptide synthetase [Metarrhizium anisopliae]
20728	ENU04522	ANI61C5443:	27-54	804-824	NAP		g2342601	618	206	2.00E-52	40	5	(Z98974) putative cytochrome p450 [Schizosaccharomyces pombe] (AL022537) putative protein [Arabidopsis thaliana]
20729	ENU04523	ANI61C1558:	22-48	805-829	NAP		g2388903	671	229	2.00E-59	53	49	(AL0223706) hypothetical protein [Schizosaccharomyces pombe] (U40374) amino-glycoside 3'-phosphotransferase [Cloning vector pMH30]
20730	ENU04524	ANI61C6309:	52-71	770-788	NAP		g3063700	160	78	5.00E-15	32	15	Human 17-Beta-Hydroxysteroid-Dehydrogenase Type 1 Complexed With 17-Beta-Estradiol []
20731	ENU04525	ANI61C5366:	1351..2378	657-676	NAP		g3169096	785	204	6.00E-52	46		
20732	ENU04526	ANI61C7102:	72-93	604-626	NAP		g1942383	154	82	3.00E-15	40	31	
20733	ENU04527	ANI61S4490:	213-231	356-375	NAP		g1244642	89	51	0.000005	32	43	
			153..507										
20734	ENU04528	ANI61C9993:	27-46	801-828	NAP		g1175408	612	34	0.033			hypothetical 107.3 KD TRP-ASP repeats containing protein C31A2.14 in chromosome I [Schizosaccharomyces pombe]
20735	ENU04529	ANI61C4851:	59-78	602-626	NAP		g3550602	257	118	5.00E-26	36	22	(AI006710) phosphatidylinositol 3-kinase [Rattus norvegicus]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Basis	Selection Database Hit	aat	Blast Score	Blast Prob	% id	% cvrg	Description	
20736	ENU04530	ANI61C3177:	23-48	770-789	NAP	g2914053	2015	426	e-119	76	30	DNA mismatch repair protein MSH2	
20737	ENU04531	ANI61C1056:	35-55	531-558	NAP	g2501152	291	134	4.00E-31	48	33	[Neurospora crassa] threonine synthase	
20738	ENU04532	ANI61S4655:	830..314		NAP	g2131314	127	41	0.000000	37	37	[Schizosaccharomyces pombe] hypothetical protein YD8142A.01 - yeast (Saccharomyces cerevisiae) (fragment) [AC00133] ORF [Emericella nidulans]	
20739	ENU04533	ANI61C1355:	22-48	303-324	NAP	g1870215	851	342	9.00E-94	99	46	(AF023634) hypothetical protein	
20740	ENU04534	ANI61C5665:	1..1604	805-824	NAP	g3150253	819	176	9.00E-52	42	24	[Schizosaccharomyces pombe]	
20741	ENU04535	ANI61C3240:	54-73	521-540	NAP	g120625	456	180	7.00E-45	60	100	G10 protein [Xenopus laevis]	
20742	ENU04536	ANI61S3332:	3384..3956	47-67	198-223	NAP	g2911462	398	107	3.00E-21	54	47	cutinase precursor (L1) [Aspergillus oryzae]
20743	ENU04537	ANI61C9348:	1..380	122-143	333-359	NAP	g2911462	398	107	2.00E-37	73	17	(AF046923) serine/threonine protein kinase [Colletotrichum trifolii]
20744	ENU04538	ANI61C4409:	813..2276	22-49	765-784	NAP	g4176523	341	104	6.00E-22	29	45	(AL035263) hypothetical protein [Schizosaccharomyces pombe]
20745	ENU04539	ANI61C9831:	1646..1	22-44	623-642	NAP	g2581903	480	124	9.00E-28	35	38	(AL031545) DEAD box ATP-dependent RNA helicase [Schizosaccharomyces pombe]
20746	ENU04540	ANI61C7608:	884..1	37-61	724-749	NAP	g4102980	121	42	0.005	20	49	(AF019082) virulent strain associated lipoprotein [Borrelia burgdorferi]
20747	ENU04541	ANI61C1617:	1230..1561	22-49	454-479	NAP	g464991	142	80	8.00E-15	40	43	ubiquitin carboxyl-terminal hydrolase YUH1 (ubiquitin thioesterase)
20748	ENU04542	ANI61C8017:	547..1	39-66	424-446	NAP	g4758430	256	93	1.00E-24			[Saccharomyces cerevisiae] geranylgeranyl diphosphate synthase [Homo sapiens]
20749	ENU04543	ANI61C4194:	2114..2587	374-393	NAP	g1168953	76	54	0.000000	32	37	citrate lyase beta chain (citrase) (citrulline subunit) [Klebsiella pneumoniae]	
20750	ENU04544	ANI61S2295:			NAP	g100753	167	46	0.000000	36	66	hydroxyproline-rich glycoprotein - sorghum [Sorghum bicolor]	
20751	ENU04545	ANI61C7450:	1431..2454	23-44	807-829	NAP	g1256839	868	191	4.00E-73	63	52	(U53329) Ran1-like protein kinase [Fusarium solani f. sp. pisii]
20752	ENU04546	ANI61C3751:	656..219	68-87	416-435	NAP	g4902874	112	48	0.00004			"(AJ242575) oxide-reductase enzyme, putative [Sinorhizobium meliloti]"

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20753	ENU04547	ANI61C1853:	25-52	411-438	NAP	g3914278	264	122	1.00E-27	55	34	cingulata]	[Glomerella pectate lyase B precursor]
20754	ENU04548	ANI61C5321:	22-49	805-829	NAP	g3183173	591	187	6.00E-48	52	53	"seryl-TRNA synthetase, cytoplasmic (serine--tRNA ligase) (SERRS) [Schizosaccharomyces pombe] (Z68905) ATP-binding cassette multidrug transporter [Emericella nidulans]	
20755	ENU04549	ANI61C1011	24-47	481-499	NAP	g1834342	1043	248	e-106	92	15	(AL031536) putative transcription factor of the GCS1-GLO3-SPS18 family [Schizosaccharomyces pombe]	
20756	ENU04550	ANI61C1045	6:..710		NAP	g3560208	274	95	7.00E-19	33	34	phosphate-repressible phosphate permease [Neurospora crassa]	
20757	ENU04551	ANI61C2588:	22-49	628-647	NAP	g130117	815	218	3.00E-79	69	39	ubiquitin-conjugating enzyme E2-18 KD (ubiquitin-protein ligase) (ubiquitin carrier protein) [Schizosaccharomyces pombe]	
20758	ENU04552	ANI61C5294:	22-46	498-521	NAP	g2501434	162	103	2.00E-22	30	92	permease [Neurospora crassa]	
			996..455										
20759	ENU04553	ANI61C6129:	72-99	412-431	NAP	g730443	80	47	0.000000	34	70	quinone oxidoreductase (NADPH:quinone reductase) (zeta-crystallin homolog protein) [	
20760	ENU04554	ANI61C1614:	56-75	777-796	NAP	g3646379	1450	199	8.00E-95	75	42	(A1001540) phenylacetyl-CoA ligase [Penicillium chrysogenum]	
20761	ENU04555	ANI61C5779:	71-90	773-799	NAP	g2443355	723	108	4.00E-23			(AB003395) ent-Kaurene synthase [Phaeosphaeria sp. L487]	
20762	ENU04556	ANI61C1114	23-42	788-815	NAP	g2625138	224	116	1.00E-25	34	14	(AF032443) ABC1 transporter; ABC-type ATPase [Magnaporthe grisea]	
20763	ENU04557	ANI61C7681:	22-49	757-780	NAP	g1817584	917	117	8.00E-26	28	19	(Y08991) adaptor protein [Homo sapiens]	
20764	ENU04558	ANI61C1919:	221-240	765-784	NAP	g4165293	962	341	2.00E-99	71	28	(X58824) cdc21 protein	
20765	ENU04559	ANI61C1065	26-45	767-786	NAP	g1346521	1027	317	8.00E-86	78	62	S-adenosylmethionine synthetase (methionine adenosyltransferase) (ADOMET synthetase) [Neurospora crassa]	
20766	ENU04560	ANI61C2670:	101-120	610-631	NAP	g604369	928	215	6.00E-70	53	34	(U17857) hMLH1 gene product	
20767	ENU04561	ANI61C4238:	22-42	772-793	NAP	g3023682	998	332	9.00E-94	79	30	[Homo sapiens]	
			1645..2569										elongation factor 2 (EF-2) [Candida albicans]

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20768	ENU04562	ANI61S2955: 1..531			NAP	g4218005	140	43	0.002	25	25	(AC006135) putative vicilin storage protein (globulin-like) [Arabidopsis thaliana]	
20769	ENU04563	ANI61C1957: 22-41	771-795	NAP		g461623	1173	92	2.00E-36	68	21	beta-galactosidase precursor (lactase) [Aspergillus niger]	
20770	ENU04564	ANI61S3141: 666..1	182-209	612-631	NAP	g2062165	797	330	6.00E-90	87	38	(AC001645) jasmonate inducible protein isolog [Arabidopsis thaliana] (AL033389) putative yeast cell division cycle CDC50 homolog	
20771	ENU04565	ANI61C3056: 33-60	801-820	NAP		g2850089	772	183	6.00E-61	52	62	[Schizosaccharomyces pombe]	
20772	ENU04566	ANI61C8012: 5408..4491	22-45	810-829	NAP	g2842699	518	173	2.00E-42	54	43	putative ubiquitin carboxyl-terminal hydrolase C6G9.08 (ubiquitin thioesterase) (ubiquitin-specific processing protease) (deubiquitinating enzyme) [Schizosaccharomyces pombe] (AL031261) conserved hypothetical protein [Schizosaccharomyces pombe] (U08104) PHOG [Penicillium chrysogenum]	
20773	ENU04567	ANI61S3854: 586..90	168-193	399-418	NAP	g3417425	202	53	5.00E-14	36	50	hypothetical 81.2 KD protein in MESI-FOL2 intergenic region [Saccharomyces cerevisiae]	
20774	ENU04568	ANI61C1100: 0-8321..9087	33-53	598-622	NAP	g643443	769	225	1.00E-78	72	39	hypothetical protein C56F8.17C in chromosome I [Schizosaccharomyces pombe]	
20775	ENU04569	ANI61C1131: 81..839	103-120	795-817	NAP	g1723773	335	144	7.00E-34	36	39	(Z98849) putative centromere protein [Schizosaccharomyces pombe]	
20776	ENU04570	ANI61S2538: 671..1	220-247	585-605	NAP	g1723448	242	120	1.00E-26	43	31	galactose-proton symport (galactose transporter) [Escherichia coli] (AL009197) hypothetical protein phosphatase [Schizosaccharomyces pombe]	
20777	ENU04571	ANI61C5097: 525..1	97-118	482-503	NAP	g2370479	146	71	7.00E-12	29	21	"probable T-complex protein 1, beta subunit (TCP-1-beta) (CCT-beta)" [Schizosaccharomyces pombe]" (U61949) Similar to cytidine deaminase. [Caenorhabditis elegans]	
20780	ENU04574	ANI61C9830: 1643..363	33-52	683-702	NAP	g1729868	1503	367	e-101	72	53		
20781	ENU04575	ANI61S3302: 567..1	180-207	443-470	NAP	g1397290	139	44	4.00E-11	47	67		

Seq num	Seq id	Contig source	5 pos	3 pos	Basis	Primer	Primer	Selection	aat	Blast	Blast	%		
						Database	Hit	ncbi gi	Score	Score	Prob	id	cvg	
20782	ENU04576	ANI61C3245:	22-42	709-735	NAP	g2342601	1176	183	1.00E-45	35	5	(X89442) peptide synthetase		
20783	ENU04577	ANI61C7535:	2557..1		NAP	g4481947	211	65	4.00E-21	36	99	[Metarhizium anisopliae] (AL035637) hypothetical protein.		
20784	ENU04578	ANI61C1091	33-52	784-803	NAP	g4454039	482	169	2.00E-41	47	31	[Schizosaccharomyces pombe] (AL035394) putative Na+/H+ - exchanging protein [Arabidopsis thaliana]		
20785	ENU04579	ANI61C6944:	38-57	781-803	NAP	g3777495	1275	284	7.00E-76	65	27	(U92083) calcium transporting ATPase [Pichia angusta]		
20786	ENU04580	ANI61C7384:	23-46	704-729	NAP	g128397	962	334	3.00E-91	99	100	nuclear movement protein NUDC [Emericella nidulans]		
20787	ENU04581	ANI61C7182:	3181..3930		NAP	g1870209	235	74	8.00E-13	46	30	(AC000133) ORF [Emericella nidulans]		
20788	ENU04582	ANI61C1122	2146..2514	27-54	761-780	NAP	g4836423	138	34	1.4		(AF119670) integral membrane protein [Magnaporthe grisea]		
20789	ENU04583	ANI61C7682:	43002..4504	78-105	749-776	NAP	g4164428	473	205	5.00E-52	49	19	(AL035247) putative pre-mRNA splicing factor rna helicase [Schizosaccharomyces pombe] (AJ012752) maltose permease [Saccharomyces cerevisiae]	
20790	ENU04584	ANI61C8016:	4149..2537	22-44	767-794	NAP	g3901117	970	135	2.00E-44	38	45	112.3 KD protein in PYK1-SNC1 intergenic region [Saccharomyces cerevisiae]	
20791	ENU04585	ANI61C1556:	505..2127	66-85	772-791	NAP	g1723187	505	80	3.00E-14	41	24	"(U75347) fatty acid synthase, beta subunit [Emericella nidulans]" probable methionyl-tRNA formyltransferase precursor [Saccharomyces cerevisiae]	
20792	ENU04586	ANI61C5421:	663..1	118-137	528-546	NAP	g1805262	336	147	6.00E-35	35	10	"(U75347) fatty acid synthase, beta subunit [Emericella nidulans]" probable methionyl-tRNA formyltransferase precursor [Saccharomyces cerevisiae]	
20793	ENU04587	ANI61C6728:	1..690	85-111	630-649	NAP	g418345	129	72	4.00E-12	39	46	(M31013) nonmuscle myosin heavy chain (NMHC) [Homo sapiens]	
20794	ENU04588	ANI61C5679:	1..1011	22-47	723-742	NAP	g189036	121	71	1.00E-11	19	20	(AF072541) xylose dehydrogenase; XDH [Galactocandida mastotermitis] (U62931) multidrug resistance protein 1 [Aspergillus flavus]	
20795	ENU04589	ANI61C2763:	1301..950	55-74	307-331	NAP	g3264834	279	118	2.00E-26	44	33	(AL033503) transcription regulatory protein [Candida albicans]	
20796	ENU04590	ANI61C7721:	441..1325	23-44	803-829	NAP	g2673947	287	98	1.00E-22	31	20	hypothetical [Aspergillus flavus]	
20797	ENU04591	ANI61C1672:	599..1	23-50	430-449	NAP	g3859681	485	128	2.00E-49	50	60	hypothetical 66.5 KD protein F02A9.5 in chromosome III []	
20798	ENU04592	ANI61C9504:	1510..986	49-72	480-504	NAP	g465847	336	83	4.00E-33				

Seq num	Seq id	Contig source	5 pos	3 pos	Primer Basis	Primer Database	Selection ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
20799	ENU04593	ANI61C9338:	2245	711-737	NAP	g2276359	1861	273	1.00E-72	38	11	(Z97992) putative phosphatidylinositol 3-kinase [Schizosaccharomyces pombe]	
20800	ENU04594	ANI61C6660:	45-64	453-477	NAP	g1709760	138	131	3.00E-30	31	100	(X56175) ORF 2 (AA 1 - 109) [Escherichia coli]	
20801	ENU04595	ANI61C9595:	106-128	389-414	NAP	g1709760	271	87	1.00E-21	50	47	putative proteasome component PRE6 (macropain subunit) (multicatalytic endopeptidase complex subunit) [Schizosaccharomyces pombe] (U53155) No definition line found	
20802	ENU04596	ANI61C6006:	22-43	709-736	NAP	g1255430	348	125	4.00E-28	37	71	[Caenorhabditis elegans] (Z81458) similar to transposable element [Caenorhabditis elegans] "proteasome (prosome, macropain) 26S subunit, non-ATrase, 12 [Homo sapiens]" KD (ubiquitin-protein ligase) (ubiquitin carrier protein) [Schizosaccharomyces pombe]	
20803	ENU04597	ANI61C7769:	1865..985		NAP	g3873958	152	92	6.00E-18	26	79	[Trichoderma harzianum] (AF074944) RRM3/PF1 helicase homolog [Schizosaccharomyces pombe]	
20804	ENU04598	ANI61C4415:	22-44	698-720	NAP	g4506221	665	60	2.00E-31	40	50	alpha-latrotoxin precursor - black widow spider [Latrodectus tredecimguttatus]	
20805	ENU04599	ANI61C5780:	23-47	518-545	NAP	g2501434	521	125	3.00E-53	63	100	hypothetical 53.3 KD protein in HXT8-CAN1 intergenic region [Saccharomyces cerevisiae]	
20806	ENU04600	ANI61C7849:	30-57	712-731	NAP	g3947746	527	220	1.00E-56	56	29	hypothetical 44.9 KD protein in SEC9-MSB2 intergenic region [Saccharomyces cerevisiae]	
20807	ENU04601	ANI61C7563:	31-50	334-360	NAP	g3309657	372	159	1.00E-38	60	15	(AL031854) putative ras related GTP-binding protein [Schizosaccharomyces pombe]	
20808	ENU04602	ANI61C1080	25-44	774-794	NAP	g102827	63	72	4.00E-12				
20809	ENU04603	ANI61C6782:	1..1076	778-805	NAP	g731421	377	98	2.00E-34	38	47		
20810	ENU04604	ANI61C4065:	1..443		NAP	g1723643	217	78	4.00E-20	41	33		
20811	ENU04605	ANI61C5853:	22-45	807-826	NAP	g3738190	706	196	2.00E-49	43	82		

Seq num	Seq id	Contig source	5 pos	3 pos	Basis	Primer	Primer	Selection	Database	Hit	ncbi gi	aat	Blast Score	Blast Prob	% id	% cvrg	Description
20812	ENU04606	ANI61C1054	39-56	724-746	NAP				g2956769	1614	169	9.00E-60	54	21	(AL072103) phosphatidylinositol phosphate phosphatase; synaptojanin-like [Schizosaccharomyces pombe]		
20813	ENU04607	ANI61C7324:	50-69	670-690	NAP	4754..5464			g2408075	436	188	4.00E-47	41	98	(Z99167) hypothetical conserved protein [Schizosaccharomyces pombe] (Saccharomyces cerevisiae)		
20814	ENU04608	ANI61C2440:	186-213	589-608	NAP	1..643			g2132014	175	92	3.00E-18	37	39	[Saccharomyces cerevisiae] (Y16563) Bassoon [Rattus norvegicus]		
20815	ENU04609	ANI61S1755:			NAP	1..588			g3413504	91	44	0.0007	22	4			
20816	ENU04610	ANI61C4426:	41-64	717-743	NAP	844..1			g2147805	319	161	5.00E-39	36	33	NarB protein - Oscillatoria chalybea [Oscillatoria chalybea]		
20817	ENU04611	ANI61C3356:	27-48	723-749	NAP	976..1			g1708850	222	93	3.00E-18	38	34	probable leukotriene A-4 hydrolase (LTA-4 hydrolase) (leukotriene A(4) hydrolase) [Saccharomyces cerevisiae] MSS51 protein [Saccharomyces cerevisiae]		
20818	ENU04612	ANI61C4165:	28-47	774-793	NAP	3186..2199			g417318	589	185	3.00E-46	44	59			
20819	ENU04613	ANI61C1138	27-46	398-416	NAP	1..971..1478			g1172568	198	80	6.00E-17	48	73	low molecular weight phosphotyrosine protein phosphatase (low molecular weight cytosolic acid phosphatase) (PTPASE) (small tyrosine phosphatase) [Schizosaccharomyces pombe] (D50497) chloride channel (ClC-5) [Rattus rattus]		
20820	ENU04614	ANI61C5427:	209-228	366-385	NAP	1940..1520			g1549231	121	38	0.000003	31	18	probable membrane protein YPL183c - yeast [Saccharomyces cerevisiae]		
20821	ENU04615	ANI61C1005	23-47	800-822	NAP	7:2999..584			g2132992	242	86	3.00E-16	27	25	[Saccharomyces cerevisiae] (AC000133) ORF [Emericella nidulans]		
20822	ENU04616	ANI61C1355:	203-222	459-478	NAP	2053..2529			g1870229	817	300	3.00E-81	97	100	"(L76169) reverse transcriptase, RNaseH [Glomerella cingulata]" (U58946) transposase [Aspergillus awamori]		
20823	ENU04617	ANI61C5998:	22-42	802-821	NAP	7885..4728			g1166378	525	86	3.00E-16			(AJ001421) Rer1 protein [Homo sapiens]		
20824	ENU04618	ANI61C1102	6:1..629	107-127	506-527	NAP	22-43		g1805251	250	120	9.00E-27	35	37	(U20323) ankyrin-like protein [Saccharomyces cerevisiae]		
20825	ENU04619	ANI61C7487:	243..1014	713-740	NAP	g2385369	466	146	9.00E-41	53	98	ematin synthetase - fungus (Fusarium script) [Fusarium script]					
20826	ENU04620	ANI61C2085:	22-48	460-479	NAP	952..441			g665573	64	44	0.0006	31	98			
20827	ENU04621	ANI61C3624:	35-54	630-649	NAP	5678..1			g481866	2935	223	8.00E-62	44	8			

Seq num	Seq id	Contig source	5 pos	3 pos	Basis	Primer	Primer	Selection	aat	Blast	Blast	%	
						Database	Hit	nebi gi	Score	Score	Prob	id	cvg
20828	ENU04622	ANI61C4110:	73-100	295-317	NAP	1..415	g2130022	117	66	1.00E-10	35	37	Description
20829	ENU04623	ANI61C3096:	23-43	777-800	NAP	1..1198	g2132857	116	41	0.014			[Avena sativa] probable membrane protein YOL158c - yeast [Saccharomyces cerevisiae]
20830	ENU04624	ANI61C5542:	22-49	429-454	NAP	165..578	g137024	321	116	1.00E-25			[Saccharomyces cerevisiae] uridylylate kinase (UK) (uridine monophosphate kinase) (UMP kinase)
20831	ENU04625	ANI61C3542:	42-61	803-829	NAP	3119..633	g2499558	386	120	1.00E-26			[Synchocystis sp.] hypothetical 84.2 KD protein SLR0473 sulfate adenylyltransferase (EC 2.7.7.4)
20832	ENU04626	ANI61C2155:	27-46	722-741	NAP	1315..1	g1084969	1548	399	e-129	97	42	- Emericella nidulans [Emericella nidulans]
20833	ENU04627	ANI61C5633:	102-129	586-612	NAP	1..685	g3929349	659	244	4.00E-64	54	47	C-14 sterol reductase (sterol C14-reductase) [Nectria haematococca]
20834	ENU04628	ANI61S4409:	29-56	272-295	NAP	1..316	g3549662	558	230	3.00E-60	96	23	(AL01394) hypothetical protein [Arabidopsis thaliana]
20835	ENU04629	ANI61C681:6	22-45	525-552	NAP	55..1	g2132903	385	174	6.00E-43	55	23	probable membrane protein YOR165w - yeast [Saccharomyces cerevisiae]
20836	ENU04630	ANI61C6221:	41-62	407-434	NAP	1..476	g115689	306	132	2.00E-30	60	38	[Saccharomyces cerevisiae] nuclear protein SNF4 (regulatory protein CAT3) [Saccharomyces cerevisiae]
20837	ENU04631	ANI61C4344:	22-46	790-809	NAP	3083..1150	g2104447	961	169	2.00E-41	39	47	(Z95396) heat shock protein 70 homolog [Schizosaccharomyces pombe]
20838	ENU04632	ANI61C9952:	219-245	614-639	NAP	858..1	g2507475	595	242	3.00E-63	46	16	paired amphipathic helix protein [Saccharomyces cerevisiae]
20839	ENU04633	ANI61C5160:	68-87	784-803	NAP	1874..488	g1353390	167	68	1.00E-10			(U34998) Rad9 [Coprinus cinereus]
20840	ENU04634	ANI61C4215:	22-45	807-829	NAP	1039..2126	g2498838	508	78	2.00E-42	47	72	meiotic recombination protein REC14 [Schizosaccharomyces pombe]
20841	ENU04635	ANI61C6750:			NAP	1549..860	g731690	152	87	9.00E-17	40	100	hypothetical 20.9 KD protein in HXT5- NRK1 intergenic region
20842	ENU04636	ANI61C8558:	28-47	455-479	NAP	236..696	g2498866	84	58	0.000000	37	36	[Saccharomyces cerevisiae] RAS suppressor protein 1 (RSU-1) (RSP-1 protein) (RSP-1) [Homo sapiens]

Seq num	Seq id	Contig source	5 pos	3 pos	Basis	Primer	Primer	Selection	Database	Hit	ncbi gi	aat	Blast Score	Blast Prob	% id	% cvrg	Description
20843	ENU04637	ANI61C9152:	26-45	537-556	NAP	9484..10108	ANT61C8418:		g4027860	858	194	6.00E-49	98	24	(U47540) TamA [Emericella nidulans]		
20844	ENTU04638	ANI61C8418:	1549..1857		NAP			g122094	461	157	5.00E-38	92	83	histone H4.2 [Emericella nidulans]			
20845	ENTU04639	ANI61C1129	96-119	725-749	NAP	7..1..1664		g1546072	707	148	5.00E-35	35	10	(U68040) polyketide synthase [Cochliobolus heterostrophus] (X55713) putative cytochrome P450 [Saccharomyces cerevisiae] (AB004690) Mis6			
20846	ENU04640	ANI61C1103	23-50	793-820	NAP	4;3908..5575		g3656	447	118	4.00E-26	28	53				
20847	ENU04641	ANI61C1269:	22-46	804-829	NAP	3063..1220		g2196560	165	32	4						
20848	ENU04642	ANI61C4393:	72-91	742-759	NAP	1..785		g120777	660	257	6.00E-68	50	53	[Schizosaccharomyces pombe] succinate-semialdehyde dehydrogenase (NADP+) (SSDH) [Escherichia coli] (AF005040) folypolyglutamate synthetase; FPGS [Neurospora crassa] "D89215) similar to Saccharomyces cerevisiae transaldolase, SWISS-PROT Accession Number P15019			
20849	ENU04643	ANI61C3785:	24-51	724-749	NAP	1270..1		g2226061	716	226	1.00E-58	46	51				
20850	ENU04644	ANI61C8146:	102-124	454-479	NAP	469..1		g1749638	387	157	5.00E-38	62	53				
20851	ENU04645	ANI61C3784:	47-66	509-533	NAP	637..1		g2326237	60	66	1.00E-17	26	63				
20852	ENU04646	ANI61C8433:	24-43	332-356	NAP	1..377		g1172766	328	146	8.00E-35						
20853	ENU04647	ANI61C8966:	44-63	711-730	NAP	5392..6501		g2132445	435	86	3.00E-16	40	27	probable membrane protein YDL148c-yeast [Saccharomyces cerevisiae)			
20854	ENTU04648	ANI61C9765:	29-48	775-798	NAP	1..1767		g1723249	2140	257	e-103	67	23	[Saccharomyces cerevisiae] hypothetical 137.2 KD protein C27F1.09C in chromosome I [Schizosaccharomyces pombe]			
20855	ENU04649	ANI61C5247:	40-59	667-686	NAP	3740..5201		g2499017	1022	173	7.00E-64	49	49	"alpha,alpha-trehalose-phosphate synthase (UDP-forming) 1 (trehalose-6-phosphate synthase) (UDP-glucose-glucosidase) (BISphosphate transferase) [Aspergillus niger]" (AE001454) fructose-BISphosphate adolase [Helicobacter pylori J99] (Z37980) hypothetical 4-hydroxyphenylacetate permease			
20856	ENTU04650	ANI61C1061	22-48	725-751	NAP	8;121..892		g4154667	126	48	0.000000	29	71				
20857	ENU04651	ANI61C388:9	22-44	672-691	NAP	35..1		g757832	187	69	2.00E-16	30	44	[Escherichia coli]			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat	Blast Score	Blast Prob	% id	% cvg	Description
20858	ENU04652	ANI61S3598: 1..644		NAP		g3913423	356	95	4.00E-19	48	59	S-adenosylmethionine decarboxylase (SAMDC) [Nicotiana tabacum]	
20859	ENU04653	ANI61C9728: 67-86	788-807	NAP		g135503	1230	438	e-122	93	58	tubulin gamma chain [Emericella nidulans]	
20860	ENU04654	ANI61C7518: 28-47	729-748	NAP		g2492661	2917	579	e-165	96	12	putative sterigmatocystin biosynthesis polyketide synthase (PKS) [Emericella nidulans]	
20861	ENU04655	ANI61S1593: 1..606		NAP		g283032	141	34	0.002	29	55	hydroxyproline-rich glycoprotein - perennial teosinte [Zea diploperennis]	
20862	ENU04656	ANI61S51:..556		NAP		g2501326	555	212	6.00E-55	72	29	pyruvate decarboxylase [Emericella nidulans]	
20863	ENU04657	ANI61C1227: 22-49	806-827	NAP		g1730031	511	190	1.00E-47	50	98	2-deoxy-D-gluconate 3-dehydrogenase (2-keto-3-deoxygluconate oxidoreductase) [Bacillus subtilis]	
20864	ENU04658	ANI61C5694: 102-129	667-692	NAP		g1169440	1343	531	e-150	97	6	"dynein heavy chain, cytosolic (DYHC)" [Emericella nidulans]	
20865	ENU04659	ANI61C5170: 51-71	710-732	NAP		g3766378	225	52	6.00E-10	42	100	(AL03907) conserved hypothetical protein [Schizosaccharomyces pombe] (AE000934) unknown	
20866	ENU04660	ANI61C9574: 23-50	449-468	NAP		g2622925	91	66	2.00E-10	28	67	[Methanobacterium thermoautotrophicum] "AFI18222" contains similarity to Iron/Ascorbate family of oxidoreductases (Pfam: PF00671, Score=307.1, E=2.2e-88, N=1)	
20867	ENU04661	ANI61C3829: 34-60	443-466	NAP		g4115913	129	82	1.00E-19	34	41	[Arabidopsis thaliana] (AC000133) ORF [Emericella nidulans]	
20868	ENU04662	ANI61C1010 5:1221..1		NAP		g1870209	414	106	2.00E-22	33	50	sperm tail-specific protein mst101(2) - fruit fly (Drosophila hydei) [] "hydroxyquinol 1,2-dioxygenase - Pseudomonas cepacia" [Burkholderia cepacia]" (AL021838) ubiquitin carboxyl-terminal hydrolase	
20869	ENU04663	ANI61S3791: 1..845		NAP		g2133632	118	48	0.00008	20	20	[Schizosaccharomyces pombe]	
20870	ENU04664	ANI61C3055: 22-44	377-398	NAP		g2120651	244	100	1.00E-20	47	38		
20871	ENU04665	ANI61C8620: 43-62	784-804	NAP		g2894281	872	257	5.00E-68	46	36		
		4660..6246											

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat	Blast Score	Blast Prob	% id	% cvrg	Description
20872	ENU04666	ANI61S1089: 1..536		NAP	g2117904	150	69	3.00E-11	34	48	ribose-phosphate pyrophosphokinase (EC 2.7.6.1) PRS1 - yeast ( <i>Candida albicans</i> )	(L48797) toxin pump [Cochliobolus carbonum]	
20873	ENU04667	ANI61C7703: 22-47	797-821	NAP	g1063421	581	74	5.00E-18	33	43	cell division control protein 31	[Saccharomyces cerevisiae]	
20874	ENU04668	ANI61C1106 5:4195..4829	66-89	589-614	NAP	g729075	326	95	5.00E-19	52	99	cyclosporin synthetase - Tolypocladium inflatum [Tolypocladium inflatum (AF010263) tartrate dehydrogenase [Agrobacterium vitis]]	[Agrobacterium vitis]
20875	ENU04669	ANI61C313:1 ..479	116-137	435-457	NAP	g1083855	133	79	2.00E-14	33	1	(U62933) multidrug resistance protein 1 [Aspergillus fumigatus]	[Aspergillus fumigatus]
20876	ENU04670	ANI61C6199: 618..1309		NAP	g2305218	501	129	3.00E-50	54	59	hypothetical 23.1 KD protein in SHP1-PTC3 intergenic region	[Saccharomyces cerevisiae] (AF078790) No definition line found [Caenorhabditis elegans]	
20877	ENU04671	ANI61C1123 0:5301..7590	22-49	700-727	NAP	g2673951	671	79	3.00E-16	31	18	probable membrane protein YOR271c - yeast ( <i>Saccharomyces cerevisiae</i> )	[Saccharomyces cerevisiae]
20878	ENU04672	ANI61C4534: 102-121 1..732	621-640	NAP	g465516	260	105	1.00E-25	48	74	probable clathrin heavy chain [Schizosaccharomyces pombe]	[Schizosaccharomyces pombe]	
20879	ENU04673	ANI61S2960: 1..547		NAP	g3329623	189	41	0.0003	24	53	probable membrane protein YPL012w - yeast ( <i>Saccharomyces cerevisiae</i> )	[Saccharomyces cerevisiae]	
20880	ENU04674	ANI61C3402: 963..1	115-134	615-634	NAP	g2132933	722	191	3.00E-60	60	72	probable elongation factor g [Schizosaccharomyces pombe]	[Schizosaccharomyces pombe]
20881	ENU04675	ANI61S4333: 1..476	29-48	436-455	NAP	g542225	448	136	7.00E-32	66	42	probable membrane protein L4.e - fission yeast (Schizosaccharomyces pombe)	[Schizosaccharomyces pombe]
20882	ENU04676	ANI61C1943: 102-124 1..574	360-381	NAP	g1705917	550	222	1.00E-57	57	11	probable clathrin heavy chain [Schizosaccharomyces pombe]	[Schizosaccharomyces pombe]	
20883	ENU04677	ANI61C9505: 1.593	71-98	540-567	NAP	g4049509	232	106	1.00E-22	31	24	(AL034563) elongation factor g [Schizosaccharomyces pombe]	[Schizosaccharomyces pombe]
20884	ENU04678	ANI61C1094 0:2454..1	41-60	626-643	NAP	g2132968	1222	135	4.00E-31	33	22	probable membrane protein YPL012w - yeast ( <i>Saccharomyces cerevisiae</i> )	[Saccharomyces cerevisiae]
20885	ENU04679	ANI61C1049 0:1..867	112-131	805-829	NAP	g4107287	223	61	8.00E-15	32	45	(AL035076) putative allantate permease [Schizosaccharomyces pombe]	[Schizosaccharomyces pombe]
20886	ENU04680	ANI61C9717: 98..1344	27-46	785-812	NAP	g4098647	751	257	7.00E-68	51	56	"(U80668) homogentisate 1,2-dioxygenase [Arabidopsis thaliana]" (AL035064) queuine tma-ribosyltransferase [Schizosaccharomyces pombe]	[Schizosaccharomyces pombe]
20887	ENU04681	ANI61C9944: 768..1	23-47	629-648	NAP	g4106673	796	171	3.00E-85	66	59		

Seq num	Seq id	Contig source	5 pos	3 pos	Primer Basis	Primer Selection	Database	Hit	ncbi gi	aat	Blast Score	Blast Prob	% id	% cvrg	Description
20888	ENU04682	ANI61C7199:	68..87	306..325	NAP		g730917	307	78	1.00E-18					"T-complex protein 1, beta subunit (TCP-1-beta) (CCT-beta)"
20889	ENU04683	ANI61C1075	24..44	803..829	NAP		g1723251	417	70	3.00E-15	29	59			[ <i>Saccharomyces cerevisiae</i> ] hypothetical 50.9 KD protein C3F10_06C in chromosome I
20890	ENU04684	ANI61C2651:	22..49	785..805	NAP		g3123261	154	70	2.00E-11					[ <i>Schizosaccharomyces pombe</i> ] meiotic recombination protein REC12
20891	ENU04685	ANI61C9331:	22..41	732..749	NAP		g1063421	519	108	1.00E-28	44	40			[ <i>Schizosaccharomyces pombe</i> ] (L48797) toxin pump [Cochliobolus carbonum]
20892	ENU04686	ANI61S29:1..			NAP		g2635181	553	213	7.00E-55	56	70			(Z99117) similar to protease [Bacillus subtilis]
20893	ENU04687	ANI61C9880:	22..41	808..829	NAP		g2498765	469	107	1.00E-28					peroxisomal membrane protein PEX16 (peroxin-16) [Yarrowia lipolytica]
20894	ENU04688	ANI61C891:1	51..69	457..481	NAP		g1805251	124	73	1.00E-16	30	29			(U58946) transposase [Aspergillus awamori]
20895	ENU04689	ANI61C3704:	69..89	805..823	NAP		g4586103	199	67	1.00E-22	33	76			(AL049638) putative protein [Arabidopsis thaliana]
20896	ENU04690	ANI61C758:3	22..48	714..741	NAP		g2497080	1119	125	5.00E-30	32	16			hypothetical 171.1 KD protein in YL16A-DAK1 intergenic region
20897	ENU04691	ANI61S2532:			NAP		g2119707	127	40	0.01	32	61			[ <i>Saccharomyces cerevisiae</i> ] proline-rich protein precursor - rat [rat]
20898	ENU04692	ANI61C883:8	22..45	456..479	NAP		g1176053	156	90	1.00E-19	34	50			hypothetical 33.3 KD protein in ADE3-SER2 intergenic region
20899	ENU04693	ANI61C2209:	22..42	719..738	NAP		g1077575	182	62	0.000000	27	41			[ <i>Saccharomyces cerevisiae</i> ] hypothetical protein YDR117c - yeast (Saccharomyces cerevisiae)
20900	ENU04694	ANI61C9811:	31..50	767..786	NAP		g120777	947	310	1.00E-83	56	58			[ <i>Saccharomyces cerevisiae</i> ] succinate-semialdehyde dehydrogenase (NADP+) (SSDH) [Escherichia coli]
20901	ENU04695	ANI61C8000:	41..60	727..749	NAP		g1703361	998	370	e-102					"ARG-6 protein precursor (contains: N-acetyl-gamma-glutamyl-phosphate reductase (N-acetyl-glutamate semialdehyde dehydrogenase) (NAGSA dehydrogenase), and acetylglutamate kinase (NAG kinase) (AGK) (N-acetyl-L-glutamate 5...[Neurospora crassa])"

Sq num	Seq id	Contig source	5 pos	Primer 3 pos	Primer Basis	Selection Database	Hit ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
20902	ENU04696	ANI61C7533:	22-46	805-829	NAP	g3830084	370	87	2.00E-16	36	75	(AL033389) alcohol dehydrogenase	
20903	ENU04697	ANI61C6751:	1..338	3582..4673	NAP	g3150262	196	80	5.00E-15	38	32	[Schizosaccharomyces pombe] (AL023634) hypothetical protein	
20904	ENU04698	ANI61C6031:	30-54	1..793	NAP	g113314	1311	482	e-135	96	7	[Schizosaccharomyces pombe] delta-(L-alpha-aminoacyl)-L-cysteinyl-D-valine synthetase (ACV synthetase) (ACVS) [Emericella nidulans]	
20905	ENU04699	ANI61C1084	51-70	6:2451..3573	NAP	g2132014	611	233	1.00E-60	45	61	hypothetical protein YOL124c - yeast (Saccharomyces cerevisiae)	
20906	ENU04700	ANI61C201:1	94-113	308-335	NAP	g2131347	264	68	2.00E-11	52	19	hypothetical protein YDL153c - yeast (Saccharomyces cerevisiae)	
20907	ENU04701	ANI61C4912:	49-72	3841..3182	NAP	g3122266	603	171	4.00E-60	65	56	eukaryotic translation initiation factor 3 delta subunit (EIF-3 delta) [Schizosaccharomyces pombe] transporter protein SMF1/ESP1 [Saccharomyces cerevisiae] (Y17243) cytochrome P450 [Gibberella fujikuroi]	
20908	ENU04702	ANI61C7350:	199-218	2513..1876	NAP	g2507129	395	112	3.00E-24	40	36	phenol 2-monoxygenase (phenol hydroxylase) [Trichosporon cutaneum] (AL022103) hypothetical protein. [Schizosaccharomyces pombe] polyketide synthase HETM [Anabaena sp.] (AC000133) ORF [Emericella nidulans]	
20909	ENU04703	ANI61C2646:	1..595	1..594..2423	NAP	g4127832	306	140	8.00E-33	39	37	[Gibberella fujikuroi] phenol 2-monoxygenase (phenol hydroxylase) [Trichosporon cutaneum] (AL022103) hypothetical protein. [Schizosaccharomyces pombe] polyketide synthase HETM [Anabaena sp.] (AC000133) ORF [Emericella nidulans]	
20910	ENU04704	ANI61C1132	23-43	703-729	NAP	g464369	221	78	8.00E-23	32	35	[Gibberella fujikuroi] phenol 2-monoxygenase (phenol hydroxylase) [Trichosporon cutaneum] (AL022103) hypothetical protein. [Schizosaccharomyces pombe] polyketide synthase HETM [Anabaena sp.] (AC000133) ORF [Emericella nidulans]	
20911	ENU04705	ANI61C7309:	71-92	545..1	NAP	g2956774	62	48	0.00003	27	72	[Gibberella fujikuroi] phenol 2-monoxygenase (phenol hydroxylase) [Trichosporon cutaneum] (AL022103) hypothetical protein. [Schizosaccharomyces pombe] polyketide synthase HETM [Anabaena sp.] (AC000133) ORF [Emericella nidulans]	
20912	ENU04706	ANI61C332:1	81-99	..558	NAP	g585251	318	134	4.00E-31	43	36	[Gibberella fujikuroi] phenol 2-monoxygenase (phenol hydroxylase) [Trichosporon cutaneum] (AL022103) hypothetical protein. [Schizosaccharomyces pombe] polyketide synthase HETM [Anabaena sp.] (AC000133) ORF [Emericella nidulans]	
20913	ENU04707	ANI61C101:1	22-46	..1001	NAP	g1870209	283	87	8.00E-24	32	50	[Gibberella fujikuroi] phenol 2-monoxygenase (phenol hydroxylase) [Trichosporon cutaneum] (AL022103) hypothetical protein. [Schizosaccharomyces pombe] polyketide synthase HETM [Anabaena sp.] (AC000133) ORF [Emericella nidulans]	
20914	ENU04708	ANI61C3232:	25-45	1917..1	NAP	g2492658	3245	541	e-153	97	14	putative sterigmatocystin biosynthesis fatty acid synthase beta subunit [Emericella nidulans]	
20915	ENU04709	ANI61C1335:	48-70	1..389	NAP	g585668	413	152	1.00E-36	62	34	polygalacturonase precursor (PG) (pectinase) [Gibberella fujikuroi] probable membrane protein YPR184w - yeast (Saccharomyces cerevisiae) [Saccharomyces cerevisiae] (X89442) peptide synthetase [Metarhizium anisopliae]	
20916	ENU04710	ANI61C1053	0:722..1		NAP	g2133039	447	198	5.00E-50	48	15		
20917	ENU04711	ANI61C4364:	30-49	1..1567	NAP	g2342601	814	123	2.00E-27	30	5		

Seq num	Seq id	Contig source	5 pos	Primer 3 pos	Primer Basis	Selection Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
20918	ENU04712	ANI61S2752:	1..605	NAP	g4760549	77	53	0.000001					(AB019494) IDN3 [Homo sapiens]
20919	ENU04713	ANI61C7196:	22-49	777-804	NAP	g3859775	415	111	2.00E-31	52	53		[Schizosaccharomyces pombe] (Z54328) putative aminopeptidase p
20920	ENU04714	ANI61C9312:	22-46	802-829	NAP	g3915187	556	132	3.00E-30	33	14		probable N-end-recognizing protein (ubiquitin-protein ligase E3 component) (N-recognin) []
20921	ENU04715	ANI61C9006:	42-61	697-716	NAP	g83716	3301	404	e-141	95	32		regulatory protein alcR - Entericella nidulans [Entericella nidulans]
20922	ENU04716	ANI61C1084	22-44	623-643	NAP	g416965	658	50	3.00E-21	37	7		"erythronolide synthase, modules 1 and 2 (ORF 1) (6-deoxyerythronolide B synthase I) (DEBS 1) []"
20923	ENU04717	ANI61C6533:	22-48	727-749	NAP	g1175451	842	152	3.00E-36				hypothetical protein C22F3.14C in chromosome I []
20924	ENU04718	ANI61C5137:	88-110	741-760	NAP	g3702632	592	137	3.00E-63	43	41		(AL031824) putative transcriptional regulator [Schizosaccharomyces pombe]
20925	ENU04719	ANI61C419:1 ..528	23-46	412-431	NAP	g1172542	388	168	3.00E-41	47	22		dolichyl-phosphate-mannose--protein mannosyltransferase 4 [Saccharomyces cerevisiae]
20926	ENU04720	ANI61C8353:	26-45	776-794	NAP	g122805	311	109	3.00E-23	30	53		6-hydroxy-D-nicotine oxidase (6-HDNO) [Arthrobacter oxidans]
20927	ENU04721	ANI61C3877:	1384..1	NAP	g3122851	2113	284	e-134	89	41		sulfur metabolite repression control protein [Entericella nidulans]	
20928	ENU04722	ANI61C8873:	8184...7035	NAP	g1175441	458	83	3.00E-15	27	31		hypothetical 98.4 KD protein C24H6.13 in chromosome I [Schizosaccharomyces pombe]	
20929	ENU04723	ANI61C1126	102-123	448-475	NAP	g4204352	396	166	1.00E-40	78	64		(U07366) eIF-5A [Candida albicans]
20930	ENU04724	ANI61C4166:	121-140	505-524	NAP	g1076211	227	45	0.0006	28	43		hypothetical protein VSP-3- Chlamydomonas reinhardtii
20931	ENU04725	ANI61C6980:	22-44	561-582	NAP	g2213560	369	164	4.00E-40	44	98		[Chlamydomonas reinhardtii] (Z27052) hypothetical protein
20932	ENU04726	ANI61C9955:	22-49	760-783	NAP	g534844	501	184	7.00E-46	55	39		[Schizosaccharomyces pombe] (UJ3672) beta-glucosidase [Candida wickerhamii]
20933	ENU04727	ANI61C1013	23-50	538-558	NAP	g2105430	316	145	4.00E-34	45	17		(U97079) U5-116kD [Mus musculus]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat	Blast Score	Blast Prob	% id	cvg	%	Description	
20934	ENU04728	ANI61S4589:	1..553	NAP	g88698	177	47	0.00008	35	54	hydroxyproline-rich glycoprotein precursor - maize [Zea mays]				
20935	ENU04729	ANI61C1053	45-64	792-819	NAP	g416643	231	65	7.00E-10	32	58	aristochene synthase (sesquiterpene cyclase) (AS) [Penicillium roquefortii] (AC004521) unknown protein [Arabidopsis thaliana]			
20936	ENU04730	ANI61C9379:	23-50	467-490	NAP	g3128203	134	63	0.000000	36	75	hypothetical 17.5 KD protein in chromosome II [Schizosaccharomyces pombe]			
20937	ENU04731	ANI61C4278:	22-42	652-671	NAP	g3915405	146	79	4.00E-14	37	96	hypothetical 17.5 KD protein in chromosome II [Schizosaccharomyces pombe]			
20938	ENU04732	ANI61C110	105-125	643-665	NAP	g3925752	276	68	1.00E-22	41	58	(AL034352) putative signal transduction protein [Schizosaccharomyces pombe] (AL021961) putative protein [Arabidopsis thaliana]			
20939	ENU04733	ANI61S3754:	31-56	371-390	NAP	g2911045	695	187	2.00E-73	95	51	(U40375) Supt6n [Mus musculus] (AF049930) PGP237-11 [Petunia x hybrida]			
20940	ENU04734	ANI61C9298:	1..508		NAP	g1401057	158	104	1.00E-21	25	14	(Z81137) Similarity to Yeast YIP1 protein (SW_P53039); cDNA EST EMBL:T01608 comes from this gene; cDNA EST EMBL:C07393 comes from this gene; cDNA EST EMBL:C07550 comes from this gene; cDNA EST EMBL:C08746 comes from this gene; ... []			
20941	ENU04735	ANI61S3133:	46-65	427-450	NAP	g4105798	164	99	2.00E-20	36	43	(Z81137) Similarity to Yeast YIP1 protein (SW_P53039); cDNA EST EMBL:T01608 comes from this gene; cDNA EST EMBL:C07393 comes from this gene; cDNA EST EMBL:C07550 comes from this gene; cDNA EST EMBL:C08746 comes from this gene; ... []			
20942	ENU04736	ANI61C7989:	71-89	418-441	NAP	g3880413	160	66	1.00E-10	33	46	(Z81137) Similarity to Yeast YIP1 protein (SW_P53039); cDNA EST EMBL:T01608 comes from this gene; cDNA EST EMBL:C07393 comes from this gene; cDNA EST EMBL:C07550 comes from this gene; cDNA EST EMBL:C08746 comes from this gene; ... []			
20943	ENU04737	ANI61C5949:	55-75	594-612	NAP	g2493011	323	151	5.00E-36	37	13	probable calcium-transporting ATPase 8 [Saccharomyces cerevisiae] (AF116827) unknown [Homo sapiens]			
20944	ENU04738	ANI61C9477:	30-49	806-829	NAP	g4768831	418	38	0.12						
20945	ENU04739	ANI61C110	1..1752	7.9439..8176	NAP	g4455787	886	195	4.00E-52	52	66	(AL035536) putative DNA polymerase accessory protein [Schizosaccharomyces pombe] hypothetical 48.1 KD protein in TUB1-CPR3 intergenic region			
20946	ENU04740	ANI61C5813:	41-60	734-761	NAP	g1730621	585	223	1.00E-61	57	56	[Saccharomyces cerevisiae] putative enoyl-CoA hydratase [Mycobacterium leprae]			
20947	ENU04741	ANI61C6657:	33-52	422-445	NAP	g1706567	89	59	0.000000	25	40				
		1283..1644				02									

Seq num	Seq id	Contig source	5 pos	3 pos	Primer Basis	Primer Selection	aat	Blast Score	Blast Prob	% id	% cvrg	Description
					Database	Hit ncbi gi	1212	322	e-103			"6-phosphogluconate dehydrogenase, decarboxylating 1 [Saccharomyces cerevisiae]"
20949	ENU04743	ANI61C3035:	105-130	416-443	NAP	g84056553	133	86	1.00E-16	39	20	(AL034583) putative exonuclease [Schizosaccharomyces pombe]
20950	ENU04744	ANI61C5064:	37-56	804-829	NAP	g2331714	212	99	5.00E-20	36	24	CDC21 protein [ ]
20951	ENU04745	ANI61C7394:	107-126	401-420	NAP	g125155	283	127	4.00E-29	41	71	Adenylylate kinase 2 (ATP-AMP transphosphorylase) [Saccharomyces cerevisiae]
20952	ENU04746	ANI61C1243:	105-125	349-371	NAP	g114251	175	51	1.00E-12	41	40	L-asparaginase I (L-asparagine amidohydrolase I) [Escherichia coli] (AL031536) fnx1p.
20953	ENU04747	ANI61C5328:	24-45	762-786	NAP	g3560207	361	89	3.00E-17	35	46	[Schizosaccharomyces pombe] (AL021287) hypothetical protein Rv3049c [Mycobacterium tuberculosis]
20954	ENU04748	ANI61C8350:	22-44	766-788	NAP	g2791647	470	89	4.00E-17	31	42	larval glue protein Lgp-3 precursor - fruit fly [Drosophila virilis] (AE01466) putative [Helicobacter pylori] j99
20955	ENU04749	ANI61S1354:			NAP	g1079170	137	52	0.000006	31	61	(AB007770) translation elongation factor 1 alpha [Aspergillus oryzae] delta-[L-alpha-amino adipyl]-L-cysteinyl-D-valine synthetase (ACV synthetase) (ACVS) [Emericella nidulans] (Z99120) similar to Na+/nucleoside cotransporter [Bacillus subtilis]
20956	ENU04750	ANI61C9637:	41-60	791-812	NAP	g4154817	480	107	1.00E-47	42	87	hypothetical hydrolase/peptidase Y4TM [Rhizobium sp. NGR234]
20957	ENU04751	ANI61C7698:	22-49	723-746	NAP	g4521247	1397	494	e-139	92	57	hydroxyproline-rich glycoprotein - perennial teosinte [Zea diploperennis] b5 reductase [Schizosaccharomyces pombe] (AL031530) putative nadh-cytochrome b5 reductase [Schizosaccharomyces pombe] (U81165) MOD-E [Podospora anserina]
20958	ENU04752	ANI61C291:1			NAP	g113314	1686	492	e-141	93	7	
						35..1						
20959	ENU04753	ANI61C1116	22-48	763-783	NAP	g2635715	530	111	1.00E-35	41	63	
20960	ENU04754	ANI61C7546:	31-51	807-828	NAP	g2497952	221	98	1.00E-19			
20961	ENU04755	ANI61S4137:	1..755		NAP	g283032	161	32	0.013	35	59	
20962	ENU04756	ANI61C936:6	49-68	494-515	NAP	g3560228	423	157	6.00E-43	50	61	
20963	ENU04757	ANI61C1316:	47-73	725-747	NAP	g2804612	1030	238	2.00E-89	83	37	
						848..1						

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	Score	Score Prob	Blast	Blast	%
20964	ENU04758	ANI61S4517:	24-47	373-393	NAP	g2330857	411	175	2.00E-43	60	10	(Z98533)
1..440												
20965	ENU04759	ANI61C3920:	22-46	723-746	NAP	g3650404	1579	148	4.00E-35	42	28	(AJ031739) eukaryotic translation initiation factor 3 subunit [Schizosaccharomyces pombe]
	2244..1					g416765	1139	164	5.00E-40	27	13	[Saccharomyces cerevisiae] general negative regulator of transcription subunit 1
20967	ENU04761	ANI61C8310:	106-125	459-479	NAP	g1703347	311	85	8.00E-26	51	67	adenine phosphoribosyltransferase 1 (APRT1) [Saccharomyces cerevisiae]
	378..1					g2493749	132	36	0.21	23	14	240 KD protein of rod photoreceptor CNG-channel [Bos taurus]
20968	ENU04762	ANI61S2708:	1..750		NAP	g1352954	224	96	2.00E-19	35	25	hypothetical 77.7 KD protein in CCT8-CCT8 intergenic region
						g136682	333	140	8.00E-33	39	99	[Saccharomyces cerevisiae] ubiquitin carboxyl-terminal hydrolase isozyme L3 (UCH-L3) (ubiquitin thiolesterase L3) [Homo sapiens] extensin-like protein - maize [Zea mays]
20971	ENU04765	ANI61C6434:	23-44	712-731	NAP	g1076802	75	46	0.0003			
	2648..1866					g1705828	1119	298	3.00E-85	95	23	chitin synthase 2 (chitin-UDP acetyl-glucosaminyl transferase 2) [Emeticella nidulans]
20972	ENU04766	ANI61C26:81	222-244	736-763	NAP	7..1						
						g730755	837	129	2.00E-50	54	45	transporter protein SMF2 [Saccharomyces cerevisiae]
20973	ENU04767	ANI61C8888:	25-52	713-737	NAP	282..1609						(AL031739) 26s proteasome regulatory subunit [Schizosaccharomyces pombe]
						g3650406	754	199	1.00E-50	47	26	killer toxin alpha and beta subunits precursor (RF2 protein) (endochitinase [Kuyveromyces lactis])
20974	ENU04768	ANI61C4526:	22-45	809-828	NAP	1314..1						"alanyl-TRNA synthetase, cytoplasmic (alanine--tRNA ligase) (ALARS) [Saccharomyces cerevisiae]" (AJ005963) 100 kDa protein [Ajellomyces capsulatus]
20975	ENU04769	ANI61C1120:	22-44	714-731	NAP	11172..12742						putative transporter C11D3.18C [Schizosaccharomyces pombe]
						g1711623	159	38	0.000000	41	11	
	1238..835					02						
20977	ENU04771	ANI61C6793:	59-78	571-591	NAP	1..648						
						g3135013	755	302	1.00E-81	68	24	
20978	ENU04772	ANI61C7746:	95-114	451-478	NAP	4718..4215	190	73	1.00E-12	25	33	

Seq num	Seq id	Contig source	5 pos	Primer 3 pos	Primer Basis	Selection	Database	Hit ncbi gi	aat Score	Blast Score	Prob	% id	% cvrg	Description
20979	ENU04773	ANI61C1049:	48-69	588-615	NAP		g3288709	996	277	e-109	89	15	(AB010442) PMR1 [Penicillium digitatum]	
20980	ENU04774	ANI61C8780:	48-65	799-826	NAP		g130333	554	154	6.00E-37	47	68	pectin lyase D precursor (PLD) (pectin lyase I) (PLI) [Aspergillus niger]	
20981	ENU04775	ANI61C1252:	114-133	435-462	NAP		g400069	841	261	5.00E-87			insertion element IS1 protein INSB [Escherichia coli]	
20982	ENU04776	ANI61C1269:	496..1		NAP		g2145993	125	69	4.00E-11	28	97	yfcA protein - Mycobacterium leprae [Mycobacterium leprae]	
20983	ENU04777	ANI61C9834:	65-84	798-816	NAP		g3402279	702	156	1.00E-54	49	78	(AJ000999) putative beta-subunit of K+ channels [Solanum tuberosum]	
20984	ENU04778	ANI61C3653:	121-140	342-361	NAP		g134920	101	47	0.00008	26	30	sulfated surface glycoprotein 185 (SSG 185) [Volvox carteri]	
20985	ENU04779	ANI61C6617:	23-42	576-595	NAP		g1079456	471	192	2.00E-49	60	62	"actin-capping protein beta chain, splice form 2 - chicken [Gallus gallus]"	
20986	ENU04780	ANI61S1139:	1..586		NAP		g1572721	133	38	0.044	31	13	(UT0136) megakaryocyte stimulating factor; MSF [Homo sapiens]	
20987	ENU04781	ANI61C8129:	22-46	621-640	NAP		g730240	249	142	3.00E-33	34	54	osmotic growth protein 1 [Saccharomyces cerevisiae]	
20988	ENU04782	ANI61C1094	223..1094		NAP		g3560228	476	98	7.00E-31	43	77	(AL031530) putative nadh-cytochrome b5 reductase [Schizosaccharomyces pombe]	
			1:1..831											
20989	ENU04783	ANI61C7234:	1296..1		NAP		g2499716	1440	303	e-109	83	55	"exopolygalacturonase precursor (exoPG) (galacturan 1,4-alpha-D-galacturonidase) (poly(1,4-alpha-D-galacturonide)galacturonohydrolase) [Aspergillus tubingensis]"	
20990	ENU04784	ANI61C9664:	6879..6438		NAP		g729650	258	98	3.00E-20	44	30	"exoglucanase I precursor (exocellulobiohydrolase I) (1,4-beta-cellulobiohydrolase) [Penicillium janthinellum]"	
20991	ENU04785	ANI61C6076:	22-45	496-515	NAP		g1197667	96	31	5.1	29	98	(U46857) vitellogenin [Anolis pulchellus]	
20992	ENU04786	ANI61C5316:	68-87	362-381	NAP		g1174622	227	84	5.00E-16	52	19	"T-complex protein 1, theta subunit (TCP-1-theta) (CCT-theta)"	
20993	ENU04787	ANI61C9088:	111-130	532-555	NAP		g2826168	193	57	0.000000	36	42	[Saccharomyces cerevisiae]" (AB010714) salicylate hydroxylase [Pseudomonas putida]	
			1167..592					1						

Seq num	Seq id	Contig source	5 pos	Primer 3 pos	Primer Basis	Selection Database	Hit ncbi gi	aat Score	blast Score	blast Prob	% id	% cvrg	Description
20994	ENU04788	ANI61C5537:	22-43	455-479	NAP	g729763	198	101	4.00E-21	38	80	30	KD heat shock protein [Emericella nidulans]
20995	ENU04789	ANI61C753:7	22-49	702-721	NAP	g1083855	150	92	4.00E-18	26	1	cyclosporin synthetase - Tolypocladium inflatum [Tolypocladium inflatum]	
20996	ENU04790	ANI61C1830:	107-129	802-821	NAP	g2501686	919	349	3.00E-95	59	16	hypothetical 187.1 KD protein in OGG1-CNA2 intergenic region	
20997	ENU04791	ANI61C8954:	93-112	556-579	NAP	g3978466	462	108	1.00E-47	45	29	[Saccharomyces cerevisiae] (AF086822) dihydroxyacetone synthase	
20998	ENU04792	ANI61C1899:	35-54	805-829	NAP	g2501202	1767	272	e-108	75	51	[Candida boidinii] protein disulfide isomerase precursor (PDI) [Aspergillus niger]	
20999	ENU04793	ANI61C3322:	164-183	454-479	NAP	g1722894	379	159	9.00E-39	52	42	"beta-xylosidase (1,4-beta-D-xylan xylohydrolase) (xylan 1,4-beta-xylosidase) / alpha-L-arabinofuranosidase (arabinosidase)	
21000	ENU04794	ANI61C1684:	22-41	781-808	NAP	g2330829	557	170	1.00E-41	40	18	[Bacteroides ovatus] (Z98530) hypothetical protein	
21001	ENU04795	ANI61C1574:	120-137	492-511	NAP	g2293194	99	57	0.000000	28	41	[Schizosaccharomyces pombe] (AF008220) yteR [Bacillus subtilis]	
21002	ENU04796	ANI61C1236:	22-45	766-792	NAP	g1253462	1460	573	e-163	03	"aminoglycoside 3'-phosphotransferase (kanamycin kinase, type I) (neomycin-kanamycin phosphotransferase, type I) (APH(3')I) [Cloning vector pHND2.2]"		
21003	ENU04797	ANI61C5865:	108-127	724-750	NAP	g2492799	589	161	8.00E-58	44	72	putative sterigmatocystin biosynthesis dehydrogenase STCV [Emericella nidulans]	
21004	ENU04798	ANI61C1994:	29-51	370-389	NAP	g4884104	110	57	0.000000	08	0	(AL050060) hypothetical protein [Homo sapiens]	
21005	ENU04799	ANI61S1320:	1..590		NAP	g3874243	147	50	0.00002	20	50	(Z70204) similar to PHD-finger; cDNA EST EMBL:T00556 comes from this gene; cDNA EST Yk344f7.5 comes from this gene [Caenorhabditis elegans]	
21006	ENU04800	ANI61C1743:	24-44	733-755	NAP	g3261605	699	185	3.00E-61	45	14	(Z74697) ppsA [Mycobacterium tuberculosis]	
21007	ENU04801	ANI61C7911:	22-48	776-797	NAP	g2894293	507	105	6.00E-28	35	47	(AL021837) hypothetical protein [Schizosaccharomyces pombe]	

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Basis	Selection	Database	Hit	ncbi gi	aat	Blast Score	Blast Prob	% id	% cvrg	Description
21008	ENU04802	ANI61C8612:	102-125	294-314	NAP		g2239205	198	90	5.00E-18	37	48	(Z97209) hypothetical protein		
21009	ENU04803	ANI61C8663:	28-49	806-828	NAP		g134854	269	92	4.00E-18	27	19	[Schizosaccharomyces pombe] transcription initiation protein SPT6		
21010	ENU04804	ANI61C1850:	25-52	720-747	NAP		g1805251	849	272	3.00E-72	54	50	(U58946) transposase [Aspergillus awamori]		
21011	ENU04805	ANI61C5897:	33-52	590-617	NAP		g1870216	1136	416	e-116	100	100	(AC000133) f4p06 [Emericella nidulans]		
21012	ENU04806	ANI61C9479:	22-44	792-818	NAP		g4056553	300	94	1.00E-18	39	34	[Schizosaccharomyces pombe] (AL034583) putative exonuclease		
21013	ENU04807	ANI61C1226:	101-120	424-444	NAP		g1710045	274	106	2.00E-22	38	21	mitochondrial respiratory chain complexes assembly protein RCA1 (TAT-binding homolog 12)		
21014	ENU04808	ANI61C6000:	22-47	806-827	NAP		g2842516	484	88	7.00E-17			[Saccharomyces cerevisiae] (AL021748) major facilitator		
			7848..5903										superfamily protein		
21015	ENU04809	ANI61C7282:	22-49	376-399	NAP		g3150141	504	128	2.00E-48	73	51	[Schizosaccharomyces pombe] (AL023594) 40s ribosomal protein s4 type		
21016	ENU04810	ANI61C1158:	43-63	791-810	NAP		g1911743	1514	320	e-103	84	65	[Schizosaccharomyces pombe] (S83229) beta-isopropylmalate dehydrogenase=isozyme [Aspergillus niger]		
21017	ENU04811	ANI61C7741:	22-42	697-724	NAP		g1705679	2474	226	5.00E-99	78	31	cell division control protein 48 [Saccharomyces cerevisiae]		
21018	ENU04812	ANI61C3249:	52-70	774-793	NAP		g1078072	247	85	8.00E-16	32	41	probable membrane protein YLR324w -yeast [Saccharomyces cerevisiae]		
21019	ENU04813	ANI61C7670:	50-69	772-791	NAP		g3043376	261	60	0.000000			[Saccharomyces cerevisiae] (AJ002528) amyR [Aspergillus oryzae]		
21020	ENU04814	ANI61C6680:	30-47	482-507	NAP		g4099032	892	176	8.00E-74	96	58	(U82084) unknown [bacteriophage SFX]		
21021	ENU04815	ANI61S2301:	71-90	363-386	NAP		g1175364	183	82	2.00E-15	39	46	hypothetical 28.0 KD protein C13C5.04 in chromosome I		
21022	ENU04816	ANI61C9378:	23-45	775-802	NAP		g2132860	280	45	0.000000	42	91	[Schizosaccharomyces pombe] probable membrane protein YOL162w -yeast [Saccharomyces cerevisiae]		
			472..1418						6				[Saccharomyces cerevisiae]		

Seq num	Seq id	Contig source	5 pos	Primer 3 pos	Primer Basis	Selection	Blast aat	Blast Blast	% id	% cvrg	Description	
21023	ENU04817	ANI61C9378:	22-48	407-434	NAP	g2132861	363	84	2.00E-29	51	- yeast (Saccharomyces cerevisiae)	
			1..456								[Saccharomyces cerevisiae]	
21024	ENU04818	ANI61C1114	32-51	393-415	NAP	g2222786	422	108	3.00E-23	63	(Z97185) hypothetical protein [Schizosaccharomyces pombe]	
		4:516..1				g131768	569	211	3.00E-54	60	quinate permease (quinate transporter) [Emeocilla nidulans]	
21026	ENU04820	ANI61C1106	30-49	670-691	NAP	g3183329	713	136	6.00E-53	57	hypothetical aminotransferase C6B12.04C [Schizosaccharomyces pombe]	
21027	ENU04821	ANI61C1024	94-115	494-519	NAP	g1293655	113	70	1.00E-11	26	(U51327) versicolorin B synthase [Aspergillus parasiticus]	
21028	ENU04822	ANI61S1471:	631..28		NAP	g418604	857	328	2.00E-93	89	hypothetical 35.6 KD protein in RPME-TDK intergenic region (ORFP) []	
21029	ENU04823	ANI61C8903:	102-125	803-829	NAP	g232152	1231	421	e-132	97	G2/mitotic-specific cyclin B [Emericella nidulans]	
21030	ENU04824	ANI61C7756:	22-49	618-643	NAP	g3451467	569	212	4.00E-54	45	gamma-synthase (AL031349) putative cystathionine gamma-synthase [Schizosaccharomyces pombe]	
21031	ENU04825	ANI61C4392:	822..1	22-43	697-715	NAP	g3947592	448	121	2.00E-46	"(AL034364) similar to homogentisate 1,2-dioxygenase (EC 1.13.11.5) (homogentisicase) (homogentisate oxygenase) (homogentisic acid oxidase); cDNA EST yk385c12.5 comes from this gene; cDNA EST EMBL:D73328 comes from this gene; cD... []"	
21032	ENU04826	ANI61S1672:	1..695		NAP	g2119707	77	55	0.000000	27	proline-rich protein precursor - rat []	
21033	ENU04827	ANI61C1097	71-90	805-829	NAP	g2496731	881	336	1.00E-91	67	hypothetical 30.2 KD protein Y4OV [Rhizobium sp. NGR234]	
21034	ENU04828	ANI61C3908:	798..1409	22-44	485-511	NAP	g586485	242	145	3.00E-34	35	hypothetical 45.5 KD protein in FIG1-GP1 intergenic region [Saccharomyces cerevisiae]
21035	ENU04829	ANI61S49:1..	530		NAP	g416876	238	47	5.00E-11	38	dihydodicarboxylate synthase (DHDPS) (vegetative protein 81) (VEG81) [Bacillus subtilis]	

Seq num	Seq id	Contig source	5 pos	Primer 3 pos	Primer Basis	Selection Database	Hit ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
21036	ENU04830	ANI61C1518:	22-43	659-678	NAP	g1168464	1254	212	2.00E-78	57	53	monoamine oxidase N (MAO-N)	
21037	ENU04831	ANI61C1133:	1291..1	4062..5481	NAP	g118381	1019	228	6.00E-59	56	58	[Aspergillus niger] ornithine decarboxylase (ODC)	
21038	ENU04832	ANI61C4437:	1625..2136	22-43	440-462	NAP	g4583351	113	64	5.00E-10	27	30	(AFI14167) lysosomal peptidase insensitive protease [Canis familiaris]
21039	ENU04833	ANI61C2465:	776..3711	57-76	795-815	NAP	g1546072	1287	147	1.00E-34	40	9	(U68040) polyketide synthase [Cochliobolus heterostrophus]
21040	ENU04834	ANI61C9269:	1761..2743	26-53	808-829	NAP	g1805251	718	249	3.00E-65	44	51	(U58946) transposase [Aspergillus awamori]
21041	ENU04835	ANI61C9769:	102-127	526-551	NAP	g1870212	903	278	2.00E-74	94	97	(AC000133) ORF [Emericella nidulans]	
21042	ENU04836	ANI61C6563:	1..495	121-144	378-405	NAP	g1351598	398	167	5.00E-41	47	31	hypothetical 59.6 KD protein [Schizosaccharomyces pombe] C4G8.07C in chromosome I
21043	ENU04837	ANI61C6365:	1..5956	39-57	728-749	NAP	g2342601	2803	145	3.00E-34	37	5	[Metarhizium anisopliae] peptide synthetase (X89442)
21044	ENU04838	ANI61C2860:	790..1	161-187	714-740	NAP	g1346361	269	142	1.00E-35	41	32	serine/threonine-protein kinase SHK2 [Schizosaccharomyces pombe]
21045	ENU04839	ANI61C9769:	596..1239	22-47	591-610	NAP	g1870213	1021	254	e-108	97	99	(AC000133) ORF [Emericella nidulans]
21046	ENU04840	ANI61C1028	7:1675..2204	60-79	443-461	NAP	g609350	549	228	3.00E-59	63	22	(U15099) methionine synthase [Saccharomyces cerevisiae]
21047	ENU04841	ANI61C1045	1:1..475	105-132	426-447	NAP	g1709181	288	117	2.00E-27	39	27	high affinity methionine permease [Saccharomyces cerevisiae]
21048	ENU04842	ANI61C2802:	2437..717	43-62	775-794	NAP	g4056555	849	86	3.00E-16			(AL034583) putative mitochondrial atp-dependent rna helicase precursor
21049	ENU04843	ANI61S4378:	1..806		NAP	g1079170	144	31	0.04	31	69	[Schizosaccharomyces pombe] larval glue protein Lgp-3 precursor - fruit fly (Drosophila virilis)	
21050	ENU04844	ANI61C2758:	1..609	105-131	523-546	NAP	g2133266	875	319	1.00E-86	96	16	[Drosophila virilis] chromosome scaffold protein sudA - nidulans
21051	ENU04845	ANI61C5221:	6482..4482	22-45	806-828	NAP	g3282216	540	56	0.0000003			(U68716) polyketide synthase homolog [Borytominia fuckeliana]
21052	ENU04846	ANI61C1008	8:1..578	35-54	497-519	NAP	g135649	263	75	2.00E-13	41	31	"2,4-dichlorophenol 6-monooxygenase (2,4-dichlorophenol hydroxylase) (2,4-DCP hydroxylase) [Plasmid pJP4]"

Seq num	Seq id	Contig source	5 pos	Primer 3 pos	Primer Basis	Selection	aat	Blast Score	Blast Prob	% id	% cvrg	Description
21053	ENU04847	ANI61C9706:	22-48	725-747	NAP	g1805262	3278	103	2.00E-45	39	13	"(U75347) fatty acid synthase, beta subunit [Emericella nidulans]"
21054	ENU04848	ANI61C3226:	58-77	676-695	NAP	g1723578	359	96	3.00E-29	50	60	probable oxidoreductase C26F1.07 in chromosome I [Schizosaccharomyces pombe] (AF104442) inhibitor resistant beta lactamase TEM-54 [Escherichia coli] (AF062655) plenty-of-prolines-101; POP101; SH3-philo-protein [Mus musculus]
21055	ENU04849	ANI61C1235:	22-49	783-810	NAP	g4557168	1419	530	e-150	97	99	(AF104442) inhibitor resistant beta lactamase TEM-54 [Escherichia coli] (AF062655) plenty-of-prolines-101; POP101; SH3-philo-protein [Mus musculus]
21056	ENU04850	ANI61S1182:	1..976		NAP	g3153821	177	34	0.99	26	29	"(AF046872) Cu,Zn-superoxide dismutase [Candida albicans]" (U51327) versicolorin B synthase [Aspergillus parasiticus] (Z68904) ATP-binding cassette multidrug transporter [Emericella nidulans]
21057	ENU04851	ANI61C7768:	24-51	468-492	NAP	g3005097	502	109	2.00E-48	67	99	"(AF046872) Cu,Zn-superoxide dismutase [Candida albicans]" (U51327) versicolorin B synthase [Aspergillus parasiticus] (Z68904) ATP-binding cassette multidrug transporter [Emericella nidulans]
21058	ENU04852	ANI61C43396:	55-76	768-787	NAP	g1293655	416	155	4.00E-37	41	37	"(AF046872) Cu,Zn-superoxide dismutase [Candida albicans]" (U51327) versicolorin B synthase [Aspergillus parasiticus] (Z68904) ATP-binding cassette multidrug transporter [Emericella nidulans]
21059	ENU04853	ANI61C1049	22-46	775-802	NAP	g1834340	4837	489	e-138	95	18	"(AF046872) Cu,Zn-superoxide dismutase [Candida albicans]" (U51327) versicolorin B synthase [Aspergillus parasiticus] (Z68904) ATP-binding cassette multidrug transporter [Emericella nidulans]
21060	ENU04854	ANI61C6622:	81-100	479-500	NAP	g131768	555	226	9.00E-59	60	34	quinate permease (quinate transporter) [Emericella nidulans]
21061	ENU04855	ANI61S1397:	552...1		NAP	g140011	497	182	1.00E-45	85	30	mitochondrial ribosomal protein S5 [Emericella nidulans]
21062	ENU04856	ANI61C1122	122-144	458-482	NAP	g2493391	359	155	1.00E-37	49	38	probable sterigmatocystin biosynthesis P450 monooxygenase STCB (cytochrome P450 62) [Emericella nidulans]
21063	ENU04857	ANI61C9762:	78-97	305-331	NAP	g731700	228	104	2.00E-22	41	31	hypothetical 42.4 KD protein in CDC12-ORC6 intergenic region [Saccharomyces cerevisiae]
21064	ENU04858	ANI61C957:1	102-125	516-543	NAP	g1703456	520	219	2.00E-56	52	18	cation-transporting ATPase PAT1 [Dictyostelium discoideum]
21065	ENU04859	ANI61C3989:	874..1	55-74	NAP	g1293655	332	78	8.00E-31	36	38	(U51327) versicolorin B synthase [Aspergillus parasiticus] (AF059777) mitogen-activated protein kinase kinase CPK1 [Cryptonectria parasitica] (AF053883) coatomer alpha subunit [Emericella nidulans]
21066	ENU04860	ANI61C5606:	1..829	66-85	NAP	g4106374	910	178	1.00E-89	73	46	translocation protein SEC66 (HSS1 protein) [Saccharomyces cerevisiae]
21067	ENU04861	ANI61S4332:	397..1		NAP	g3170523	637	258	1.00E-68	99	10	(AF053883) coatomer alpha subunit [Emericella nidulans]
21068	ENU04862	ANI61C9112:	22-48	725-752	NAP	g464738	138	58	0.000000	09		

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database	Hit ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description	
21069	ENU04863	ANI61C320:1	744..2877	NAP	g940860	461	147	8.00E-35	51	29	(X90565) MYO2	[Saccharomyces cerevisiae]		
21070	ENU04864	ANI61C6479:	97-116	651-672	NAP	g1749498	176	95	5.00E-19	28	77	(D89145) similar to <i>Saccharomyces cerevisiae</i> ORF YGL092W	[Schizosaccharomyces pombe]	
21071	ENU04865	ANI61C7648:	27-50	373-400	NAP	g1170421	180	60	3.00E-13	40	21	HUS2 protein	[Saccharomyces cerevisiae]	
21072	ENU04866	ANI61C7910:	1..428	NAP	g113314	3671	454	e-136	89	7	delta-(L-alpha-aminoacyl)-L-cysteinyl-D-valine synthetase (ACVS)	(ACVS) [Emmericella nidulans]		
21073	ENU04867	ANI61C1224:	64-91	638-663	NAP	g462071	797	290	7.00E-85			"fatty acid synthase, subunit beta		
21074	ENU04868	ANI61C9303:	27-54	805-829	NAP	g4755188	521	73	8.00E-24			[Yarrowia lipolytica]" (AC007018) unknown protein		
21075	ENU04869	ANI61C2783:	22-44	677-695	NAP	g2414579	545	216	1.00E-55	49	44	[Arabidopsis thaliana] (Z99292) flavoprotein		
21076	ENU04870	ANI61C1014	6:1022..265	50-69	635-657	NAP	g1730743	387	183	9.00E-46	46	77	[Schizosaccharomyces pombe] hypothetical 34.9 KD protein in MSK1-PDA2 intergenic region	
21077	ENU04871	ANI61C3868:	22-49	435-461	NAP	g2494018	214	89	3.00E-17	35	79	maltose O-acetyltransferase (maltose transacetylase)	[Escherichia coli]	
21078	ENU04872	ANI61C1035	22-49	515-534	NAP	g2315274	419	76	1.00E-32	49	51	(Y11113) endoglucanase IV [Hypocreja jecorina]		
21079	ENU04873	ANI61C8581:	22-42	799-819	NAP	g3980401	213	127	7.00E-29	33	97	(AC004561) putative tropinone reductase	[Arabidopsis thaliana]	
21080	ENU04874	ANI61C27:1..271	24-51	715-742	NAP	g586352	1238	134	1.00E-30	34	22	hypothetical 124.0 KD protein in PCS60-ABDI intergenic region		
21081	ENU04875	ANI61C1053	185-204	810-829	NAP	g2851424	181	100	1.00E-20	25	75	[Saccharomyces cerevisiae] hypothetical 37.5 KD protein in DEGA-NPRB intergenic region		
21082	ENU04876	ANI61C7988:	40-59	665-691	NAP	g1175361	150	55	0.000000	29	51	[Bacillus subtilis] hypothetical 48.5 KD protein		
		770..1				4						C13C5_02 in chromosome I		
21083	ENU04877	ANI61C1202:	22-41	786-808	NAP	g2342601	790	166	2.00E-40	37	5	[Schizosaccharomyces pombe] (X89442) peptide synthetase		
21084	ENU04878	ANI61C5153:	40-59	768-787	NAP	g1706176	977	316	2.00E-85	71	25	[Metarrhizium anisopliae] cutinase transcription factor 1 alpha		
		216..1177										[Fusarium solani f. sp. pisii]		

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	aat	Blast Score	Blast Prob	% id	% cvrg	Description
21085	ENU04879	ANI61C6712:	22-49	722-749	NAP	g1709997	726	48	0.0001			DNA repair protein RAD18
21086	ENU04880	ANI61C499:7	63-82	806-829	NAP	g2909648	548	157	5.00E-47	53	95	[Schizosaccharomyces pombe] (AL021943) echA5 [Mycobacterium tuberculosis]
21087	ENU04881	ANI61C4145:	64-90	485-504	NAP	g1078626	954	346	5.00E-95	99	12	bimD protein - <i>Emericella nidulans</i>
21088	ENU04882	ANI61C7661:	102-123	291-310	NAP	g464435	303	126	6.00E-29	53	26	[Aspergillus niger] acid phosphatase precursor
21089	ENU04883	ANI61C6082:	68-87	804-826	NAP	g1805261	645	166	1.00E-44	40	13	"(U75347) fatty acid synthase, alpha subunit [Emericella nidulans]" (AC002534) hypothetical protein [Arabidopsis thaliana] (AF097728) pyruvate carboxylase [Aspergillus terreus]
21090	ENU04884	ANI61S373:1.	42-61	257-276	NAP	g2392764	335	141	4.00E-34	78	17	(AF071202) ABC transporter MOAT-B [Homo sapiens] (AC000133) ORF [Emericella nidulans]
21091	ENU04885	ANI61C3838:	23-46	807-826	NAP	g3335173	373	71	1.00E-17			
21092	ENU04886	ANI61C1035	60-79	791-810	NAP	g1870208	2179	466	e-130	96	23	(AF097728) pyruvate carboxylase [Aspergillus terreus]
21093	ENU04887	ANI61C4237:	31-50	807-829	NAP	g91..2338	891..2338					(AF071202) ABC transporter MOAT-B [Homo sapiens] (AC000133) ORF [Emericella nidulans]
21094	ENU04888	ANI61C1042	22-43	810-829	NAP	g2495217	1971	436	e-121	78	57	glucokinase (glucose kinase) (GLK) [Aspergillus niger]
21095	ENU04889	ANI61C5224:	23-50	801-827	NAP	g1077569	1088	208	3.00E-75	53	37	probable membrane protein YDR109c - yeast (Saccharomyces cerevisiae) [Saccharomyces cerevisiae]
21096	ENU04890	ANI61C3404:	22-48	790-810	NAP	g2131132	213	90	1.00E-17	24	19	UDPGlucose--glycoprotein glucosidophosphotransferase (EC 2.7.8.19) - fission yeast (Schizosaccharomyces pombe) [Schizosaccharomyces pombe] (AL035226) putative structure specific recognition protein, possible chromatin-associated HMG protein
21097	ENU04891	ANI61C2738:	35-54	780-805	NAP	g4160575	539	122	2.00E-49	53	42	[Schizosaccharomyces pombe] hypothetical 25.3 KD protein in TIM23-ARE2 intergenic region [Saccharomyces cerevisiae]
21098	ENU04892	ANI61C1038	151-170	702-721	NAP	g1730665	121	67	2.00E-10	29	91	
21099	ENU04893	ANI61C2329:	30-54	795-820	NAP	g4507295	250	85	4.00E-16	28	99	syntaxis 7 [Homo sapiens]
			1177..2017									

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database	Hit ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvg	%
21100	ENU04894	ANT61C1038	22..46	535..562	NAP		g3790261	371	160	1.00E-38	43	65	(AL031966) putative quinone oxidoreductase [Schizosaccharomyces pombe]
21101	ENU04895	ANI61S1377:	70..89	378..397	NAP		g2494062	740	292	8.00E-79	98	51	hypothetical 30.8 KD protein in GIP-FDRA intergenic region [Escherichia coli] (AL033534) acetyl-coa acetyltransferase
21102	ENU04896	ANT61C1013	22..49	766..789	NAP		g3873546	1129	190	6.00E-75	57	66	D-amino acid oxidase (DAMOX) (DAO) (DAO) [Nectria haematoxocca]
21103	ENU04897	ANT61C1117	105..128	377..401	NAP		g129302	329	132	2.00E-30	43	47	"lysyl-tRNA synthetase, cytoplasmic (lysine--tRNA ligase) (LYSRS) [Saccharomyces cerevisiae]", "Chain A, Aspartate Aminotransferase From Saccharomyces Cerevisiae Cytoplasm ["hypothetical protein YGL244w - yeast (Saccharomyces cerevisiae) (Saccharomyces cerevisiae)]
21104	ENU04898	ANT61C4968:	22..48	769..788	NAP		g135139	1151	348	3.00E-95	57	47	"lysyl-tRNA synthetase, cytoplasmic (lysine--tRNA ligase) (LYSRS) [Saccharomyces cerevisiae]", "Chain A, Aspartate Aminotransferase From Saccharomyces Cerevisiae Cytoplasm ["hypothetical protein YGL244w - yeast (Saccharomyces cerevisiae) (Saccharomyces cerevisiae)]
21105	ENU04899	ANT61C6717:	27..46	806..829	NAP		g3660282	574	88	9.00E-30	39	54	"lysyl-tRNA synthetase, cytoplasmic (lysine--tRNA ligase) (LYSRS) [Saccharomyces cerevisiae]", "Chain A, Aspartate Aminotransferase From Saccharomyces Cerevisiae Cytoplasm ["hypothetical protein YGL244w - yeast (Saccharomyces cerevisiae) (Saccharomyces cerevisiae)]
21106	ENU04900	ANT61C6446:	22..48	706..730	NAP		g1077167	152	73	3.00E-12	23	53	"lysyl-tRNA synthetase, cytoplasmic (lysine--tRNA ligase) (LYSRS) [Saccharomyces cerevisiae]", "Chain A, Aspartate Aminotransferase From Saccharomyces Cerevisiae Cytoplasm ["hypothetical protein YGL244w - yeast (Saccharomyces cerevisiae) (Saccharomyces cerevisiae)]
21107	ENU04901	ANT61C989:1	63..86	774..801	NAP		g1546072	903	55	0.000000	21	9	(U68040) polyketide synthase [Cochliobolus heterostrophus] YPT1-related protein 2
21108	ENU04902	ANT61C4177:	22..44	428..447	NAP		g141305	472	172	6.00E-47			[Schizosaccharomyces pombe] putative translational activator C18G6.05C (GCN1 homolog) [Schizosaccharomyces pombe] (AF043230) trehalose-6-phosphate synthase subunit 1 [Emericella nidulans]
21109	ENU04903	ANT61C7502:	27..50	795..822	NAP		g1351721	1692	296	2.00E-85	56	10	glucose oxidase precursor (glucose oxyhydrase) (GOD) (beta-D-glucosidase) [Talaromyces flavus] (AF067650) sarcosine dehydrogenase [Rattus norvegicus]
21110	ENU04904	ANT61C7090:	23..43	794..813	NAP		g3170246	1708	398	e-128	98	49	glucose oxidase precursor (glucose oxyhydrase) (GOD) (beta-D-glucosidase) [Talaromyces flavus] (AF067650) sarcosine dehydrogenase [Rattus norvegicus]
21111	ENU04905	ANT61C4732:	96..115	302..321	NAP		g3287841	94	54	0.000000	30	19	glucose oxidase precursor (glucose oxyhydrase) (GOD) (beta-D-glucosidase) [Talaromyces flavus] (AF067650) sarcosine dehydrogenase [Rattus norvegicus]
21112	ENU04906	ANT61C5835:	1256..1		NAP		g3283373	230	82	4.00E-15	30	28	glucose oxidase precursor (glucose oxyhydrase) (GOD) (beta-D-glucosidase) [Talaromyces flavus] (AF067650) sarcosine dehydrogenase [Rattus norvegicus]

Seq num	Seq id	Contig source	5 pos	3 pos	Primer Basis	Primer Database	Selection Hit	aat	Blast Score	Blast Prob	% id	% cvrg	Description
21113	ENU04907	ANI61C6337:	71..90	800..819	NAP	g3451309	427	140	6.00E-45	40	95	(AL031324)	transcription initiation factor IIE beta subunit (TFIIE-beta) [Schizosaccharomyces pombe] (AB021703) fr [Neurospora crassa]
21114	ENU04908	ANI61C6864:	22..48	804..824	NAP	g4063002	937	228	4.00E-59	42	35	(Z97052)	putative ubiquinone biosynthesis methyltransferase [Schizosaccharomyces pombe] hypothetical 24.4 KD protein C22E12.02 in chromosome I [Schizosaccharomyces pombe] quinate 5-dehydrogenase (EC 1.1.1.24) - Emericella nidulans []
21115	ENU04909	ANI61S4630:	561..258		NAP	g2213547	201	95	1.00E-19	46	33	(AF053883)	coatomer alpha subunit [Emericella nidulans]
21116	ENU04910	ANI61C4391:	33..52	411..430	NAP	g1723516	327	144	4.00E-34	59	53	hypothetical 38.2 KD protein in SUB1-ARGR1 intergenic region [Saccharomyces cerevisiae]	
21117	ENU04911	ANI61C1164:	31..53	247..266	NAP	g101797	469	195	8.00E-50	85	33	hypothetical 53.5 KD protein C1F5.07C in chromosome I [Schizosaccharomyces pombe] (X94769)	
21118	ENU04912	ANI61C8818:	122..142	397..416	NAP	g3170523	546	191	2.00E-48	94	10	choline dehydrogenase [Rattus rattus]	
21119	ENU04913	ANI61C2376:	30..49	786..805	NAP	g2497129	446	111	6.00E-24	38	72	melanin biosynthetic polyketide synthase PKS1 - Colletotrichum lagenarium [Colletotrichum lagenarium]	
21120	ENU04914	ANI61C3368:	22..41	800..827	NAP	g1351682	425	82	3.00E-16	28	48	lysophospholipase precursor (phospholipase B) [Penicillium chrysogenum]	
21121	ENU04915	ANI61C9569:	24..43	804..829	NAP	g1154950	129	47	2.00E-11	27	35	sterol O-acyltransferase 2 (sterol-ester synthase 2) [Saccharomyces cerevisiae]	
21122	ENU04916	ANI61C8170:	1..2682	28..47	NAP	g2147662	1979	238	4.00E-62	46	12	ran GTPASE activating protein 1 (RNA1 protein) [Schizosaccharomyces pombe]	
21123	ENU04917	ANI61C6409:	95..114	551..577	NAP	g730338	774	289	1.00E-77	67	36		
21124	ENU04918	ANI61C9456:	46..65	734..757	NAP	g1173091	497	171	4.00E-42	49	63		
21125	ENU04919	ANI61C9369:	84..106	500..527	NAP	g1703371	253	93	8.00E-24	43	22		

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database	Hit ncbi gi	Score	Score Prob	% id	% cvrg	Description
21126	ENU04920	ANI61C7770:	72-91	689-710	NAP	g1352918	517	179	6.00E-45	44	55	CAAX prenyl protease 1 (prenyl protein-specific endoprotease 1) (PPSEP 1) (A-factor converting enzyme) [Saccharomyces cerevisiae] (AJ011965) oxidoreductase [Claviceps purpurea]
21127	ENU04921	ANI61C8438:	37-56	745-764	NAP	g4499843	609	91	2.00E-19	38	53	(AJ011965) oxidoreductase [Claviceps purpurea] (L47346) alpha-glucoside permease [Saccharomyces cerevisiae]
21128	ENU04922	ANI61S3872:	181-202	432-459	NAP	g992919	185	91	4.00E-18	32	26	[U32375] tartrate dehydrogenase [Agrobacterium vitis]
21129	ENU04923	ANI61C2942:	22-43	643-660	NAP	g984373	687	198	2.00E-69	66	58	(AL023534) putative methionine aminopeptidase 1
21130	ENU04924	ANI61C1073	117-136	418-439	NAP	g3130036	372	128	2.00E-37	60	35	[Schizosaccharomyces pombe] (AL031179) atp synthase delta chain family; oligomycin sensitivity conferring protein
21131	ENU04925	ANI61C7314:	44-63	480-507	NAP	g3395587	183	53	1.00E-14	45	52	[Schizosaccharomyces pombe] (AL031179) atp synthase delta chain family; oligomycin sensitivity conferring protein
21132	ENU04926	ANI61C2478:	22-48	454-478	NAP	g118292	258	109	1.00E-23	38	100	4-carboxymuconolactone decarboxylase (CMD) [Acinetobacter calcoaceticus]
21133	ENU04927	ANI61C4431:	27-46	807-828	NAP	g2132120	139	175	5.00E-43	27	19	hypothetical protein YOR296w - yeast (Saccharomyces cerevisiae)
21134	ENU04928	ANI61C6376:	22-47	805-828	NAP	g3548818	348	134	1.00E-30	37	64	[AC005313] unknown protein [Arabidopsis thaliana]
21135	ENU04929	ANI61C8026:	26-45	613-632	NAP	g2130442	1140	129	5.00E-34	33	29	hypothetical protein SPAC8A4.01C - fission yeast (Schizosaccharomyces pombe) (fragment)
21136	ENU04930	ANI61C5280:	40-59	605-624	NAP	g2120955	387	175	2.00E-43	46	67	[Schizosaccharomyces pombe] ORF5 - Alcaligenes eutrophus
21137	ENU04931	ANI61C7663:	1840-2502	1639..1	NAP	g2493479	860	196	2.00E-49	47	21	[Ralstonia eutropha] "dynactin, 150 KD isoform (150 KD dynein-associated polypeptide) (DP-150) (DAP-150) (P150-glued)
21138	ENU04932	ANI61S996:1.	28-48	249-273	NAP	g2494589	129	58	0.000000	37	22	[Neurospora crassa] putative folylpolyglutamate synthase (folylpoly-gamma-glutamate synthetase) (FPGS) [Saccharomyces cerevisiae]
		.300										

Seq num	Seq id	Contig source	5 pos	3 pos	Primer Basis	Primer Selection	aat	Blast	Blast	%				
					Database Hit	ncbi gi	Score	Score	Prob	% id	cvg	Description		
21139	ENU04933	ANI61C1866:	42-61	435-463	NAP	g2997731	650	222	1.00E-57	68	48	(AF054512) endoglucanase V [Aspergillus aculeatus]		
21140	ENU04934	ANI61C7308:	1576..1092	1..637	13-132	524-543	NAP	g2117031	538	190	7.00E-51	62	37	(X94220) rhamnogalacturonase [Aspergillus niger]
21141	ENU04935	ANI61C6373:	1..3346	22-49	680-702	NAP	g1546072	828	75	7.00E-13			(U68040) polyketide synthase [Cochliobolus heterostrophus]	
21142	ENU04936	ANI61C1004	3..4535..1974	22-47	809-829	NAP	g2465160	1351	92	5.00E-38	41	24	(Z99753) hypothetical protein [Schizosaccharomyces pombe]	
21143	ENU04937	ANI61C6032:	1..657	152-171	533-558	NAP	g1723241	167	72	4.00E-12	29	29	hypothetical protein C26A3.15C in chromosome I [Schizosaccharomyces pombe]	
21144	ENU04938	ANI61C3309:	27-46	768-787	NAP	g2440206	1169	155	7.00E-59	56	33	(Z99532) putative integral membrane protein [Schizosaccharomyces pombe] "dynein heavy chain, cytosolic (DYHC)" [Emericella nidulans]"		
21145	ENU04939	ANI61C9915:	906..1	58-81	805-825	NAP	g1169440	1451	321	e-150	97	6	(X89442) peptide synthetase [Metarhizium anisopliae]	
21146	ENU04940	ANI61C4247:	1..1862	23-45	752-778	NAP	g2342601	1009	261	6.00E-69	47	5	hypothetical 49.0 KD protein UFD4-CAP1 intergenic region [Saccharomyces cerevisiae]	
21147	ENU04941	ANI61C3772:	1125..814	72-91	253-272	NAP	g549657	284	98	2.00E-20	54	24	chromatin assembly factor 1 P90 subunit (CAF-1 90 KD subunit) (RAP1 localization factor 2) [Saccharomyces cerevisiae]	
21148	ENU04942	ANI61C7930:	1..1336	44-63	611-632	NAP	g3334134	203	48	0.00006	30	36	subunit (CAF-1 90 KD subunit) (RAP1 localization factor 2) [Saccharomyces cerevisiae]	
21149	ENU04943	ANI61C9002:	1069..579	57-76	447-466	NAP	g3687473	191	52	2.00E-10	44	99	(AL031798) WD repeat protein [Schizosaccharomyces pombe]	
21150	ENU04944	ANI61S3829:	1..529	1..529	712-731	NAP	g758803	90	46	0.0001	24	33	(U23828) peritrophin-95 precursor [Lucilia cuprina]	
21151	ENU04945	ANI61C4391:	2057..1	22-40	g3114719	949	72	4.00E-12	38	13	(Z68906) ATP-binding multidrug cassette transporter [Botryotinia fuckeliana] (AL021287) hypothetical protein Rv3049c [Mycobacterium tuberculosis]			
21152	ENU04946	ANI61C1720:	1181..1	116-138	721-748	NAP	g2791647	409	82	9.00E-23	29	48	(Saccharomyces cerevisiae) [Saccharomyces cerevisiae]	
21153	ENU04947	ANI61C1069	1..435	22-48	383-402	NAP	g2132249	348	123	6.00E-28	56	72	hypothetical protein YPL252c - yeast [Arabidopsis thaliana]	
21154	ENU04948	ANI61S3700:	457..1	113-132	408-428	NAP	g2462832	700	184	6.00E-69	92	26	[Arabidopsis thaliana]	

Seq num	Seq id	Contig source	5 pos	3 pos	Basis	Primer	Selection	aat	Blast Score	Blast Prob	% id	% cvg	Description
21155	ENU04949	ANI61C8568:	22-45	453-475	NAP	g4176522	291	136	2.00E-31	30	47	(AL035263) hypothetical protein	
21156	ENU04950	ANI61C8225:	39-62	806-829	NAP	g3264834	810	109	1.00E-45	46	77	[Schizosaccharomyces pombe] (AF072541) xylose dehydrogenase; XDH [Galactocandida mastotermitis]	
21157	ENU04951	ANI61C4401:	22-43	663-690	NAP	g1351102	282	124	2.00E-34	44	53	putative agmatinase precursor (agmatine ureohydrolase) (AUH) [Schizosaccharomyces pombe] (AB013376) unknown [Bacillus halodurans]	
21158	ENU04952	ANI61S4151:	31-51	245-271	NAP	g4514357	215	82	1.00E-17	35	100	(AB013376) unknown [Bacillus halodurans]	
21159	ENU04953	ANI61C1075	197-216	568-587	NAP	g730745	327	132	2.00E-30	38	17	osomolarity two-component system protein SLN1 [Saccharomyces cerevisiae]	
21160	ENU04954	ANI61C279:1	111-129	501-526	NAP	g3319315	271	104	5.00E-22	49	15	(AF074951) cellobiose dehydrogenase [Thielavia heterothallica]	
21161	ENU04955	ANI61C1025:	23-48	428-447	NAP	g1723260	396	173	8.00E-43	52	27	hypothetical GTP-binding protein C3F10.16C in chromosome I	
21162	ENU04956	ANI61C9690:	27-54	688-715	NAP	g1166378	569	111	8.00E-24	32	25	[Schiosaccharomyces pombe] "L76169" reverse transcriptase, RNaseH [Glomerella cingulata]" (AF095741) unknown [Rattus norvegicus]	
21163	ENU04957	ANI61C1050	32-51	472-491	NAP	g3747107	96	67	1.00E-10	35	38	alpha-glucuronidase precursor (alpha-glucosiduronase) [Aspergillus tubingensis]	
21164	ENU04958	ANI61C7276:	6137..5602		NAP	g3912991	237	110	8.00E-24	39	19	coat assembly complex beta adaptin subunit [Rattus norvegicus]	
21165	ENU04959	ANI61C5836:	56-77	597-624	NAP	g4557469	620	185	4.00E-66			hypothetical 62.3 KD protein in PTP3-IV1 intergenic region	
21166	ENU04960	ANI61C5110:	22-43	712-731	NAP	g731485	811	159	5.00E-73	51	48	[Saccharomyces cerevisiae]	
21167	ENU04961	ANI61C5433:			NAP	g1001338	87	65	2.00E-12	27	50	(D64006) Ap-4-A phosphoylase II [Synchocystis sp.] hypothetical 36.4 KD protein in POP2-HOL1 intergenic region	
21168	ENU04962	ANI61C3958:	79-98	370-389	NAP	g1730686	96	39	0.014	25	45	[Saccharomyces cerevisiae]	
21169	ENU04963	ANI61C84:10	22-41	712-731	NAP	g2132651	712	249	3.00E-65	42	48	probable membrane protein YLL028w -yeast (Saccharomyces cerevisiae)	
21170	ENU04964	ANI61S1096:	38-57	445-464	NAP	g2673951	655	210	3.00E-58	66	16	[Saccharomyces cerevisiae] (U62933) multidrug resistance protein 1 [Aspergillus fumigatus]	

Seq num	Seq id	Contig source	5 pos	3 pos	Primer Basis	Primer Database	Selection Hit	aat ncbi gi	Score 431	Blast 180	Prob 4.00E-45	% id 62	% cvrg 23	Description
21171	ENU04965	ANI61C5094:	107-126	353-372	NAP	g584806								"ATP synthase alpha chain, mitochondrial precursor [Neurospora crassa]"
21172	ENU04966	ANI61C3659:	48-68	291-310	NAP	g849206	519	213	4.00E-55	74	26	(U28373) Etf1p: Elongation factor 2 (Swiss Prot accession number P32324). Note that the entire gene is not included in this cosmid.		
21173	ENU04967	ANI61C2382:	49-76	614-641	NAP	g1351604	150	52	2.00E-10	26	66	hypothetical 40.0 KD protein C4G8.14C in chromosome I [Z99165] hypothetical protein [Schizosaccharomyces pombe]		
21174	ENU04968	ANI61C1180:	22-47	684-709	NAP	g2408064	161	94	9.00E-19	29	23	(Z99162) hypothetical protein [Schizosaccharomyces pombe] (AB003109) beta-glucosidase [Humicola grisea var thermoidea] hypothetical 102.7 KD protein in PRP16-SRP40 intergenic region [Saccharomyces cerevisiae]		
21175	ENU04969	ANI61C2243:	22-41	728-749	NAP	g2408021	352	120	1.00E-26	37	41	[AB003109] beta-glucosidase [Humicola grisea var thermoidea] hypothetical 102.7 KD protein in PRP16-SRP40 intergenic region [Saccharomyces cerevisiae]		
21176	ENU04970	ANI61C2141:	22-43	658-677	NAP	g4249560	1044	268	1.00E-90	72	51	[Saccharomyces cerevisiae]		
21177	ENU04971	ANI61C9921:	24-51	539-565	NAP	g549643	191	79	3.00E-14	33	18	MINN9 protein [Candida albicans]		
21178	ENU04972	ANI61C2170:	23-42	714-740	NAP	g1709064	782	314	5.00E-85	57	75	(L28110) LON gene of <i>S. cerevisiae</i> is downstream of the HAP3 gene; Putative ATP-binding motif bp 1960 to bp 1986.; Putative catalytic site serine of serine proteases from bp 3109 to bp 3111 [Saccharomyces cerevisiae]		
21179	ENU04973	ANI61C7073:	68-88	360-381	NAP	g454438	317	111	2.00E-30	60	10	"branched-chain amino acid aminotransferase, mitochondrial precursor (BCAT) (TWT1 protein) [Saccharomyces cerevisiae]" (Y15839) fatty acid transporter protein [Cochliobolus heterostrophus] (AB025967) choriogenin Minor [Oryzias latipes]		
21180	ENU04974	ANI61C1121	52-71	601-628	NAP	g731024	387	138	3.00E-32	40	49	[Laccaria bicolor] iucB protein - <i>Escherichia coli</i> [Escherichia coli]		
21181	ENU04975	ANI61C2031:	69-96	356-383	NAP	g2687850	120	77	9.00E-14	24	25	[U93506] symbiosis-related protein [Escherichia coli]		
21182	ENU04976	ANI61S4631:	502..1		NAP	g4589850	142	62	0.000000	32	26	[Oryzias latipes]		
21183	ENU04977	ANI61C7290:	1..517		NAP	g2072023	420	138	3.00E-32	53	100	[Laccaria bicolor]		
21184	ENU04978	ANI61C6657:	916..186	103-123	421-440	NAP	g1073534	185	89	2.00E-17	39	43	[Escherichia coli]	
			1..416											

Seq num	Seq id	Contig source	5 pos	Primer 3 pos	Primer Basis	Selection Database	Hit ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
21185	ENU04979	ANI61C1051	28-55	807-829	NAP	g1085432	147	38	0.07	0.07	0.07	0.07	mucin (clone PGM-2A) - pig [Sus scrofa]
21186	ENU04980	ANI61C7282:	31-58	465-489	NAP	g4262216	336	138	2.00E-32	35	64	(AC006161) putative DNA binding protein [Arabidopsis thaliana]	
21187	ENU04981	ANI61S1306: 1..655			NAP	g4218005	179	49	0.00003	21	31	(AC006135) putative vicilin storage protein (globulin-like) [Arabidopsis thaliana]	
21188	ENU04982	ANI61C1082	116-135	662-686	NAP	g4538673	116	70	1.00E-11	26	57	"(AL09474) putative lipid metabolism protein, sphingomyelinase family similarity [Schizosaccharomyces pombe]"	
21189	ENU04983	ANI61C1252: 36-55	729..1091	418-436	NAP	g773414	434	183	8.00E-46	92	66	(U23751) beta galactosidase [Cloning vector pBBR1MCS-5]	
21190	ENU04984	ANI61C439:9	319..9705		NAP	g2330831	228	108	3.00E-23	26	53	(Z98530) myo-inositol transporter [Schizosaccharomyces pombe]	
21191	ENU04985	ANI61C8782: 29-50	942..1	720-739	NAP	g1351343	1615	547	e-155	98	26	positive regulator of purine utilisation [Emericella nidulans]	
21192	ENU04986	ANI61C295:6 925..7990	157-184	797-824	NAP	g2648302	278	103	2.00E-32	44	86	"(AE000952) 2-hydroxyhepta-2,4-diene-1,7-dioate isomerase [hpcE-2] [Archaeoglobus fulgidus]"	
21193	ENU04987	ANI61C6797: 62-81	1073..1	715-735	NAP	g2146821	548	91	1.00E-17	36	39	alpha-glucoside transport protein - yeast [Saccharomyces cerevisiae] []	
21194	ENU04988	ANI61C346:8 06..369	139-166	433-452	NAP	g3136049	132	63	0.000000	36	38	(AL023592) putative phosphatidylinositol-glycan-class c protein [Schizosaccharomyces pombe] (AF029346) chloride channel protein 3 [Oryctolagus cuniculus]	
21195	ENU04989	ANI61C7116: 2155..1			NAP	g2599548	1110	223	1.00E-57	40	34	(D90748) Spermidine/putrescine transport system permease protein PotB. [Escherichia coli]	
21196	ENU04990	ANI61C4598: 441..1	22-42	437-461	NAP	g1651554	745	294	2.00E-79	98	65	aflatoxin biosynthesis polyketide synthase (PKS) [Aspergillus parasiticus]	
21197	ENU04991	ANI61C5425: 724..1	96-115	597-616	NAP	g2492660	334	129	2.00E-29	36	11	hypothetical 50.8 KD protein in MIR1-STE18 intergenic region [Saccharomyces cerevisiae]	
21198	ENU04992	ANI61C8486: 2325..3743	22-42	807-829	NAP	g1176339	671	209	2.00E-53	43	60		

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	Score	Score	Blast Prob	% id	% cvrg	Description
21199	ENU04993	ANI61C948:1 ..580		NAP		g2190551	170	108	4.00E-23	28	38	"(AC001229) Similar to <i>C. elegans</i> hypothetical protein K07C5.6 (gb Z71181). ESTs	
21200	ENU04994	ANI61C4231: 22-41	414-435	NAP		g3859773	141	73	1.00E-12	32	20	(Z98598) hypothetical protein [Arabidopsis thaliana] "glucosidase 1/S2 precursor (glucan 1,4-alpha-glucosidase) (1,4-alpha-D-glucan glucosidase) (Saccharomyces cerevisiae var. diastaticus)"	
21201	ENU04995	ANI61C6504: 65-84	729-747	NAP		g728850	110	35	0.61			[Schizosaccharomyces pombe]	
21202	ENU04996	ANI61C1933: 1..571		NAP		g4249560	560	225	2.00E-58	66	34	(AB003109) beta-glucosidase [Humicola grisea var. thermoidea] (Z98981) hypothetical protein [Schizosaccharomyces pombe]	
21203	ENU04997	ANI61C6870: 1120..1	22-49	806-829	NAP	g2388995	360	148	4.00E-35	36	56	synapsin I splice form a - human []	
21204	ENU04998	ANI61S913:1..754		NAP		g107749	124	71	1.00E-11	27	34	"ankyrin 1, erythrocyte form 3 - human []" (Z98977) hypothetical protein [Schizosaccharomyces pombe] (Z93388) predicted using Genefinder; cDNA EST EMBL:D70912 comes from this gene; cDNA EST EMBL:D73452 comes from this gene; cDNA EST EMBL:D71574 comes from this gene; cDNA EST EMBL:D74229 comes from this gene; cDNA EST EMBL:D727... []	
21205	ENU04999	ANI61C2450: 1269..1	74-93	712-731	NAP	g1360744	340	84	3.00E-25	34	14	"ankyrin 1, erythrocyte form 3 - human []" (Z98977) hypothetical protein [Schizosaccharomyces pombe] (Z93388) predicted using Genefinder; cDNA EST EMBL:D70912 comes from this gene; cDNA EST EMBL:D73452 comes from this gene; cDNA EST EMBL:D71574 comes from this gene; cDNA EST EMBL:D74229 comes from this gene; cDNA EST EMBL:D727... []	
21206	ENU05000	ANI61S719:4 91..1	23-41	451-470	NAP	g2656001	211	92	2.00E-18	39	20	[Schizosaccharomyces pombe]	
21207	ENU05001	ANI61C1120 5:9128..8237	22-49	802-829	NAP	g3879734	269	79	2.00E-18	38	93	cDNA EST EMBL:D70912 comes from this gene; cDNA EST EMBL:D73452 comes from this gene; cDNA EST EMBL:D71574 comes from this gene; cDNA EST EMBL:D74229 comes from this gene; cDNA EST EMBL:D727... []	
21208	ENU05002	ANI61C7395: 906..2125	22-47	744-764	NAP	g1723736	720	187	7.00E-47	43	43	hypothetical 68.3 KD protein in PDX1-SNGL intergenic region [Saccharomyces cerevisiae]	
21209	ENU05003	ANI61C3250: 1100..1	60-79	726-743	NAP	g2625138	574	233	1.00E-60	39	17	(AF032443) ABC1 transporter; ABC-type ATPase [Magnaporthe grisea] putative sterigmatocystin biosynthesis fatty acid synthase beta subunit [Emericella nidulans]	
21210	ENU05004	ANI61C587: 1..969	22-42	804-829	NAP	g2492658	1336	314	7.00E-85	99	12		

Seq num	Seq id	Contig source	5 pos	3 pos	Primer Basis	Primer Selection	aat	Blast Score	Blast Prob	% id	% cvrg	Description
					Database Hit	ncbi gi	Score					
21211	ENU05005	ANI61C9398:	102-124	523-547	NAP	g2851654	282	71	4.00E-22	43	31	2-dehydro-3-deoxyphosphogalactonate aldolase (6-phospho-2-dehydro-3-deoxygalactonate aldolase) (2-oxo-3-deoxygalactonate 6-phosphate aldolase) / galactonate dehydratase [Escherichia coli]
21212	ENU05006	ANI61C1139	22-47	795-814	NAP	g2498757	378	96	3.00E-19	31	52	peroxisomal membrane protein PAS2 (peroxin-3) [Pichia pastoris]
21213	ENU05007	ANI61C5990:	102-124	250-267	NAP	g2499716	206	94	3.00E-19	45	22	"exopolygalacturonase precursor (exoPG) (galacturan 1,4-alpha-galacturonidase) (poly(1,4-alpha-D-galacturonide)galacturonohydrolase) [Aspergillus tubingensis]" (AL023290) amino acid permease [Schizosaccharomyces pombe]
21214	ENU05008	ANI61C5102:	139-163	426-445	NAP	g3116147	179	67	2.00E-14	34	27	osomolarity two-component system protein SLN1 [Saccharomyces cerevisiae]
21215	ENU05009	ANI61C1061	26-46	722-749	NAP	g730745	63	48	0.00006	27	16	quinate 5-dehydrogenase (EC 1.1.1.24) – Emericella nidulans [Schizosaccharomyces pombe] methylenetetrahydrofolate dehydrogenase (NAD+)
21216	ENU05010	ANI61C5586:	1296..2033		NAP	g101797	1141	455	e-127	91	74	[Saccharomyces cerevisiae] (AC000133) ORF [Emericella nidulans]
21217	ENU05011	ANI61C1129	164-183	336-358	NAP	g417321	189	83	8.00E-16	46	33	replication factor-A protein 2 (single-stranded DNA-binding protein P30 subunit) [Schizosaccharomyces pombe] (AB004535) ATP-dependent RNA helicase MSS116 precursor [Schizosaccharomyces pombe]
21218	ENU05012	ANI61C1543:	928..625		NAP	g1870219	78	45	0.0002	30	99	hypothetical protein MJ0304 [Methanococcus jannaschii] (X89442) peptide synthetase [Metarhizium anisopliae]
21219	ENU05013	ANI61C8821:	24-50	791-818	NAP	g2498849	263	123	1.00E-27	33	86	
21220	ENU05014	ANI61C7941:	118-137	719-736	NAP	g2257514	387	157	6.00E-40	38	51	
			928..1									
21221	ENU05015	ANI61C5148:	110-129	454-473	NAP	g2493491	44	46	0.0002	25	92	
21222	ENU05016	ANI61C7063:	1..550		NAP	g2342601	1262	77	1.00E-13	27	4	
			3083..1									

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21223	ENU05017	ANI61C2576:	24-44	786-805	NAP		g1711573	610	156	6.00E-46	48	76	"probable succinyl-COA ligase (GDP-forming), alpha-chain precursor (succinyl-COA synthetase, alpha chain) (SCS-alpha) []"
21224	ENU05018	ANI61S335:5	63-90	486-509	NAP		g3360271	877	353	7.00E-97	97	20	(AC005824) putative selenium-binding protein [Arabidopsis thaliana] UDP-glucose 4-epimerase (galactowaldenase) / aldose 1-epimerase (mutarotase)
21225	ENU05019	ANI61C1118	22-45	525-548	NAP		g535169	422	129	4.00E-45	49	27	[Saccharomyces cerevisiae]
21226	ENU05020	ANI61C9007: 102-125	553-584	NAP			g730017	282	83	5.00E-20	50	26	cystathione gamma-synthase (O-succinylhomoserine (thiol)-lyase) []
21227	ENU05021	ANI61C1183: 68-87	717-736	NAP			g1723281	1051	122	3.00E-27	33	29	probable ATP-dependent DNA helicase C4H3.05 [Schizosaccharomyces pombe]
21228	ENU05022	ANI61C8411: 30-57	779-799	NAP			g1175914	811	248	4.00E-65	42	34	hypothetical 95.4 KD protein in SEC4-MSH4 intergenic region
21229	ENU05023	ANI61C1834: 104-131	756-782	NAP			g2353165	186	46	0.0002	34	97	[AF015561] RO10 [Neurospora crassa]
21230	ENU05024	ANI61S578:6	24..1	NAP			g1705828	157	69	9.00E-12	33	18	chitin synthase 2 (chitin-UDP acetyl-glucosaminyl transferase 2)
21231	ENU05025	ANI61C1040	41-60	795-822	NAP		g2791526	118	41	0.000000	32	63	[Emericella nidulans] (AL02246) echA14 [Mycobacterium tuberculosis]
21232	ENU05026	ANI61C1120	22-48	781-802	NAP		g4033481	233	69	2.00E-20	29	53	putative tartrate transporter [Agrobacterium vitis]
21233	ENU05027	ANI61C3812: 545..1	22-49	503-524	NAP		g3522935	63	57	0.000000	25	59	(AC00441) putative alcohol dehydrogenase [Arabidopsis thaliana]
21234	ENU05028	ANI61C2852: 1883..1	84-103	714-736	NAP		g2833193	594	85	6.00E-16	28	34	HOS3 protein [Saccharomyces cerevisiae]
21235	ENU05029	ANI61C5843: 1..941	61-81	806-829	NAP		g2267601	306	120	1.00E-26	33	47	(AF009417) cytochrome P450 [Myrothecium roridum] (Y17243) cytochrome P450 [Gibberella fujikuroi]
21236	ENU05030	ANI61C626:1	80-99	718-735	NAP		g4127832	601	144	6.00E-47	41	51	hypothetical 118.6 KD protein C29E6.03C in chromosome I [Schizosaccharomyces pombe]
21237	ENU05031	ANI61C8459: 233..1	33-53	805-828	NAP		g1351618	585	67	1.00E-10			
		9479...5897											

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database	Hit ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
21238	ENU05032	ANI61C1121:	22-42	802-829	NAP	g124871	489	151	6.00E-46	40	87	Inorganic pyrophosphatase (pyrophosphate phospho-hydrolase) (PPASE) [Kluyveromyces lactis] (AL03261) sulfate permease [Schizosaccharomyces pombe] (AC000133) ORF [Emeicella nidulans]	
21239	ENU05033	ANI61C4611:	28-47	728-747	NAP	g3417410	1275	252	2.00E-66	50	31	(AL03261) sulfate permease [Schizosaccharomyces pombe] (AC000133) ORF [Emeicella nidulans]	
21240	ENU05034	ANI61C1027	22-48	782-808	NAP	g1870209	2360	476	e-134	85	51	"(U95181) 2,5 dihydroxyphenylacetate oxidase [Caenorhabditis elegans]" hypothetical protein YKL201c - yeast (Saccharomyces cerevisiae) []	
21241	ENU05035	ANI61C1047	33-52	413-432	NAP	g4056552	379	114	2.00E-36	59	43	"(U95181) 2,5 dihydroxyphenylacetate oxidase [Caenorhabditis elegans]" hypothetical protein YKL201c - yeast (Saccharomyces cerevisiae) []	
21242	ENU05036	ANI61C8687:	43-62	626-645	NAP	g3912991	2086	419	e-116	67	33	alpha-glucuronidase precursor (alpha-glucosiduronase) [Aspergillus tubingensis] (AJ022172) protein kinase [Schizosaccharomyces pombe] (S59774) RNA polymerase subunit [Saccharomyces cerevisiae]	
21243	ENU05037	ANI61C7437:	102-126	454-473	NAP	g2980827	114	80	8.00E-15	41	32	ATP-dependent protease LA 2 [Myxococcus xanthus]	
21244	ENU05038	ANI61C6321:	62-80	747-766	NAP	g1680605	442	100	1.00E-42	52	99	hypothetical 27.5 KD protein in SPO1-SIS1 intergenic region [Saccharomyces cerevisiae]	
21245	ENU05039	ANI61C2198:	141-162	718-745	NAP	g547861	611	246	2.00E-64	48	32	[Pichia pastoris) []	
21246	ENU05040	ANI61C4414:	22-46	801-828	NAP	g1730705	400	90	6.00E-38	42	92	[Schizosaccharomyces pombe] (Z79700) hypothetical protein Rv0976c [Mycobacterium tuberculosis] (AL022600) putative mannose-1-phosphate gaanyl transferase [Schizosaccharomyces pombe] peroxisomal assembly protein 5 - yeast (Pichia pastoris) []	
21247	ENU05041	ANI61C6703:	51-73	805-829	NAP	g3261634	474	171	7.00E-42	42	40	extensin-like protein - maize [Zea mays]	
21248	ENU05042	ANI61C1053	22-42	616-634	NAP	g3080527	872	206	2.00E-52	43	65	hypothetical 87.5 KD protein in ACS1-GCV3 intergenic region [Saccharomyces cerevisiae]	
21249	ENU05043	ANI61S1767:	39-58	457-478	NAP	g539079	698	285	2.00E-76	70	16	"(U95181) 2,5 dihydroxyphenylacetate oxidase [Caenorhabditis elegans]" hypothetical protein YKL201c - yeast (Saccharomyces cerevisiae) []	
21250	ENU05044	ANI61S3339:	1..831	7:1..972	NAP	g1076802	116	37	0.000002	30	21		
21252	ENU05046	ANI61C9718:	25-48	292-316	NAP	g4100190	153	87	5.00E-17	40	26		
21253	ENU05047	ANI61S371:1.	665..328		NAP	g539218	96	43	0.002	16	30		
			.490										

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Primer Database Hit	aat ncbi gi	Score	blast Score	blast Prob	% id	cvg	%	Description
21254	ENU05048	ANT61C8803:	31..50	806..829	NAP	g4502091	410	160	1.00E-38	33	7			"ankyrin 2, neuronal [Homo sapiens]"
21255	ENU05049	ANI61C8498:	22..47	808..829	NAP	g4176530	2328	277	3.00E-86	57	22	(AL035263) putative condensin subunit [Schizosaccharomyces pombe] (X00790) cytochrome oxidase I [Emericella nidulans]		
21256	ENU05050	ANI61C1137:	5241..1481		NAP	g4468948	1258	490	e-138	92	49	homocitrate dehydratase [Saccharomyces cerevisiae]		
21257	ENU05051	ANI61C4514:	431..1282		NAP	g729967	150	75	1.00E-13	36	39	"Chain A, Phenol Hydroxylase From Trichosporon Cutaneum ["] 3-phytase precursor [Bacillus sp.]		
21258	ENU05052	ANI61C5723:	23..50	665..692	NAP	g3318897	453	221	4.00E-57	41	42			
21259	ENU05053	ANI61C7280:	22..46	802..821	NAP	g3914344	344	128	6.00E-29					
21260	ENU05054	ANI61C1544:	728...1942		NAP	g3828341	165	98	1.00E-19	30	18	(AB004305) mBLVR [Mus musculus]		
21261	ENU05055	ANI61C8211:	69..87	747..766	NAP	g1077413	809	260	2.00E-87	66	99	hypothetical protein YLR186w - yeast (Saccharomyces cerevisiae)		
21262	ENU05056	ANI61S9:1..5	86		NAP	g2465558	162	79	2.00E-14	37	74	(AF011545) YedB [Bacillus subtilis]		
21263	ENU05057	ANI61C9836:	22..45	804..828	NAP	g1351714	749	154	8.00E-37	34	55	putative transporter C11D3.18C [Schizosaccharomyces pombe]		
21264	ENU05058	ANI61C8454:	3361..1728	48..68	NAP	g2132208	739	210	1.00E-53	41	31	hypothetical protein YPL150w - yeast (Saccharomyces cerevisiae)		
			1381..2692										[Saccharomyces cerevisiae]	
21265	ENU05059	ANI61S13:69	8..1	157..174	618..645	NAP	g2804470	120	81	7.00E-15	28	16	(AF043701) contains similarity to ankyrin repeats and protein kinases [Caenorhabditis elegans]	
21266	ENU05060	ANI61C5161:	34..53	627..647	NAP	g3668157	513	82	5.00E-15			(AL031764) putative exocyst complex component [Schizosaccharomyces pombe]		
21267	ENU05061	ANI61C229:1	33..59	624..643	NAP	g419963	226	73	3.00E-12	44	83	snRNP protein B - fruit fly (Drosophila melanogaster) [Drosophila melanogaster]		
21268	ENU05062	ANI61C728:2	672..672		NAP	g3025214	231	80	1.00E-17	36	36	hypothetical 65.9 KD protein in SSP120-HAP1 intergenic region [Saccharomyces cerevisiae]		
21269	ENU05063	ANI61C9372:	4572..3951	115..134	388..407	NAP	g2146853	325	90	1.00E-17	45	32	alpha-galactosidase (EC 3.2.1.22) III precursor - fungus (Trichoderma reesei) [Hypocrealejecorina]	

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database	Hit ncbi gi	aat Score	Score	Blast Prob	% id	cvg	%	Description
21270	ENU05064	ANI61C6066:	192-211	455-479	NAP	g833697	633	254	4.00E-67	83	100			catabolic 3-dehydrogenase - Emericella nidulans [Emericella nidulans]
21271	ENU05065	ANI61C1113	64-82	786-804	NAP	g2507475	365	93	2.00E-18	36	9			Paired amphipathic helix protein [Saccharomyces cerevisiae]
21272	ENU05066	ANI61C3518:	210-237	571-598	NAP	g538067	157	44	0.0008	29	14			(M77661) putative polyprotein [Magnaporthe grisea] (AF051914) C-4 methyl sterol oxidase
21273	ENU05067	ANI61C9741:	55-74	794-813	NAP	g2970627	725	289	2.00E-77	50	86			[Candida albicans] putative mitochondrial carrier protein C12B10.09 [Schizosaccharomyces pombe]
21274	ENU05068	ANI61C9993:	107-130	673-699	NAP	g1723552	325	130	1.00E-29	44	62			
21275	ENU05069	ANI61C4742:	73-92	621-638	NAP	g3183171	784	318	2.00E-86	61	25			"probable alanyl-tRNA synthetase, cytoplasmic (alanine--tRNA ligase) (ALAR5) [Schizosaccharomyces pombe]"
21276	ENU05070	ANI61S4634:	227..538		NAP	g731584	114	31	6	35	60			hypothetical 17.1 KD protein in PUR5 3'region [Saccharomyces cerevisiae] (D83967) YfkN [Bacillus subtilis]
21277	ENU05071	ANI61C6461:	101-120	679-696	NAP	1..799								
21278	ENU05072	ANI61C720:1	47-66	800-824	NAP	g4505823	640	267	8.00E-71	48	94			pirin [Homo sapiens]
21279	ENU05073	ANI61C276:1	42-67	765-788	NAP	g2224775	595	226	2.00E-58	43	71			(Z97025) pyruvate carboxylase [Bacillus subtilis]
21280	ENU05074	ANI61C9649:	1..1530	26-45	NAP	g1546072	555	167	8.00E-41	37	11			(U68040) polyketide synthase [Cochliobolus heterostrophus] (AL034491) similar to yeast transcription initiation factor iif, alpha subunit [Schizosaccharomyces pombe]"
21281	ENU05075	ANI61S1135:	626..1		NAP	g4008576	172	53	0.000002	34	37			
21282	ENU05076	ANI61S1439:	58..57		NAP	g3329623	156	45	0.0007	17	69			(AF078790) No definition line found [Caenorhabditis elegans]
21283	ENU05077	ANI61C1060	94-116	798-817	NAP	8:1239..1								positive regulator of purine utilisation [Emericella nidulans]
21284	ENU05078	ANI61C8743:	3864..4464		NAP	g3646453	331	138	3.00E-32	38	100			(AL031603) putative succinate dehydrogenase cytochrome b subunit precursor [Schizosaccharomyces pombe]"
21285	ENU05079	ANI61C7969:			NAP	g208131	126	64	5.00E-10	42	98			(M77169) beta-galactosidase alpha-peptide [Shuttle vector pJIR1457]
			486..170											

Seq num	Seq id	Contig source	5 pos	3 pos	Primer Basis	Primer	Selection	aat	Blast Score	Blast Score	% id	% cvrg	Description
					ncbi gi	Database Hit	g400269	1494	377	e-104	64	52	
21287	ENU05081	ANI61C6968:	28-48	808-829	NAP		g1399263	1443	469	e-131	96	60	dehydrogenase precursor (acylating) (MMSDH) [Rattus norvegicus] (U28383) cystathione beta-lyase [Emericella nidulans]
21288	ENU05082	ANI61C1441:	121-141	664-683	NAP		g462168	617	248	3.00E-65	46	9	translational activator GCN1 [Saccharomyces cerevisiae] (AJ238717) ZRP protein [Rattus norvegicus]
21289	ENU05083	ANI61C249;5	93-112	317-344	NAP		g4757128	78	55	0.000000	3		hydroxyproline-rich glycoprotein - perennial teosinte [Zea diploperennis] (AF06241) splicing factor hPRP17 [Homo sapiens]
21290	ENU05084	ANI61S3273:	23..158		NAP		g283032	92	49	0.00003	27	57	(U62931) multidrug resistance protein 1 [Aspergillus flavus]
21291	ENU05085	ANI61C6213:	22-41	805-829	NAP		g3283220	1109	200	1.00E-71	56	51	(M59935) negative-acting regulatory protein [Emericella nidulans] (AL022299) putative serine palmitoyltransferase [Schizosaccharomyces pombe] (AJ132442) phenylacetate 2-hydroxylase [Emericella nidulans] beta-glucuronidase (GUS) (beta-D-glucuronoside glucuronosohydrolase) [Escherichia coli] (AB002377) KIAA0379 [Homo sapiens]
21292	ENU05086	ANI61C3458:	102-121	666-685	NAP		g2673947	594	226	2.00E-58	52	18	DNA repair protein RAD8 [Schizosaccharomyces pombe] (AL035637) putative protease subunit; chaperonin [Schizosaccharomyces pombe]
21293	ENU05087	ANI61S1524:	1..499		NAP		g168082	69	48	0.00004	35	17	major subunit [Staphylococcus aureus] (AL0222103) transmembrane transporter lizlp [Schizosaccharomyces pombe]
21294	ENU05088	ANI61C5043:	38-57	750-769	NAP		g3006156	905	175	6.00E-70	52	52	
21295	ENU05089	ANI61C1208:	8761..10108		NAP		g4867801	1922	49	0.00004			
21296	ENU05090	ANI61C2406:	118-137	638-658	NAP		g584839	599	239	1.00E-62			
21297	ENU05091	ANI61C1087	6:481..1		NAP		g2224699	97	67	9.00E-11	27	18	
21298	ENU05092	ANI61C721;5	93..1	65-87	468-492	NAP	g548669	313	151	3.00E-36	44	17	
21299	ENU05093	ANI61C1097	29-56	719-746	NAP		g4481954	1614	363	e-100	74	31	
21300	ENU05094	ANI61C5311:	22-45	463-482	NAP		g543325	188	92	3.00E-20	33	56	small nuclear ribonucleoprotein U1A - mouse [Mus musculus]
21301	ENU05095	ANI61S3796:	1..494		NAP		g4490609	361	109	6.00E-28	53	22	major subunit [Staphylococcus aureus] (AL0222103) transmembrane transporter lizlp [Schizosaccharomyces pombe]
21302	ENU05096	ANI61S2956:	35-53	287-306	NAP		g2956768	109	45	0.00001	29	33	
			1..451										

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat	Blast Score	Blast Prob	% id	% cvrg	Description
21303	ENTU05097	ANI61C9512:	23-50	736-757	NAP	g3183392	386	92	2.00E-36	45	99		C17A5.08 in chromosome I precursor [Schizosaccharomyces pombe]
21304	ENU05098	ANI61C6112:	26-45	722-749	NAP	g2633022	585	225	4.00E-58	43	31		(Z99107) yetA [Bacillus subtilis]
21305	ENU05099	ANI61C3343:	22-49	420-439	NAP	g1076211	101	33	1.6				hypothetical protein VSP-3- [Chlamydomonas reinhardtii]
		983...1											[Chlamydomonas reinhardtii] (AF007865) bacitracin synthetase I; BacA [Bacillus licheniformis]
21306	ENU05100	ANI61C1093	22-44	808-829	NAP	g2982194	494	163	1.00E-39	38	5		(AF052061) polygalacturonase [Ophiostoma novo-ulmi]
21307	ENU05101	ANI61C9439:	102-123	414-438	NAP	g2967835	312	70	1.00E-27	55	34		(L35487) mannanase [Aspergillus aculeatus]
21308	ENU05102	ANI61C1118	104-130	396-422	NAP	g558311	294	132	9.00E-31	52	34		putative sterigmatocystin biosynthesis ketoreductase STCE [Emericella nidulans]
21309	ENU05103	ANI61C7701:	59-76	773-792	NAP	g2492756	1193	372	e-102	95	92		(AF059534) severin kinase [Dictyostelium discoideum]
21310	ENU05104	ANI61C2235:	45-64	799-826	NAP	g3075511	823	58	0.000000	27	49		proline-rich protein MP2 - mouse (fragment) []
21311	ENU05105	ANI61C5581:	1..502		NAP	g91209	123	57	0.000000	29	67		hypothetical protein VSP-3- [Chlamydomonas reinhardtii] (Y07919) beta-prime-adaptin protein [Mus musculus]
21312	ENU05106	ANI61C9514:	118-138	525-552	NAP	g1076211	60	43	0.001	27	34		transcription elongation factor S-II (TFIIS) [Schizosaccharomyces pombe] (Z99531) ubiquitin system protein [Schizosaccharomyces pombe]
21313	ENU05107	ANI61C4192:	42-61	722-749	NAP	g2398720	1362	271	4.00E-72	51	27		ARP2/3 complex 20 KD subunit (P20-ARC) [Homo sapiens] (AF068065) Gp900; mucin-like glycoprotein [Cryptosporidium parvum]
21314	ENU05108	ANI61C2192:	40-58	431-450	NAP	g1351227	385	148	2.00E-35	43	57		hypothetical 49.1 KD protein C11D3.06 in chromosome I [Schizosaccharomyces pombe]
21315	ENU05109	ANI61C1130	48-71	782-806	NAP	g2440180	473	32	6.9				
21316	ENU05110	ANI61C7737:	60-80	484-507	NAP	g3121766	329	128	8.00E-30	72	68		
21317	ENU05111	ANI61S2227:	1616..1089		NAP	g4063042	154	39	0.033	30	11		
21318	ENU05112	ANI61C123:9	24-43	794-813	NAP	g1351703	856	284	7.00E-76	56	58		
		66..1											

Seq num	Seq id	Contig source	5 pos	Primer 3 pos	Primer Basis	Selection Database Hit	nebi gi	aat Score	Blast Score	Blast Prob	% id	cvg	% Description
21319	ENU05113	ANi61C5332:	27-46	802-829	NAP	g4033486	299	75	7.00E-13				[Agrobacterium vitis]
21320	ENU05114	ANi61C4918:	22-44	724-749	NAP	g1352677	1333	369	e-101	91	37		serine/threonine protein phosphatase 2B catalytic subunit (calmodulin-dependent calcineurin A subunit) [Emericella nidulans]
21321	ENU05115	ANi61C3944:	23-50	797-817	NAP	g3764029	825	168	6.00E-53	43	9	(AB001995) TellP	
21322	ENU05116	ANi61C8015:	69-88	756-775	NAP	g1362793	263	69	5.00E-11	33	99	[Schizosaccharomyces pombe] emopamil-binding protein - human [Homo sapiens]	
21323	ENU05117	ANi61C5643:	27-45	671-694	NAP	g1483603	128	105	3.00E-22	36	8	(X98690) Pristinamycin I synthase 2 [Streptomyces pristinaespiralis]	
21324	ENU05118	ANi61C3986:	41-60	776-796	NAP	g2342601	437	188	5.00E-47	34	5	(X89442) peptide synthetase [Metarrhizium anisopliae]	
21325	ENU05119	ANi61C8013:	45-71	805-829	NAP	g2388946	958	85	2.00E-33	36	48	"(Z98978) SPAC27E2.06c, putative methionyl-tRNA synthetase, leu539aa, similar eg. to YGR171C, SYMM_YEAST, P22438, methionyl-tRNA synthetase; mitochondrial, (575aa), fasta scores, opt:396, E:0, (39.9% identity in 546 aa o... [ ]" putative sterigmatocystin biosynthesis polyketide synthase (PKS) [Emericella nidulans]	
21326	ENU05120	ANi61C2723:	34-53	735-754	NAP	g2492661	1471	440	e-123	97	11	[U20808] auxin-induced protein [Vigna radiata]	
21327	ENU05121	ANi61S2128:	107-125	390-407	NAP	g1184121	130	66	1.00E-10	31	46	DNA-directed RNA polymerase I 190 KD polypeptide (A190)	
21328	ENU05122	ANi61C1070	23-47	656-683	NAP	g2507346	1768	335	2.00E-91	54	16	[Saccharomyces cerevisiae] (U32622) toluenesulfonate zinc-independent alcohol dehydrogenase [Comamonas testosterone] (AL021070) ppsB [Mycobacterium tuberculosis]	
21329	ENU05123	ANi61C4506:	102-128	453-472	NAP	g1790870	214	75	4.00E-13	44	50	(AC002292) Phosphatidylinositol 3-kinase [Arabidopsis thaliana]	
21330	ENU05124	ANi61C4658:	23-43	799-823	NAP	g3261497	676	232	3.00E-60	43	18	hypothetical 83.4 KD protein in DSK2-CAT8 intergenic region [Saccharomyces cerevisiae]	
21331	ENU05125	ANi61C4699:	489...1		NAP	g2462752	404	167	5.00E-41	51	20		
21332	ENU05126	ANi61C4285:	42-61	765-784	NAP	g2497216	610	244	5.00E-64	49	35		

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos Basis	Selection Database Hit	aat ncbi gi	Blast Score	Blast Prob	% id	% cvrg	Description
21333	ENU05127	ANI61C7878:	22-42	528-547 NAP	g1945326	184	91	5.00E-18	27	13	(Z72902) ORF YGR116w [Saccharomyces cerevisiae]
21334	ENU05128	ANI61S1312:	1..585	NAP	g1572721	137	41	0.008	28	15	(U70136) megakaryocyte stimulating factor; MSF [Homo sapiens]
21335	ENU05129	ANI61C4899:	34-53	781-800 NAP	g57554	201	101	5.00E-21	32	47	(X65296) carboxylesterase [Rattus rattus]
21336	ENU05130	ANI61C3565:	74-93	711-730 NAP	g3913798	1464	439	e-122	72	52	"exogucanase I precursor (exocellulobiohydrolase D) (1,4-beta-cellulobiohydrolase D) (beta-glucarcellulobiohydrolase D) [Aspergillus aculeatus]" Lipase 2 (triacylglycerol lipase) [Saccharomyces cerevisiae]
21337	ENU05131	ANI61C9214:	218-244	802-829 NAP	g1729921	198	57	0.000000	39	55	hypothetical 26.6 KD sensory transduction protein in IDH 3' region [Bacillus subtilis]
21338	ENU05132	ANI61S831:	.724	NAP	g1176993	383	168	3.00E-41	44	88	threonine dehydratase precursor (threonine deaminase) [Arxula adeninivorans]
21339	ENU05133	ANI61C4796:	22-47	528-547 NAP	g3915105	474	160	8.00E-39	61	33	(L41670) fumarylacetate hydrolase [Emericella nidulans]
21340	ENU05134	ANI61C2653:	92-111	540-559 NAP	g1130507	141	83	2.00E-15	31	46	(D90908) hypothetical protein [Synechocystis sp.]
21341	ENU05135	ANI61S957:	188-215	486-513 NAP	g1652748	345	150	5.00E-36	48	65	methyltetrahydrofolate dehydrogenase (NAD <sup>+</sup> )
21342	ENU05136	ANI61C953:	22-43	653-679 NAP	g417321	527	205	2.00E-52	59	64	[Saccharomyces cerevisiae] hypothetical protein (LAC12 3' region - yeast (Kluyveromyces marxianus var. lactis) [Kluyveromyces lactis]
21343	ENU05137	ANI61C1080	114-133	550-570 NAP	g82852	614	231	3.00E-63	61	45	probable uroporphyrin-III C-methyltransferase (urogen III methylase) (SUMT) (uroporphyrinogen III methylase) (UROMT)
21344	ENU05138	ANI61C4415:	51-70	537-555 NAP	g549009	201	67	4.00E-21	33	34	[Saccharomyces cerevisiae] (AF079317) flavoprotein subunit p-
			61..675								cresol methylhydroxylase [Sphingomonas aromaticivorans] (AJ132432) fimbrial [Gibberella pulicaris]
21345	ENU05139	ANI61C55:39	113-132	458-476 NAP	g3378433	233	80	6.00E-19	38	34	
		00..3276									
21346	ENU05140	ANI61C489:5	118-135	507-528 NAP	g4185903	717	291	2.00E-78	80	32	
		51..1									

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database	Hit	ncbi gi	aat	Blast Score	Blast Prob	% id	% cvrg	Description	
21347	ENU05141	ANI61C3097:	113-132	625-647	NAP	g417038	640	193	2.00E-64	65	45			[Saccharomyces cerevisiae] transcriptional activator GCN5	
21348	ENU05142	ANI61C1204:	205-228	685-712	NAP	g4539186	192	111	7.00E-24	31	58			(AL049485) probable zinc-binding alcohol dehydrogenase [Streptomyces coelicolor]	
21349	ENU05143	ANI61C1041	27-47	662-689	NAP	g731836	448	155	4.00E-50	51	37			probable mannosyltransferase KTR7 [Saccharomyces cerevisiae]	
21350	ENU05144	ANI61C4688:	22-40	730-752	NAP	g549443	1580	257	e-126	96	12			conidial green pigment synthase [Emericella nidulans]	
21351	ENU05145	ANI61C8490:	40-59	773-792	NAP	g112984	1245	158	3.00E-70	68	53			"aspartate aminotransferase, mitochondrial precursor (Transaminase A) (glutamate oxaloacetate transaminase-2) [Mus musculus]"	
21352	ENU05146	ANI61C1856:	22-46	449-476	NAP	g3560223	121	66	1.00E-10	29	48			(AL031523) hypothetical protein [Schizosaccharomyces pombe]	
21353	ENU05147	ANI61C33:86	22-47	718-744	NAP	g3184060	578	123	6.00E-50	49	26			(AL023776) ubiquitin carboxy-terminal hydrolase [Schizosaccharomyces pombe] (AF064069) aryl-alcohol oxidase precursor [Pleurotus eryngii]	
21354	ENU05148	ANI61C726:6	22-46	562-581	NAP	g3851524	190	97	1.00E-19	30	32			(AL033389) alcohol dehydrogenase [Schizosaccharomyces pombe] (AL031824) putative transcriptional regulator [Schizosaccharomyces pombe]	
21355	ENU05149	ANI61C2963:	32-59	331-354	NAP	g3850084	156	75	3.00E-13	32	46			"(U75347) fatty acid synthase, alpha subunit [Emericella nidulans]"	
21356	ENU05150	ANI61C8811:	49-68	336-356	NAP	g3702632	300	128	2.00E-29	48	18			hypothetical 33.7 KD protein in ISC10 3'region [Saccharomyces cerevisiae]	
21357	ENU05151	ANI61C2538:	53-73	410-434	NAP	g731385	165	72	2.00E-12	34	48			hydroxyproline-rich glycoprotein precursor - maize [Zea mays]	
21358	ENU05152	ANI61S1367:	1..457		NAP	g82698	210	45	0.0008	32	70			"(U75347) fatty acid synthase, alpha subunit [Emericella nidulans]" glucose oxidase precursor (glucose oxyhydrase) (GOD) (beta-D-glucosidase)	
21359	ENU05153	ANI61C6372:	1..720		NAP	g1805261	169	67	9.00E-11	33	9			[Talaromyces flavus]	
21360	ENU05154	ANI61C1057	7:1534..2318	22-44	700-719	NAP	g3287841	828	187	8.00E-47	63	43			hypothetical 68.5 KD protein in SCSS3-SUP44 intergenic region [Saccharomyces cerevisiae]
21361	ENU05155	ANI61C7117:	25-48	375-398	NAP	g1723913	499	209	1.00E-53	63	27				
			2458..2946												

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database	Hit ncbi	gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description	
21362	ENU05156	ANI61C3955:	120-138	486-505	NAP		g731968		486 203	1.00E-51	50	61		hypothetical 35.9 KD protein in HXT8-CRT1 intergenic region	
21363	ENU05157	ANI61C4224:	22-43	803-826	NAP		g4557481		761 148	4.00E-35	31	18		[Saccharomyces cerevisiae] canalicular multispecific organic anion transporter [Homo sapiens]	
21364	ENU05158	ANI61C7037:	1..1762		NAP		g4154078		195 93	7.00E-26	37	26		(AL035161) putative efflux protein [Streptomyces coelicolor]	
21365	ENU05159	ANI61C856:2	57-76	451-470	NAP		g1170131		209 103	7.00E-22	37	35		glucarate dehydratase subunit (GDH) [Pseudomonas putida]	
21366	ENU05160	ANI61C8308:	26-46	806-829	NAP		g1351678		130 43	0.003				hypothetical 41.5 KD protein C1F5_03C in chromosome I	
21367	ENU05161	ANI61C102	26-53	723-749	NAP		g82798		844 197	4.00E-71	55	15		[Schizosaccharomyces pombe] DNA-directed RNA polymerase (EC 2.7.7.6) 1189K chain - fission yeast (Schizosaccharomyces pombe)	
21368	ENU05162	ANI61S395:5	105-126	442-461	NAP		g4574121		146 85	4.00E-16	32	30		(AF009415) choline dehydrogenase [Staphylococcus xylosus]	
21369	ENU05163	ANI61C9793:	22-48	781-803	NAP		g2342601		1701 158	4.00E-38	30	5		(X89442) peptide synthetase [Metarhizium anisopliae]	
21370	ENU05164	ANI61C7505:	69-88	774-796	NAP		g1363761		598 73	6.00E-15				probable membrane protein YPR194c - yeast (Saccharomyces cerevisiae)	
21371	ENU05165	ANI61C2147:	33-52	455-477	NAP		g1723578		296 130	2.00E-30	48	53		[Saccharomyces cerevisiae] probable oxidoreductase C26F1.07 in chromosome I [Schizosaccharomyces pombe]	
21372	ENU05166	ANI61C1526:	46-64	803-822	NAP		g4456821		1167 306	5.00E-99	76	56		(AL035548) casein kinase i homolog ck1 [Schizosaccharomyces pombe]	
21373	ENU05167	ANI61C865:8	2630..1517	22-43	761-780	NAP		g3183368		810 191	7.00E-59	58	41		hypothetical 64.0 KD protein C20G4.05C in chromosome I
21374	ENU05168	ANI61S2442:	1..533		NAP		g1805261		251 94	5.00E-19	43	9		[Schizosaccharomyces pombe] ("U75347) fatty acid synthase, alpha subunit [Emericella nidulans]" (AL035064) protein kinase skp1p	
21375	ENU05169	ANI61C8742:	940..1	22-47	728-749	NAP	g4106669		791 225	1.00E-69	73	57		[Schizosaccharomyces pombe] (AJ000999) putative beta-subunit of K+ channels [Solanum tuberosum]	
		719..1					g3402279		415 152	9.00E-40	61	48			



Seq num	Seq id	Contig source	5 pos	Primer 3 pos	Primer Basis	Selection Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
21391	ENU05185	ANi61C6380:	33-52	797-817	NAP	g2342601	653	101	9.00E-21	25	5	(X89442) peptide synthetase [Metarhizium anisopliae]	
21392	ENU05186	ANi61S2843:	528..1		NAP	g1352946	366	136	1.00E-31	49	60	hypothetical 32.6 KD protein in DAL5-TH11 intergenic region [Saccharomyces cerevisiae]	
21393	ENU05187	ANi61C5497:	27-54	808-829	NAP	g2739355	2771	429	e-119	71	25	(AC003972) pNORF1 [Homo sapiens]	
21394	ENU05188	ANi61C5368:	22-44	787-806	NAP	g1729996	139	54	9.00E-11	32	75	TOXD protein [Cochliobolus carbonum]	
21395	ENU05189	ANi61C9887:	191-218	533-556	NAP	g3875727	225	65	2.00E-22	49	28	(Z70751) similar to 4-coumarate-CoA ligase; cDNA EST EMBL:CT7240 comes from this gene; cDNA EST EMBL:C08540 comes from this gene [Caenorhabditis elegans]	
21396	ENU05190	ANi61C8675:	24-43	725-744	NAP	g3121988	339	112	9.00E-30	34	48	betaine aldehyde dehydrogenase (BADH) [Rhodococcus sp.]	
21397	ENU05191	ANi61C3613:	22-48	332-356	NAP	g1711469	257	116	6.00E-26	47	29	dibenzothiophene desulfurization enzyme C (DBT sulfur dioxygenase)	
21398	ENU05192	ANi61C8895:	37-64	723-749	NAP	g102551	926	360	1.00E-98	65	17	Caenorhabditis elegans kinesin-related protein unc-104 - [Caenorhabditis elegans]	
21399	ENU05193	ANi61C2996:	75-95	666-685	NAP	g3913980	435	157	9.00E-44	50	49	probable kynureinase (L-kynureanine hydrolase) [Saccharomyces cerevisiae] (U53663) Nopp44/46 [Trypanosoma brucei]	
21400	ENU05194	ANi61C5409:	71-90	265-284	NAP	g1314705	85	35	0.18	31	33	NPL4 protein [Saccharomyces cerevisiae]	
21401	ENU05195	ANi61C1209:	22-44	748-775	NAP	g462739	216	106	3.00E-22	35	34	"(AC003970) Similar to Glucose-6-phosphate dehydrogenases, [Arabidopsis thaliana]" putative glycosyltransferase HOCl precursor [Saccharomyces cerevisiae]	
21402	ENU05196	ANi61S3756:	27-47	553-572	NAP	g3482917	544	142	1.00E-51	74	26	probable helicase MOT1 [Aspergillus niger]	
			593..1									Multidrug resistance-associated protein 4 [Homo sapiens]	
21403	ENU05197	ANi61C1055	22-41	788-808	NAP	g1352891	153	95	7.00E-19	24	69	NADPH-ferrithemoprotein reductase (EC 1.6.2.4) - Aspergillus niger	
21404	ENU05198	ANi61C4595:	67-87	492-516	NAP	g417308	457	94	8.00E-32			[Aspergillus niger]	
21405	ENU05199	ANi61C4356:	40-59	600-621	NAP	g481285	356	159	1.00E-38	36	32	Multidrug resistance-associated protein 4 [Homo sapiens]	
21406	ENU05200	ANi61C3342:	22-41	476-495	NAP	g3219829	178	60	5.00E-15	36	99		
			1571..1021										

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	Score	Score	Blast Prob	% id	% cvrg	Description
21407	ENU05201	ANi61C1135	22-48	497-521	NAP	g481230	148	88	5.00E-17	32	43	L-iditol 2-dehydrogenase (EC 1.1.1.14)	
21408	ENU05202	ANi61C7939:	22-41	519-539	NAP	g3567	217	96	2.00E-20	40	60	[Rattus norvegicus] precursor - rat [X55731] COX11 (AA 1-277)	
21409	ENU05203	ANi61C7448:	591...1		NAP	g1272506	444	125	7.00E-43	87	100	[Saccharomyces cerevisiae] [Candida maltsa] (D43686) L41 ribosomal protein	
21410	ENU05204	ANi61C2343:	3462..3016		NAP	g1652639	52	75	3.00E-13	26	12	(D90907) sensory transduction	
21411	ENU05205	ANi61C1286:	65-84	728-747	NAP	g2440190	606	187	1.00E-46	36	18	histidine kinase [Synechocystis sp.] (Z98602) putative protein transport	
21412	ENU05206	ANi61S281:1	1033...1		NAP	g433011	114	66	2.00E-10	29	53	protein sec7 homolog [Schizosaccharomyces pombe] (S62929) PRB1L precursor	
			2..632									protein=basic proline rich proteins (Ps, PmF, PmS, and Pe) precursor {C-terminal} [Homo sapiens]	
21413	ENU05207	ANi61C5167:	221-239	605-624	NAP	g3417437	226	102	3.00E-21	34	64	(AL031263) putative GTPase-activator protein for Rho-like GTPases	
21414	ENU05208	ANi61C2551:	27-47	775-795	NAP	g2072499	148	86	3.00E-16	29	31	[Schizosaccharomyces pombe] (U9690) myb-related transcription factor [Strongylocentrotus purpuratus] (U35661) colony 1 [Ophiostoma ulmi]	
21415	ENU05209	ANi61C9694:	703..1628	217-238	722-741	NAP	g998355	239	127	8.00E-29	30	33	
21416	ENU05210	ANi61C9624:	4641..3789	22-49	555-581	NAP	g1175373	390	137	6.00E-34	46	29	hypothetical 72.5 KD protein C2F7.10 in chromosome 1
21417	ENU05211	ANi61C6114:	1365..1999		NAP	g2388934	189	56	0.000000	38	23	[Schizosaccharomyces pombe] (Z98977) hypothetical protein	
21418	ENU05212	ANi61C7669:	296..1060	24-51	730-749	NAP	g3282044	1676	390	e-113	76	18	[Schizosaccharomyces pombe] (Y13967) alpha-aminoacidate reductase large subunit [Penicillium chrysogenum]
21419	ENU05213	ANi61C3906:	1364...1		NAP	g1710858	431	182	2.00E-45	50	65	putative SEC14 cytosolic factor (phosphatidylinositol/phosphatidyl-choline transfer protein) (PIP/C TP) [Schizosaccharomyces pombe]	
21420	ENU05214	ANi61C5852:	1.1.799	120-139	726-746	NAP	g730212	798	180	2.00E-89	72	90	NADH-ubiquinone dehydrogenase 24 KD subunit precursor [Neurospora crassa]
21421	ENU05215	ANi61C9289:	1..1309	22-46	807-829	NAP	g538067	523	161	6.00E-39	34	20	(M77661) putative pol polyprotein [Magnaporthe grisea]

Seq num	Seq id	Contig source	5 pos	Primer 3 pos	Primer Basis	Selection Database	nebi hit	aat gi	blast score	blast prob	% id	% cvrg	Description
21422	ENU05216	ANI61C7651:	28-51	787-806	NAP	g3978134	541	83	6.00E-32	48	24	(U65409) Sla2p [Yarrowia lipolytica]	
21423	ENU05217	ANI61C320:1	102-129	654-677	NAP	g2995360	481	99	6.00E-36	56	48	"DEAD/H (Asp-Glu-Ala-Asp/His) box protein. [Schizosaccharomyces pombe]"	
21424	ENU05218	ANI61C6917: 36-57	348-374	NAP	g4758126	241	62	0.000000	001			"DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide, Y chromosome [Homo sapiens]"	
21425	ENU05219	ANI61C9553: 23-44	801-828	NAP	g118233	452	55	2.00E-19				allantose permease [Saccharomyces cerevisiae]	
21426	ENU05220	ANI61C9720: 45-64	810-829	NAP	g1352079	1801	289	e-107	70	30		beta-glucosidase 1 precursor (gentiobiose) (cellobiose) (beta-D-glucoside glucohydrolase) [Aspergillus aculeatus]	
21427	ENU05221	ANI61C2169: 59-78	562-581	NAP	g4539264	662	241	4.00E-63	58	58		(AL049495) conserved hypothetical protein [Schizosaccharomyces pombe]	
21428	ENU05222	ANI61C4363: 27-50	711-731	NAP	g417305	702	190	1.00E-47	46	41		"mannosyl-oligosaccharide alpha-1,2-mannosidase (MAN(9)-alpha-mannosidase) [Saccharomyces cerevisiae]"	
21429	ENU05223	ANI61S1929: 111-134	521-544	NAP	g113314	891	356	5.00E-98	93	5		delta-[L-alpha-aminoacetyl]-L-cysteinyl-D-valine synthetase (ACVS) [Emericella nidulans]	
21430	ENU05224	ANI61C7050: 32-51	757-780	NAP	g2773302	270	179	2.00E-44	35	51		(AF040720) xylosidase/arabinosidase [Selenomonas ruminantium]	
21431	ENU05225	ANI61C6970: 22-49	797-824	NAP	g543961	210	85	8.00E-16				cell division control protein 14 [Schizosaccharomyces pombe] (Y12503) Man9-mannosidase [Sus scrofa]	
21432	ENU05226	ANI61C784:5 61..1	24-43	428-455	NAP	g2154997	247	134	3.00E-31	40	26		
21433	ENU05227	ANI61S3090: 1..457		NAP	g100210	156	37	0.09	32	45		extensin precursor (clone Tom L-4) - tomato [Lycopersicon esculentum] hypothetical protein YLR419w - yeast (Saccharomyces cerevisiae)	
21434	ENU05228	ANI61C3808: 743..1	101-120	617-640	NAP	g1363750	204	65	5.00E-20	30	15		[Saccharomyces cerevisiae]
21435	ENU05229	ANI61C1125 7:485..1	67-87	437-456	NAP	g4557387	157	70	4.00E-14	37	32		fumarylacetateacetate [Homo sapiens]
21436	ENU05230	ANI61C9186: 4850..1262	59-78	791-810	NAP	g4585936	1397	192	3.00E-48	38	21		(AC007211) putative helicase [Arabidopsis thaliana]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Basis	Database	Hit ncbi gi	aat Score	blast Score	blast Prob	% id	cvg %	Description	
21437	ENU05231	ANI61C2296:	22-49	779..801	NAP	g1217600	149	92	3.00E-19	27	48	(D38215)ter3	[Streptomyces aureofaciens]	
21438	ENU05232	ANI61C8809:	4890..5915	310..1320	NAP	g416657	576	162	2.00E-42	52	73	Anti-silencing protein 1	[Saccharomyces cerevisiae]	
21439	ENU05233	ANI61C1071	64-83	719-738	NAP	g2342601	1457	214	1.00E-57	40	5	(X89442) peptide synthetase	[Metarhizium anisopliae]	
21440	ENU05234	ANI61C79:28	22-46	630-649	NAP	g1174617	494	129	1.00E-42	64	33	"T-complex protein 1, epsilon subunit (TCP1-epsilon)(CCT-epsilon) []"	(AL023287) Satp	
21441	ENU05235	ANI61C9059:	29..3543	99-120	NAP	g3116126	93	61	0.000000	28	30	[Schizosaccharomyces pombe]	[U68040] polyketide synthase	
21442	ENU05236	ANI61C8724:	1..533	22-47	800-827	NAP	g1546072	493	70	2.00E-11			[Cochliobolus heterostrophus]	[AE000735] ATP dependent protease ATPase subunit clpX [Aquifex aeolicus]
21443	ENU05237	ANI61C4628:	1944..3970	108-126	548-567	NAP	g2983756	265	119	2.00E-26	42	40	(U48234) spU2AF23	[Schizosaccharomyces pombe]
			1..650										Copper amine oxidase 1 [Aspergillus niger]	
21444	ENU05238	ANI61C4376:	823..1527	22-45	646-673	NAP	g2347143	660	266	1.00E-70	59	99	Hypothetical protein YOR004w - yeast (Saccharomyces cerevisiae)	[Saccharomyces cerevisiae]
21445	ENU05239	ANI61C4928:	1597..1	72-91	781-807	NAP	g2501339	673	207	9.00E-53	51	35	putative ubiquitin carboxyl-terminal hydrolase C6G9.08 (ubiquitin thiolesterase) (ubiquitin-specific processing protease) (deubiquitinating enzyme) [Schizosaccharomyces pombe]	[X89715] AOF1001 [Saccharomyces cerevisiae]
21446	ENU05240	ANI61C9658:	2293..1816	72-89	434-456	NAP	g2132029	150	58	0.000000	37	56	hypothetical 33.7 KD protein in ISC10 region [Saccharomyces cerevisiae]	(AL035218) hypothetical protein
21447	ENU05241	ANI61C4358:	704..1569	31-49	719-738	NAP	g2842699	369	164	5.00E-40	42	50	hypothetical 68.8 KD protein C2F7.07C in chromosome I	[Schizosaccharomyces pombe]
21448	ENU05242	ANI61C4668:	1..996	38-57	726-747	NAP	g1177622	216	49	0.00004	28	27	[Schizosaccharomyces pombe]	[Schizosaccharomyces pombe]
21449	ENU05243	ANI61C1134	8:618..1	22-46	524-548	NAP	g4160578	154	79	2.00E-14	31	54	hypothetical 33.7 KD protein in ISC10 region [Saccharomyces cerevisiae]	(AL035218) hypothetical protein
21450	ENU05244	ANI61C639:7	12..322	22-45	452-479	NAP	g731385	158	94	8.00E-19	37	50	[Schizosaccharomyces pombe]	[U68040] polyketide synthase
21451	ENU05245	ANI61C7684:	640..1399	72-91	718-739	NAP	g1175370	177	120	1.00E-26	30	39	[Schizosaccharomyces pombe]	[Cochliobolus heterostrophus]

Seq num	Seq id	Contig source	5 pos	3 pos	Primer Basis	Primer Selection	aat	Blast	Blast	%	
					Database Hit	ncbi gi	Score	Score	Prob	id	cvg
21452	ENU05246	ANI61C8831:	22-43	453-478	NAP	g2132738	460	175	2.00E-43	61	98
2353..2820											
21453	ENU05247	ANI61C6666:	23-44	490-514	NAP	g2894269	245	117	7.00E-26	32	49
734..1											
21454	ENU05248	ANI61C5501:	23-50	725-748	NAP	g462414	1454	123	8.00E-64	69	45
605..2159											
21455	ENU05249	ANI61S150:5	110-130	376-399	NAP	g4263543	584	229	9.00E-60	85	15
74..155											
21456	ENU05250	ANI61S310:5	183-210	340-365	NAP	g3913727	496	142	8.00E-38	98	20
86..201											
21457	ENU05251	ANI61C5962:	22-48	779-801	NAP	g1351928	292	66	3.00E-25	38	65
1..1303											
21458	ENU05252	ANI61C6706:	37-54	803-829	NAP	g1166378	515	79	2.00E-25	34	24
2398..1											
21459	ENU05253	ANI61C8887:	118-137	372-399	NAP	g2132861	92	45	0.00002	32	56
1..420											
21460	ENU05254	ANI61C1016	27-50	700-723	NAP	g2738309	251	98	8.00E-20	31	51
0:827..1											
21461	ENU05255	ANI61C6324:	29-56	723-742	NAP	g730431	914	258	6.00E-70	62	27
1123..1											
21462	ENU05256	ANI61C1002:	2743..3805		NAP	g2804298	532	118	3.00E-36	38	51
21463	ENU05257	ANI61C4431:	56-75	460-484	NAP	g731809	182	91	4.00E-18	40	99
2430..1926											
21464	ENU05258	ANI61C6829:	110-129	389-416	NAP	g3764029	318	146	6.00E-35	51	5
21465	ENU05259	ANI61C1930:			NAP	g1170566	697	172	4.00E-54	47	51
1240..1											
21466	ENU05260	ANI61C3261:	22-47	737-759	NAP	g2370466	2515	146	2.00E-34	29	5
1..3275											
21467	ENU05261	ANI61C2859:	23-42	785-804	NAP	g1421604	431	177	7.00E-44	40	48
99..1099											

શ્રી મંત્રી સુધી દ્વારા નિર્ધારિત કરેલી અધ્યક્ષ વિભાગીઓ

Sed num	Seq id	Contig source	5 pos	3 pos	Primer Basis	Primer Selection	aat	Blast Score	Blast Prob	% id	cvg	%	
21468	ENU05262	ANI61C4819:	121-146	256-280	NAP	g3219530	226	106	5.00E-23	52	52	(AJ006688) IgE-binding protein	
21469	ENU05263	ANI61C1017	172-191	538-557	NAP	g558311	520	118	1.00E-51	57	51	[Aspergillus fumigatus] [L35487] mannanase [Aspergillus aculeatus]	
21470	ENU05264	ANI61C9994:	22-49	804-829	NAP	g4507293	354	185	3.00E-46	43	81	syntaxis 5A [Homo sapiens]	
21471	ENU05265	ANI61S1430:	26..1083	1..745	NAP	g4218005	156	62	0.000000	21	35	(AC006135) putative vicilin storage protein (globulin-like) [Arabidopsis thaliana]	
21472	ENU05266	ANI61C746:1	122-142	337-358	NAP	g418296	268	123	5.00E-28			vacuolar ATP synthase 95 KD subunit (vacuolar ATPase 95 KD subunit)	
21473	ENU05267	ANI61C2820:	22-44	490-509	NAP	g3169065	219	104	4.00E-22	32	19	(AL023704) putative translocation elongation factor-Tu fa mily	
21474	ENU05268	ANI61C7326:	50-75	308-335	NAP	g2499454	219	104	2.00E-22	46	34	[Schizosaccharomyces pombe] pectinesterase precursor (pectin methylesterase) (PE) [Aspergillus aculeatus]	
21475	ENU05269	ANI61C7855:	22-43	801-828	NAP	g2132944	430	183	1.00E-45	40	87	probable membrane protein YOR311c - yeast (Saccharomyces cerevisiae)	
21476	ENU05270	ANI61C1495:	102-126	464-483	NAP	g3850070	575	120	1.00E-56	58	28	[Saccharomyces cerevisiae] (AL033385) transketolase	
21477	ENU05271	ANI61C7628:	1..635	27-52	NAP	g2905657	323	138	1.00E-32	59	31	[Schizosaccharomyces pombe] (AF047469) arsenite translocating ATPase [Homo sapiens]	
21478	ENU05272	ANI61C7236:	1..386	22-42	NAP	g1077557	101	55	0.000000	30	26	probable membrane protein YDR061w - yeast (Saccharomyces cerevisiae)	
21479	ENU05273	ANI61C7050:	965..2783	22-40	NAP	g1929089	253	36	0.46			[Saccharomyces cerevisiae] (Z93777) hypothetical protein Rv1215c	
21480	ENU05274	ANI61C5946:	1.992	39-58	NAP	g4160583	578	218	4.00E-56	50	73	[Mycobacterium tuberculosis] (AL025218) conserved hypothetical protein [Schizosaccharomyces pombe] o-pyrocatechuate decarboxylase (EC 4.1.1.46) - Aspergillus niger (fragments) []	
21481	ENU05275	ANI61C8772:	51..569	22-45	NAP	g2133256	318	129	2.00E-30	68	39	(AL023534) major facilitator family transporter [Schizosaccharomyces pombe]	
21482	ENU05276	ANI61C1063	3:1017..1	47-66	755-780	NAP	g3130032	378	165	4.00E-40	35	48	







Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Primer Database Hit	aat ncbi gi	Blast Score	Blast Score	Blast Prob	% id	% cvrg	Description
21526	ENU05320	ANI61C1071	22-45	790-809	NAP	g549602	195	50	0.000002	32	75	hypothetical	32.0 KD protein in SAP190-SPO14 intergenic region
21527	ENU05321	ANI61C2481:	61-80	806-829	NAP	g1654028	262	49	0.00005				[Saccharomyces cerevisiae] (Z81360) hypothetical protein Rv1726
21528	ENU05322	ANI61S2482:	250..1826 77..598		NAP	g2465144	86	58	0.000000	32	63	[Mycobacterium tuberculosis] (Z99753) hypothetical protein	
21529	ENU05323	ANI61C7829:	211-235	626-649	NAP	g2266908	143	86	3.00E-16	38	70	[Schizosaccharomyces pombe] (AE001274) PXNC; L4171.2 [Leishmania major]	
21530	ENU05324	ANI61C2803:	29-53	386-405	NAP	g1711410	106	64	4.00E-10	27	34	[Streptomyces pristinaespiralis] (PLA synthase subunit A)	
21531	ENU05325	ANI61C1039	22-42	728-751	NAP	g1706694	601	238	3.00E-63	52	34	"lanosterol synthase (oxidosqualene--lanosterol cyclase) (2,3-epoxysqualene--lanosterol cyclase) (OSC) [Schizosaccharomyces pombe]" HUS1 protein [Schizosaccharomyces pombe]	
21532	ENU05326	ANI61C5507:	25-44	802-829	NAP	g3219811	312	77	2.00E-13	32	70	(AL031534) Chaperonin hsp78p [Schizosaccharomyces pombe]	
21533	ENU05327	ANI61C8456:	27-48	611-638	NAP	g3560150	2216	359	1.00E-98	65	34	Synapsins IA and IB []	
21534	ENU05328	ANI61S1345:	2215..1 1..703		NAP	g135153	105	52	0.000004	26	32	"ATP synthase alpha chain, mitochondrial precursor [Neurospora crassa]" hypothetical 100.5 KD protein C1B9.04 in chromosome I	
21535	ENU05329	ANI61C1768:	70-89	721-740	NAP	g584806	1414	492	e-138	83	51	[Schizosaccharomyces pombe] hypothetical 77.8 KD protein in MRPS28-HXT7 intergenic region	
21536	ENU05330	ANI61C5226:	22-49	804-823	NAP	g1723540	910	61	3.00E-13	36	27	[Saccharomyces cerevisiae] (X14612) myb protein [Gallus gallus]	
21537	ENU05331	ANI61C3227:	22-47 1..1072	732-755	NAP	g2501559	681	142	5.00E-61	45	38	[Caenorhabditis elegans] (AF071221) N-carbamyl-L-amino acid amidohydrolase [Arthrobacter aurescens]	
21538	ENU05332	ANI61C2826:	67-87 728..24	651-672	NAP	g63628	107	40	0.000000	35	79		
21539	ENU05333	ANI61C991:1	46-70 .340	280-299	NAP	g1945500	98	59	0.000000	30	25	(U13644) F56D2.2 gene product	
21540	ENU05334	ANI61C1082	22-41	577-603	NAP	g3249039	245	120	1.00E-26	36	53	(AF071221) N-carbamyl-L-amino acid amidohydrolase [Arthrobacter aurescens]	

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database	Hit ncbi gi	aat Score	Blast Score	Prob	% id	% evrg	Description
21541	ENU05335	ANI61C1043:	22-45	803-822	NAP	g3687510	372	123	2.00E-27	58	65	(AL031788) ubiquitin-conjugating enzyme [Schizosaccharomyces pombe]	
21542	ENU05336	ANI61C4716:	22-41	313-332	NAP	g1084771	445	183	7.00E-46	70	77	ribosomal protein L18a.e.c13 - yeast (Saccharomyces cerevisiae)	
21543	ENU05337	ANI61C2614:	39-62	724-749	NAP	g543806	1224	299	2.00E-80	58	40	"glucoamylase precursor (glucan 1,4-alpha-glucosidase) (1,4-alpha-D-glucan glucohydrolase) [Aspergillus oryzae] (Z99163) WD repeat protein [Schizosaccharomyces pombe] (Y11322) SEC61 protein [Yarrowia lipolytica]	
21544	ENU05338	ANI61C1067	36-55	802-829	NAP	g4884474	624	121	7.00E-49	46	(D78351) nuclease O [Aspergillus oryzae] (AL031856) putative involvement in protein glycosylation in the golgi		
21545	ENU05339	ANI61C7406:	41-62	645-664	NAP	g2076715	737	288	2.00E-78	67	67	[Schizosaccharomyces pombe] (Y11322) SEC61 protein [Yarrowia lipolytica]	
21546	ENU05340	ANI61C1013	1-2643..3799		NAP	g1834315	855	217	1.00E-55	52	67	(D78351) nuclease O [Aspergillus oryzae]	
21547	ENU05341	ANI61S2200:	23-45	415-438	NAP	g3738162	502	180	6.00E-45	70	32	[Schizosaccharomyces pombe] Aquaporin 9 [Homo sapiens]	
21548	ENU05342	ANI61C9766:	46-65	375-398	NAP	g3913082	99	53	0.000000	33	38	(U00050) similar to enoyl-CoA hydratases; highest similarity to YKRS_YEAST [Caenorhabditis elegans]	
21549	ENU05343	ANI61C8029:	45-72	265-284	NAP	g485111	168	73	6.00E-13	36	26	(U46690) ATP-dependent RNA helicase [Mus musculus]	
			1..315									(AL034352) putative oxalyl-CoA decarboxylase [Schizosaccharomyces pombe]	
21550	ENU05344	ANI61S1642:	22-49	327-348	NAP	g1335873	264	108	2.00E-23	50	24	(U05811) serine/threonine protein kinase [Trichoderma reesei]	
21551	ENU05345	ANI61C659:1	174-193	342-361	NAP	g4581500	133	64	4.00E-10	33	18	D-lactate dehydrogenase [Kluuyeromyces lactis]	
21552	ENU05346	ANI61C2064:	40-59	726-751	NAP	g458284	1502	269	1.00E-94	85	37	NADH-ubiquinone oxidoreductase 51 KD subunit precursor (complex I-51KD) (CL-51KD) [Aspergillus niger]	
21553	ENU05347	ANI61C4060:	116..1		NAP	g3023651	435	172	3.00E-42	37	48		
21554	ENU05348	ANI61S4097:	1..331		NAP	g2499312	127	57	0.000000	36	22		

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database	Hit	ncbi gi	aat	Blast Score	Blast Prob	% id	cvg	%	Description
21555	ENU05349	AN161C2044:	488..893	NAP		g2851654	219	110	7.00E-24	46	22	2-dehydro-3-deoxyphosphogalactonate aldolase (6-phospho-2-dehydro-3-deoxygalactonate aldolase) (2-oxo-3-deoxygalactonate 6-phosphate aldolase) / galactonate dehydratase [Escherichia coli]			
21556	ENU05350	AN161C9912:	22-47	480-505	NAP	g1125833	569	167	3.00E-55	80	78	(U43283) Similar to ras-related protein; coded for by C. elegans cDNA CEESK32F; coded for by C. elegans cDNA yk82h5.3; coded for by C. elegans cDNA yk82h5.5; coded for by C. elegans cDNA yk168c1.3; coded for by C. elegans cDNA yk168c1.5 [Cae...]			
21557	ENU05351	AN161C55:78	24-47	498-520	NAP	g4895135	87	78	4.00E-14			(AFI27374) MmcR [Streptomyces lavendulae]			
21558	ENU05352	AN161C8078:	37-59	722-749	NAP	g3355628	1981	267	6.00E-71	48	17	(X91867) CPC3 protein [Neurospora crassa]			
21559	ENU05353	AN161C806:2	22-43	725-745	NAP	g3114719	1435	217	1.00E-67	50	16	(Z68906) ATP-binding multidrug cassette transporter [Botryotinia fuckeliana]			
21560	ENU05354	AN161C2673:	58-83	729-746	NAP	g547901	760	262	6.00E-78	64	70	"Malate dehydrogenase, mitochondrial precursor [Saccharomyces cerevisiae]" hypothetical 103.0 KD protein in RADI10-PRS4 intergenic region			
21561	ENU05355	AN161C1129	103-122	516-535	NAP	g2497072	315	96	3.00E-32	47	18	[Saccharomyces cerevisiae] (U62931) multidrug resistance protein 1 [Aspergillus flavus]			
21562	ENU05356	AN161C1032	108-127	727-748	NAP	g2673947	1501	272	2.00E-72	52	21	(U97002) similar to acyl-CoA dehydrogenases and epoxide hydrolases [Caenorhabditis elegans] hypothetical protein YPL009c - yeast (Saccharomyces cerevisiae)			
21563	ENU05357	AN161C949:5	22-47	787-814	NAP	g1938424	293	94	3.00E-22	35	25	[Saccharomyces cerevisiae] (AB010442) PMR1 [Penicillium digitatum]			
21564	ENU05358	AN161C7361:	37-56	773-800	NAP	g1077257	282	111	8.00E-24	27	27	hypothetical 27.3 KD protein C9G1.08C in chromosome I [Schizosaccharomyces pombe]			
21565	ENU05359	AN161C179:1	22-44	755-780	NAP	g3288709	1767	377	e-104	63	19				
21566	ENU05360	AN161C9217:	31-56	707-733	NAP	g3183391	118	78	7.00E-14	29	97				
			..1794												
			135..888												

Sed num	Seq id	Contig source	5 pos	Primer 3 pos	Primer Basis	Selection Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
21567	ENU05361	ANI61C1120	22-45	786-805	NAP	g3702641	498	124	9.00E-28	41	86	(AL031825) similar to human 75k autoantigen [Schizosaccharomyces pombe]	
21568	ENU05362	ANI61C1045	34-55	728-747	NAP	g2342601	1392	174	8.00E-43	32	5	(X89442) peptide synthetase [Metarhizium anisopliae]	
21569	ENU05363	ANI61C8576:	23-41	802-829	NAP	g586858	223	81	1.00E-14	42	94	hypothetical 21.4 KD protein in DACA-SERS intergenic region [Bacillus subtilis]	
21570	ENU05364	ANI61C258:1	46-65	773-792	NAP	g2132903	436	73	2.00E-12	24	33	probable membrane protein YOR165w - yeast (Saccharomyces cerevisiae) [Saccharomyces cerevisiae]	
21571	ENU05365	ANI61C1091	7-2457..3107		NAP	g2144323	357	143	1.00E-33	46	14	xanthine dehydrogenase (EC 1.1.1.204) / xanthine oxidase (EC 1.1.3.22) - rat [D49832] stearoyl-acyl carrier protein desaturase [Sesamum indicum]	
21572	ENU05366	ANI61S4059:	183-208	527-554	NAP	g1020096	596	252	1.00E-66	76	41	Versicolorin reductase (VER-1) [Aspergillus parasiticus]	
21573	ENU05367	ANI61C1047	63-82	806-825	NAP	g2506150	325	101	5.00E-21	35	88	probable sterigmatocystin biosynthesis P450 MONOxygenase STCF (cytochrome P450 60A2) [Emericella nidulans]	
21574	ENU05368	ANI61C7245:	22-41	596-618	NAP	g2493389	343	159	2.00E-38	35	53	(U70136) megakaryocyte stimulating factor; MSF [Homo sapiens] (Z97341) hypothetical protein [Arabidopsis thaliana] (X92655) gluconate [Schizosaccharomyces pombe]	
21575	ENU05369	ANI61S3950:	1..807		NAP	g1572721	143	40	0.022	27	18	probable calcium-transferring ATPase 7 [Saccharomyces cerevisiae] (AF023156) carnitine acetyl transferase FacC [Emericella nidulans] iucB protein - Escherichia coli [Escherichia coli]	
21576	ENU05370	ANI61C5314:	22-44	666-693	NAP	g2245026	104	78	6.00E-14	35	100	Photosystem I P700 chlorophyll A apoprotein A2 [Nicotiana tabacum] (Z97211) probable involvement in ergosterol synthesis [Schizosaccharomyces pombe]	
21577	ENU05371	ANI61C4173:	24-43	629-652	NAP	g2624405	163	98	6.00E-20	27	30		
21578	ENU05372	ANI61C1147	2..1..2042	22-46	669-688	NAP	g731806	1647	347	6.00E-95	63	23	
21579	ENU05373	ANI61C5508:	855..1		NAP	g2511761	1185	458	e-128	86	34		
21580	ENU05374	ANI61C8155:	1..398	104-123	352-371	NAP	g1073534	165	75	2.00E-15	38	36	
21581	ENU05375	ANI61S365:5	25..1	182-204	462-484	NAP	g131154	895	364	e-100	94	23	
21582	ENU05376	ANI61C4338:	667..1	38-57	550-573	NAP	g2239236	674	255	3.00E-67	66	16	

Seq num	Seq id	Contig source	5 pos	Primer 3 pos	Primer Basis	Selection Database	aat ncbi	Blast gi	Score	Prob	% id	% cvrg	Description
21583	ENU05377	ANI61C2934:	27-46	748-768	NAP		g1345571	376	104	2.00E-40	47	25	[Pisum sativum] starch branching enzyme II (X80010)
21584	ENU05378	ANI61C403:1 ..2381	335..1201	71-90	806-824	NAP	g2842700	1133	155	4.00E-56	41	15	hypothetical 192.5 KD protein [Schizosaccharomyces pombe] C6G9.10C in chromosome I
21585	ENU05379	ANI61C196:1 130..2491	22-44	764-790	NAP		g538067	809	227	7.00E-59	43	20	[Magnaporthe grisea] (M77661) putative pol polyprotein ATP-dependent protease LA
21586	ENU05380	ANI61S822:6 60..160	215-234	414-433	NAP		g3913995	217	63	0.000000	39	19	[Azospirillum brasilense] uracil phosphoribosyltransferase (UMP pyrophosphorylase) (UPRTase) [Saccharomyces cerevisiae]
21587	ENU05381	ANI61C2843: 533..1	72-91	409-428	NAP		g120609	238	93	9.00E-20			
21588	ENU05382	ANI61C9743: 26-45 2636..1864	731-752	NAP			g1730032	230	89	4.00E-17	32	99	2-deoxy-D-glucuronate 3-dehydrogenase (2-keto-3-deoxygluconate oxidoreductase) [Escherichia coli]
21589	ENU05383	ANI61C1137: 1..333		NAP			g83727	544	218	1.00E-56	96	33	hypothetical nox3 protein - <i>Emericella nidulans</i> mitochondrial (SGC3) [Emericella nidulans]
21590	ENU05384	ANI61C3195: 40-59 68..609	468-487	NAP			g1168269	223	95	3.00E-22	38	53	"arabinan endo-1,5-alpha-L-arabinosidase A precursor (endo-1,5-alpha-L-arabinanase A) (ABN A) [Aspergillus niger]" (AB010442) PMR1 [Penicillium digitatum]
21591	ENU05385	ANI61C966:6 8..566	37-62	390-417	NAP		g3288709	623	245	5.00E-66	78	11	probable aflatoxin biosynthesis P450 monooxygenase ORD1 (cytochrome P450 60A1) [Aspergillus parasiticus] "arabinan endo-1,5-alpha-L-arabinosidase A precursor (endo-1,5-alpha-L-arabinanase A) (ABN A) [Aspergillus niger]" (AF067655) plenty-of-prolines-10; POP101; SH3-philo-protein [Mus musculus]
21593	ENU05387	ANI61C2144: 1..645	103-122	520-540	NAP		g1168269	189	103	1.00E-21	31	64	mitochondrial respiratory function protein homolog [Schizosaccharomyces pombe]
21594	ENU05388	ANI61S1049: 1..735		NAP			g3153821	127	50	0.00001	23	27	
21595	ENU05389	ANI61C6621: 621..1	26-45	497-520	NAP		g1709097	286	121	2.00E-29	37	50	

Seq num	Seq id	Contig source	5 pos	3 pos	Basis	Primer Database	Selection Hit	ncbi gi	aat Score	Score	Prob	% id	% cvrg	Description	
21596	ENU05390	AN161C5111:	108-127	654-673	NAP		g3560142	252	123	1.00E-27	36	29	(AL031534)	Major facilitator superfamily protein	
21597	ENU05391	AN161C7295:	22-45	800-827	NAP		g3139137	259	98	2.00E-26	41	22	(AF063864)	essential nuclear protein [Schizosaccharomyces pombe] McM3p [Schizosaccharomyces pombe]	
21598	ENU05392	AN161C5341:	22-49	766-787	NAP		g3395584	868	273	8.00E-73	52	24	(AL031179)	importin beta subunit [Schizosaccharomyces pombe]	
21599	ENU05393	AN161C6532:	118-137	448-473	NAP		g2388906	396	183	6.00E-46	57	54	(Z98974)	hypothetical protein [Schizosaccharomyces pombe]	
21600	ENU05394	AN161C986:1	113-139	476-503	NAP		g3023676	495	187	5.00E-49	48	31	probable translation initiation factor EIF-2B epsilon subunit (EIF-2B GDP-GTP exchange factor)		
21601	ENU05395	AN161C7272:	54-73	372-399	NAP		g1723230	305	123	6.00E-28	45	58	[Schizosaccharomyces pombe]	hypothetical 28.5 KD protein C1D4.08 in chromosome I	
21602	ENU05396	AN161C1104	107-129	609-628	NAP		g3978466	567	215	2.00E-55	51	31	(AF086822)	dihydroxyacetone synthase [Candida boidinii]	
21603	ENU05397	AN161C1017	137-156	722-749	NAP		g1546072	249	118	6.00E-26	34	10	(U68040)	polyketide synthase [Cochliobolus heterostrophus]	
21604	ENU05398	AN161C6174:	39-57	555-574	NAP		g731878	197	105	3.00E-22	29	25	AXL2 protein precursor (SRO4 protein)	[Saccharomyces cerevisiae] (K03205) salivary proline-rich protein precursor [Homo sapiens]	
21605	ENU05399	AN161S1311:	1..713		NAP		g190504	97	45	0.0004			[Saccharomyces cerevisiae]	regulator Y protein GAL4 (X89442) peptide synthetase [Saccharomyces cerevisiae]	
21606	ENU05400	AN161C9864:	54-73	803-822	NAP		g1169823	368	33	3.1			[Metarhizium anisopliae]		
21607	ENU05401	AN161C1033	24-41	625-645	NAP		g2342601	2035	119	1.00E-42	43	5	(AF132563)	BcDNA.LD14392 [Drosophila melanogaster]	
21608	ENU05402	AN161C9342:	36-55	703-723	NAP		g4689350	727	298	3.00E-80			[Drosophila melanogaster]	Maltose permease MAL3T (maltose transport protein MAL3T)	
21609	ENU05403	AN161C4212:	23-48	707-730	NAP		g585446	660	180	9.00E-45	33	45	[Saccharomyces cerevisiae]	[Saccharomyces cerevisiae] (X05204) arom polypeptide	
21610	ENU05404	AN161C6072:	26-47	803-829	NAP		g3834343	1545	436	e-121	97	17	[Emericella nidulans]		
21611	ENU05405	AN161C3958:	1..926	126-149	287-306	NAP		g3219962	210	88	2.00E-17	46	33	C17H9.08	[Schizosaccharomyces pombe]
		1437..1101													

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat	Blast Score	Blast Prob	% id	% cvrg	Description
21612	ENU05406	ANI61C937:1	102-127	440-465	NAP	g4587971	772	277	2.00E-74	96	12	(AF082072) ABC transporter protein	
21613	ENU05407	ANI61C2980:	56-77	527-546	NAP	g2462911	321	105	9.00E-32	42	28	AtC [Emericella nidulans]	
21614	ENU05408	ANI61S3826:	146-165	507-524	NAP	g2327063	174	45	0.0005	22	23	(AF001305) protease I [Pneumocystis carinii f. sp. carinii]	
21615	ENU05409	ANI61C9451:	41-61	625-649	NAP	g2076715	914	231	6.00E-91	76	51	(Y11322) SEC61 protein [Yarrowia lipolytica]	
21616	ENU05410	ANI61C199:6	32..198		NAP	g539218	106	42	0.003	20	25	hypothetical protein YKL20lc - yeast (Saccharomyces cerevisiae)	
21617	ENU05411	ANI61C1002	25-52	807-829	NAP	g1586814	736	205	3.00E-52	48	63	glycerol-3-phosphate dehydrogenase [Schizosaccharomyces pombe]	
21618	ENU05412	ANI61C3264:	22-45	766-783	NAP	g2414609	1146	354	4.00E-97	69	53	(Z99295) citrate lyase [Schizosaccharomyces pombe]	
21619	ENU05413	ANI61C7483:	22-46	691-718	NAP	g584766	537	173	2.00E-42	66	99	ADP-ribosylation factor-like protein 1 [Saccharomyces cerevisiae]	
21620	ENU05414	ANI61C9092:	54-73	765-782	NAP	g4581500	838	252	2.00E-66	50	47	(AL034352) putative oxalyl-CoA decarboxylase [Schizosaccharomyces pombe]	
21621	ENU05415	ANI61C3548:	1816..1030		NAP	g126791	816	233	2.00E-73	88	42	mRNA maturase B11 (COBA intron protein)	
21622	ENU05416	ANI61C2656:	87-114	562-581	NAP	g731288	474	175	3.00E-43	43	27	hypothetical 87.5 KD protein in ACSI-GCV3 intergenic region	
21623	ENU05417	ANI61C1514:	1..1308		NAP	g2493965	1869	244	e-108	84	20	[Saccharomyces cerevisiae] xanthine dehydrogenase (purine hydroxylase I) [Emericella nidulans]	
21624	ENU05418	ANI61C305:2	799..1	22-44	723-749	NAP	g2459997	1553	144	3.00E-49	45	20	(AF012898) protein phosphatase Ssd1 homolog [Candida albicans]
21625	ENU05419	ANI61C9125:	1..431	22-44	378-397	NAP	g3646447	92	53	0.000001	35	69	"(AL031603) peroxisomal membrane protein pmp20p, Ahpc-TSA family protein [Schizosaccharomyces pombe]"
21626	ENU05420	ANI61C5598:	100-118	462-481	NAP	g1805262	292	131	3.00E-30	49	7	"(U75347) fatty acid synthase, beta subunit [Emericella nidulans]"	
21627	ENU05421	ANI61C2807:	109-130	465-487	NAP	g4262222	299	105	2.00E-22	39	30	"(AC006200) putative RNA helicase A, 3' partial [Arabidopsis thaliana]"	
21628	ENU05422	ANI61C8964:	844..335	108-127	375-394	NAP	g2493143	335	72	3.00E-23	74	66	vacuolar ATP synthase 16 KD proteolipid subunit [Candida tropicalis]
			6972..6519										

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database	Hit ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
21629	ENU05423	ANI61C9643:	34-53	724-743	NAP	g1723575	515	83	2.00E-15				chromosome I [Schizosaccharomyces pombe]
21630	ENU05424	ANI61C4970:	22-46	795-822	NAP	g699196	560	141	8.00E-33	42	52		(U15181) 4-coumarate-coA ligase [Mycobacterium leprae]
21631	ENU05425	ANI61C1099	22-49	766-785	NAP	g3114719	588	196	1.00E-49	48	15		(Z68906) ATP-binding multidrug cassette transporter [Botryotinia fuckeliana]
21632	ENU05426	ANI61C5574:	59-86	410-437	NAP	g3947855	244	67	2.00E-20	45	60		(AL034381) putative Golgi membrane protein [Schizosaccharomyces pombe] (L24441) kinesin light chain [Loligo pealii]
21633	ENU05427	ANI61C9448:	22-48	806-829	NAP	g403179	367	114	3.00E-42	34	55		(AF048790) No definition line found [Caenorhabditis elegans]
21634	ENU05428	ANI61S991:1..576			NAP	g3329623	165	57	0.000000	21	57		(AJ001157) hymA [Emericella nidulans]
21635	ENU05429	ANI61C9118:1..1241	25-47	802-824	NAP	g3163927	1659	187	e-106	99	63		(AL033389) putative allantoin permease [Schizosaccharomyces pombe]
21636	ENU05430	ANI61C1327:804..1520			NAP	g3850093	228	124	7.00E-28	30	47		G protein beta subunit like - mouse [Mus musculus]
21637	ENU05431	ANI61C9639:9628..9095	122-141	489-513	NAP	g2137308	66	42	0.003	23	47		"(U75347) fatty acid synthase, alpha subunit [Emericella nidulans]" (AL008883) glnA4 [Mycobacterium tuberculosis]
21638	ENU05432	ANI61C1236:3252..1	36-60	714-736	NAP	g1805261	1628	259	1.00E-68	48	15		(X89442) peptide synthetase [Metarhizium anisopliae]
21639	ENU05433	ANI61C1001	79-98	275-294	NAP	g2612805	142	80	1.00E-14	37	21		hypothetical oxidoreductase in PTA-ROCC intergenic region [Bacillus subtilis]
21640	ENU05434	ANI61C2961:1..314..1	31-50	770-789	NAP	g2342601	645	152	4.00E-36	41	4		
21641	ENU05435	ANI61C1258:1..467	53-75	398-417	NAP	g732372	90	50	0.000000	37	38		
21642	ENU05436	ANI61C2743:1213..1800	22-49	542-567	NAP	g2707191	124	36	0.22	38	53		(U94.86) glutamine rich protein similar to glutenins [Glomerella cingulata]
21643	ENU05437	ANI61C3684:1985..2821	28-55	784-811	NAP	g4502229	435	122	7.00E-40	53	100		ADP-ribosylation factor-like 2 [Homo sapiens]
21644	ENU05438	ANI61C9235:1..631	106-128	561-580	NAP	g549795	384	161	4.00E-39				GTP-binding protein YPT51/VPS21 [Saccharomyces cerevisiae]

Seq num	Seq id	Contig source	5 pos	3 pos	Primer Basis	Primer Selection	aat	Blast	Blast	% id	% cvg	Description
						Database Hit	ncbi gi	Score	Score Prob			(AL021046) hypothetical PHD finger domain protein [Schizosaccharomyces pombe]
21645	ENU05439	ANI61C6976:	23-45	638-657	NAP	g2706459	179	85	5.00E-16	26	75	[Schizosaccharomyces pombe] (Z99167) putative helicase
21646	ENU05440	ANI61C8570:			NAP	g2408082	806	96	1.00E-27	37	28	[Schizosaccharomyces pombe] putative methylenetetrahydrofolate reductase [Saccharomyces cerevisiae]
21647	ENU05441	ANI61C1109	4:1..910		NAP	g1709159	449	120	2.00E-49	42	39	"long chain alpha-hydroxy acid oxidase=FMN-dependent alpha-hydroxy acid-oxidizing enzyme {EC 1.1.3.15} [rats, kidney, Peptide, 352..2514 aa]"
21648	ENU05442	ANI61C4289:	24-44	803-829	NAP	g238482	269	135	4.00E-31	36	73	DNA repair protein RHP54 [Schizosaccharomyces pombe] (Y13917) yngF [Bacillus subtilis]
21649	ENU05443	ANI61C1038	27-49	722-749	NAP	g3123262	1765	341	e-115	73	33	Pisatin demethylase (cytochrome P450 57A1) [Nectria haematococca mpVII] (Z69793) R03A10.3 [Caenorhabditis elegans]
21650	ENU05444	ANI61C5267:	222-241	503-530	NAP	g2266427	229	99	1.00E-21	43	67	NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 3 - Emericella nidulans mitochondrion (SGC3) [] (AL023517) putative iron-sulfur binding oxidoreductase [Streptomyces coelicolor]
21651	ENU05445	ANI61C1038	22-43	802-829	NAP	g3929362	648	92	4.00E-36	42	45	homolog (MTS2 protein) [Schizosaccharomyces pombe] (Z98560) hypothetical protein [Schizosaccharomyces pombe] (Z68905) ATP-binding cassette multidrug transporter [Emericella nidulans]
21652	ENU05446	ANI61C7643:	22-45	760-779	NAP	g3878874	351	124	9.00E-28	34	49	putative 60S ribosomal protein YEL050C [Saccharomyces cerevisiae] probable membrane protein YDL246c - yeast [Saccharomyces cerevisiae]
21653	ENU05447	ANI61S4583:	405..1		NAP	g01813	585	141	1.00E-33	91	99	[Saccharomyces cerevisiae]
21654	ENU05448	ANI61C1798:	120-141	260-279	NAP	g3130015	75	50	0.000005	27	19	
21655	ENU05449	ANI61C9805:	186-213	551-570	NAP	g547935	581	106	1.00E-47	72	41	
			3895..3285									
21656	ENU05450	ANI61C1029	72-91	717-736	NAP	g2330803	2374	353	1.00E-96	58	19	[Schizosaccharomyces pombe] (Z98560) hypothetical protein [Schizosaccharomyces pombe] (Z68905) ATP-binding cassette multidrug transporter [Emericella nidulans]
21657	ENU05451	ANI61C617:8	96-120	700-727	NAP	g1834342	1276	472	e-139	97	18	putative 60S ribosomal protein YEL050C [Saccharomyces cerevisiae] probable membrane protein YDL246c - yeast [Saccharomyces cerevisiae]
21658	ENU05452	ANI61C1022	27-48	810-829	NAP	g418426	594	233	1.00E-60	54	59	
21659	ENU05453	ANI61S4056:	9:876..8		NAP	g2117435	101	64	5.00E-10	27	33	
			358..1									

Seq num	Seq id	Contig source	5 pos	3 pos	Basis	Database	Hit	ncbi gi	Score	Score	Prob	% id	cvg	%	Description
21660	ENU05454	ANI61C9713:	98-118	336-362	NAP	g2995374	273	120	6.00E-27	53	56	(AL022245)	hypothetical	21.5 kd	protein [Schizosaccharomyces pombe]
21661	ENU05455	ANI61C6683:	110-129	451-471	NAP	g1565203	151	92	2.00E-18	32	41	(D87894)	chitinase	[Rhizopus microsporus var. oligosporus]	
21662	ENU05456	ANI61C1044	28-48	686-710	NAP	g2132863	600	238	4.00E-62	45	38	probable membrane protein	YOR001w	- yeast (Saccharomyces cerevisiae) [Saccharomyces cerevisiae]	
21663	ENU05457	ANI61C5918:	42-61	765-784	NAP	g416900	422	115	6.00E-25	42	46	probable aldehyde dehydrogenase	[Pseudomonas sp.]		
21664	ENU05458	ANI61S1481:	863..1		NAP	g1334398	166	32	6.9	29	75	(X15081)	MURF2 protein (AA 1-348)	[Criithidia fasciculata]	
21665	ENU05459	ANI61C9981:	42-62	724-749	NAP	g3023272	2834	458	e-128	76	28	alpha-glucosidase precursor (maltase) (AGL)	[Aspergillus oryzae]		
21666	ENU05460	ANI61C1118	31-50	616-641	NAP	g2308977	977	100	2.00E-52	99	11	(AB000125)	chitin synthase	[Emericella nidulans]	
21667	ENU05461	ANI61C6359:	23-50	803-829	NAP	g3021303	1362	359	e-127	100	10	(Y15996)	acetyl-CoA carboxylase	[Emericella nidulans]	
21668	ENU05462	ANI61C540:1	104-123	722-741	NAP	g3947883	562	215	4.00E-55	44	55	(AL034382)	putative Trp-Asp repeat protein	[Schizosaccharomyces pombe]	
21669	ENU05463	ANI61C1212:	53-76	463-482	NAP	g4505739	119	45	0.0003	26	100	prefoldin 1	[Homo sapiens]		
21670	ENU05464	ANI61C739:6	33-54	626-650	NAP	g4210899	68	54	0.000001	22	48	(AF045609)	OrfL	[Sinorhizobium meliloti]	
21671	ENU05465	ANI61C3278:	108-131	701-724	NAP	g3116113	454	212	3.00E-54	53	29	(AL023286)	probable atp-dependent rna helicase	[Schizosaccharomyces pombe]	
21672	ENU05466	ANI61C2706:	65-84	317-343	NAP	g1168403	183	81	4.00E-15	41	15	regulatory protein ALCR	[1]		
21673	ENU05467	ANI61C1097	90-114	370-389	NAP	g731385	147	68	4.00E-11	35	46	hypothetical	33.7 KD protein in ISC10		
21674	ENU05468	ANI61C558:3	26-46	803-829	NAP	g522302	959	143	8.00E-45	39	23	3region	[Saccharomyces cerevisiae]		
21675	ENU05469	ANI61C2976:	23-47	805-826	NAP	g3868931	342	125	9.00E-37	39	66	(L35053)	endonuclease	[Magnaporthe grisea]	
21676	ENU05470	ANI61C4309:	48-67	762-781	NAP	g1654096	1237	78	4.00E-50	54	8	(AB014769)	glutamyl cyclase	[Bothrops jararaca]	
21677	ENU05471	ANI61S1014:	1..3926		NAP	g3037018	170	33	0.011	27	92	(Y09076)	RAD3	[Schizosaccharomyces pombe]	
			335..931											subunit 5	[Bodo saltans]

Seq num	Seq id	Contig source	5 pos	Primer 3 pos	Primer Basis	Selection Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
21678	ENU05472	ANi61S1690:	1..793	NAP		g786117	159	49	0.00003	17	52	(L41834) nuclear protein [Ensis minor]	
21679	ENU05473	ANi61C1127:	63-90	551-575	NAP	g3006175	448	191	3.00E-48	53	33	(AL022305) putative transcription factor [Schizosaccharomyces pombe]	
21680	ENU05474	ANi61C6111:	22-44	1449..1	NAP	g117619	450	122	4.00E-27	34	41	Choline transport protein [Saccharomyces cerevisiae]	
21681	ENU05475	ANi61C3619:	41-60	769..1	NAP	g4033411	533	222	3.00E-57	44	27	putative importin beta-2 subunit (karyopherin beta-2 subunit) (importin 10M) (transportin) (TRN) [Schizosaccharomyces pombe]	
21682	ENU05476	ANi61C4102:	112-131	321-343	NAP	g416963	402	171	2.00E-42			C-5 sterol desaturase [Saccharomyces cerevisiae]	
21683	ENU05477	ANi61C1696:	70-89	1..368	625-644	NAP	g2501730	328	92	5.00E-18	29	75	Peroxisome assembly protein PER8 (peroxin-10) [Pichia angusta] (AL025218) possible involvement in nuclear protein localisation
21684	ENU05478	ANi61C1763:	22-45	3169..4384	748-767	NAP	g4160581	644	227	2.00E-61	48	67	[Schizosaccharomyces pombe] Hexokinase [Schistosoma mansoni] 5'region (ORFA) [Listeria monocytogenes]
21685	ENU05479	ANi61C7954:	24-44	1192..2771	807-826	NAP	g2833327	329	100	2.00E-20	33	54	hypothetical oxidoreductase in INLA (U87965) putative G-protein [Mus musculus]
21686	ENU05480	ANi61C5158:	22-48	205..943	695-714	NAP	g140925	419	144	3.00E-37	37	99	hypothetical oxidoreductase in INLA (U87965) putative G-protein [Mus musculus]
21687	ENU05481	ANi61C3007:	23-46	962..1	714-741	NAP	g1916927	769	286	2.00E-76	55	48	(Z98530) hypothetical protein [Acetomonium sp.]
21688	ENU05482	ANi61C9656:	40-59	627..1	495-520	NAP	g2330829	307	123	8.00E-28	35	13	[Schizosaccharomyces pombe] (AB010110) ascorbate oxidase
21689	ENU05483	ANi61C4620:	183-203	971..403	528-548	NAP	g2780359	448	194	3.00E-49	49	34	[Saccharomyces cerevisiae]
21690	ENU05484	ANi61C7917:	28-55	1162..1	724-749	NAP	g1077412	376	136	3.00E-31	42	22	hypothetical protein YLR187w - yeast (Saccharomyces cerevisiae)
21691	ENU05485	ANi61C1002	38-56	1:2095..5786	764-784	NAP	g2492658	1339	111	6.00E-24	27	14	putative sterigmatocystin biosynthesis fatty acid synthase beta subunit [Emericella nidulans]
21692	ENU05486	ANi61C3789:	221-240	1..794	738-764	NAP	g4481951	583	243	8.00E-64	41	11	(AL035637) putative alpha-glucan synthase [Schizosaccharomyces pombe]
21693	ENU05487	ANi61C1946:	53-75	653..1	515-534	NAP	g113701	422	185	2.00E-46	46	38	Acetamidase [Emericella nidulans]

Seq num	Seq id	Contig source	5 pos	Primer 3 pos	Primer Basis	Selection Database	Hit ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description	
21694	ENU05488	ANI61C2383:	22-45	438-457	NAP	g417567	136	84	8.00E-16				2) [Schizosaccharomyces pombe] protein-tyrosine phosphatase 2 (PTPase	
21695	ENU05489	ANI61C8573:	22-47	798-825	NAP	g4836505	296	64	0.000000	002			(AF124929) putative deacetylcephalosporin C acetyltransferase [Streptomyces clavuligerus]	
21696	ENU05490	ANI61C1008	65-84	806-829	NAP	g559964	194	102	3.00E-21	40	74		(J05282) insect-type dehydrogenase [Pseudomonas cepacia]	
21697	ENU05491	ANI61C513:1	102-129	617-640	NAP	g4557525	590	208	2.00E-53	54	44		dihydrolipoamide dehydrogenase precursor [Homo sapiens]	
21698	ENU05492	ANI61C8488:	68-86	435-453	NAP	g1723495	168	61	0.000000	39	23		hypothetical 63.2 KD protein C1F3.09 in chromosome I	
			759..1235				007							
21699	ENU05493	ANI61C9883:	25-44	661-687	NAP	g2326833	704	200	9.00E-51	38	33		[Schizosaccharomyces pombe] (Z73502) ORF YPL147w	
21700	ENU05494	ANI61C1003:	23-49	802-829	NAP	g1653242	559	70	2.00E-11	28	53		[Saccharomyces cerevisiae] (D90912) hypothetical protein	
21701	ENU05495	ANI61C855:1	128-147	408-428	NAP	g1749490	138	82	4.00E-15	31	69		[Synechocystis sp.] "D89141) similar to Saccharomyces cerevisiae hypothetical 27.6KD protein in chromosome VII, SWISS-PROT Accession Number P46948	
			..585											
21702	ENU05496	ANI61C1018	22-48	365-392	NAP	g1437475	134	64	8.00E-10	30	38		[Schizosaccharomyces pombe]" " (D86544) hydroxyquinol-1, 2-dioxxygenase [Ralstonia pickettii]" (AL034564) putative protease; endopeptidase [Schizosaccharomyces pombe]	
21703	ENU05497	ANI61C1003	51-70	515-534	NAP	g4049543	131	60	0.000000	33	39		[Schizosaccharomyces pombe] (AL022244) hypothetical protein	
21704	ENU05498	ANI61C1042	22-43	804-829	NAP	g2995339	199	91	8.00E-18	27	32		[Schizosaccharomyces pombe]	
21705	ENU05499	ANI61C1057	41-60	788-807	NAP	g113314	4339	538	e-152	99	7		delta-(L-alpha-aminoacyl)-L-cysteinyl-D-valine synthetase (ACVS synthetase) (ACVS) [Emericella nidulans]	
			0:1..2533											
21706	ENU05500	ANI61C5776:	206-225	681-701	NAP	g4826880	94	62	0.000000	004			oxidase (cytochrome c) assembly 1-like [Homo sapiens]	
21707	ENU05501	ANI61C6356:	1424..697	22-49	725-749	NAP	g3702200	717	252	2.00E-66	47	43		(AJ011686) methylenetetrahydrofolate reductase [Schizosaccharomyces pombe]
			998..1											

Seq num	Seq id	Contig source	5 pos	Primer 3 pos	Primer Basis	Selection Database Hit	ncbi gi	Score	Score Prob	% id	% cvrg	Description
21708	ENU05502	ANI61C4103:	42-61	795-814	NAP	g13466660	464	145	5.00E-34	37	58	Salicylate hydroxylase (salicylate 1-monooxygenase) [Pseudomonas putida]
21709	ENU05503	ANI61C1102	25-46	390-413	NAP	g133356	258	115	2.00E-25			DNA-directed RNA polymerase III largest subunit (C160) [Saccharomyces cerevisiae]
21710	ENU05504	ANI61C9104:	45-64	762-781	NAP	g1173383	328	163	1.00E-39	37	66	SCN1 protein [Schizosaccharomyces pombe] (AL035439) putative NADPH cytochrome reductase
21711	ENU05505	ANI61C1296:	22-43	728-749	NAP	g4500377	415	143	6.00E-38	36	47	[Schizosaccharomyces pombe] "U75347" fatty acid synthase, beta subunit [Emericella nidulans]" (AB010714) salicylate hydroxylase [Pseudomonas putida]
		1318...1				g1805262	2017	391	e-108	77	13	(U32622) toluenesulfonate zinc-independent alcohol dehydrogenase [Comamonas testosteroni] alpha-amylase (EC 3.2.1.1) 3 precursor - Aspergillus oryzae [Aspergillus oryzae]
21712	ENU05506	ANI61C6074:			NAP	g2826168	235	106	2.00E-22	39	49	Acetamidase [Emericella nidulans]
21713	ENU05507	ANI61C9521:	37-57	661-679	NAP	g1790870	191	90	7.00E-18	38	44	(U32622) toluenesulfonate zinc-independent alcohol dehydrogenase [Comamonas testosteroni] alpha-amylase (EC 3.2.1.1) 3 precursor - Aspergillus oryzae [Aspergillus oryzae]
21714	ENU05508	ANI61C4432:	40-66	303-325	NAP	g67385	736	154	7.00E-52	42	52	Importin alpha subunit (karyopherin alpha subunit) (serine-rich RNA polymerase I suppressor protein) [Schizosaccharomyces pombe] "Z97338" strong similarity to protein phosphatase 2A regulatory chain, 74K [Arabidopsis thaliana]" Proteasome component C11 (macropain subunit C11) (proteinase YSCE subunit 11) (multicatalytic endopeptidase complex subunit C11) [Saccharomyces cerevisiae]
21715	ENU05509	ANI61C7537:	23-42	740-765	NAP	g113701	170	81	5.00E-15	28	28	(AF043595) xyloglucan-specific endo-beta-1,4-glucanase precursor [Aspergillus aculeatus]"
21716	ENU05510	ANI61C8019:	178-195	422-446	NAP	g3122272	717	261	4.00E-69	70	37	
21717	ENU05511	ANI61C3497:	61-80	388-413	NAP	g2244898	254	132	3.00E-30	29	26	
21718	ENU05512	ANI61C2554:	42-66	730-749	NAP	g730378	502	141	4.00E-48			
21719	ENU05513	ANI61C3764:	23-47	494-517	NAP	g4105147	848	175	8.00E-69	68	100	"(AF043595) xyloglucan-specific endo-beta-1,4-glucanase precursor [Aspergillus aculeatus]"
21720	ENU05514	ANI61C7285:	23-42	729-751	NAP	541..1312						

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	aat	Blast Score	Blast Prob	% id	% cvrg	Description	
21721	ENU05515	ANi61C3973:	37-64	713-737	NAP	g730881	1645	210	1.00E-87	64	33	"threonyl-tRNA synthetase, cytoplasmic (threonine--tRNA ligase)" (THRRS) [Saccharomyces cerevisiae]	
21722	ENU05516	ANi61C3026:	22-49	392-419	NAP	g1362793	168	84	8.00E-16	35	69	[Homo sapiens] emopamil-binding protein - human	
21723	ENU05517	ANi61C4961:	121-140	799-824	NAP	g1666269	261	83	2.00E-29	40	75	(Z82021) cytochrome P450 [Agaricus bisporus]	
21724	ENU05518	ANi61C7020:	23-42	762-780	NAP	g3219785	885	288	4.00E-77	58	65	putative cysteine synthase (O-acetylserine sulfhydrylase) (O-acetylserine (thiol)-lyase) (CSASE) [Schizosaccharomyces pombe]	
21725	ENU05519	ANi61S2922:	22-45	398-420	NAP	g1723436	610	221	2.00E-57	74	14	hypothetical 119.9 KD protein C56R8.03 in chromosome I	
21726	ENU05520	ANi61C7675:	146-168	506-525	NAP	g538605	828	265	8.00E-88	86	41	[Schizosaccharomyces pombe] glutamate dehydrogenase (NADP+) (EC 1.4.1.4) - Emericella nidulans [Emericella nidulans]	
21727	ENU05521	ANi61C8815:	117-136	570-589	NAP	g2894300	256	90	2.00E-17	43	36	(AL021837) hypothetical protein [Schizosaccharomyces pombe] (Z68905) ATP-binding cassette multidrug transporter [Emericella nidulans]	
21728	ENU05522	ANi61C1562:	1..621	22-49	727-747	NAP	g1834342	1513	512	e-144	96	18	[Homo sapiens] (X95073) Translin associated protein X [Homo sapiens]
21729	ENU05523	ANi61C2594:	4976..1196	22-46	810-829	NAP	g401013	4308	384	e-120	73	21	DNA-directed RNA polymerase II 138 KD polypeptide (RNA polymerase II subunit 2) [Schizosaccharomyces pombe]
21730	ENU05524	ANi61C8067:	1..1111	62-81	780-799	NAP	g2407176	1822	553	e-157	98	27	(AF016850) alpha-mannosidase [Emericella nidulans]
21731	ENU05525	ANi61S775:.	.984		NAP	g4240179	204	39	0.029	26	29	(AB020652) KIAA0845 protein [Homo sapiens]	
21732	ENU05526	ANi61C3351:	4228..4741	22-43	468-493	NAP	g3982753	86	70	1.00E-11	32	37	(AF070937) gibberellin 3 beta-hydroxylase [Arabidopsis thaliana]
21733	ENU05527	ANi61C1027	4..2881..3490	57-77	482-509	NAP	g1770576	154	51	8.00E-14	31	54	[Homo sapiens] GTPase-activating protein [Schizosaccharomyces pombe]
21734	ENU05528	ANi61C5396:	1061..3386	24-43	805-829	NAP	g462156	1450	172	2.00E-42			tracylglycerol lipase (EC 3.1.1.3) I-yeast (Geotrichum candidum) (strain CBS 178.71) []
21735	ENU05529	ANi61C1028	0-2033..475	35-54	809-829	NAP	g2117970	341	71	1.00E-11			

Seq num	Seq id	Contig source	5 pos	Primer 3 pos	Primer Basis	Selection Database Hit	aat ncbi gi	Score	Score	Blast Prob	% id	% cvrg	Description
21736	ENU05530	ANI61S302:1.	41-60	438-457	NAP	g2245050	599	172	1.00E-63	72	6	(Z97342) resistance gene homolog [Arabidopsis thaliana]	
21737	ENU05531	ANI61C6674:	31-50	487-507	NAP	g1906796	349	133	2.00E-32	44	70	(D85181) fungal sterol-C5-desaturase homolog [Homo sapiens]	
21738	ENU05532	ANI61S1332:	1..724		NAP	g4759100	115	45	0.0004			"splicing factor, arginine/serine-rich 11 [Homo sapiens]"	
21739	ENU05533	ANI61C2473:	48-67	658-677	NAP	g226788	501	178	6.00E-44	37	14	erythrocyte ankyrin [Homo sapiens]	
21740	ENU05534	ANI61C3738:	107-126	546-565	NAP	g2924771	126	95	6.00E-19	27	53	(AC002334) putative dimethylaniline monooxygenase [Arabidopsis thaliana]	
21741	ENU05535	ANI61C3590:	32-51	427-448	NAP	g1749552	224	72	8.00E-28	33	35	"(D89172) similar to <i>Saccharomyces cerevisiae</i> transketolase 2(TK2), SWISS-PROT Accession Number P33315 [Schizosaccharomyces pombe]"	
21742	ENU05536	ANI61C8544:	25-44	804-828	NAP	g2791647	454	110	8.00E-35	33	47	(AL021287) hypothetical protein Rv3049c [Mycobacterium tuberculosis]	
21743	ENU05537	ANI61S3134:	551..1		NAP	g4558826	242	106	2.00E-22	42	41	(AF076691) aureobasidin-resistance protein; AurA [Emericella nidulans]	
21744	ENU05538	ANI61C4840:	34-53	770-797	NAP	g3914984	432	181	5.00E-45	39	7	Ferrichrome siderophore peptide synthetase [Ustilago maydis]	
21745	ENU05539	ANI61C1550:	41-60	423-442	NAP	g4456808	130	52	0.000002	33	22	(AJ236923) ifc3 protein [Shewanella frigidimarina]	
21746	ENU05540	ANI61C9547:	118-138	478-503	NAP	g3136025	165	104	4.00E-22	33	62	(AL023587) putative DNA repair protein [Schizosaccharomyces pombe]	
21747	ENU05541	ANI61C5119:	598..1		NAP	g2909514	88	47	8.00E-10	34	48	(AL021932) hypothetical protein Rv0439c [Mycobacterium tuberculosis]	
21748	ENU05542	ANI61C6475:	166-185	369-388	NAP	g121649	389	115	2.00E-42	52	14	GRR1 protein [Saccharomyces cerevisiae]	
21749	ENU05543	ANI61C1044	39-58	803-822	NAP	g1708621	930	231	1.00E-67	57	23	serine/threonine-protein kinase PMK1 [Schizosaccharomyces pombe]	
21750	ENU05544	ANI61C6941:	62-81	804-829	NAP	g1171738	809	240	1.00E-62	48	52	nonsense-mediated mRNA decay protein 3 [Saccharomyces cerevisiae]	
21751	ENU05545	ANI61C1198:	83-109	692-719	NAP	g1652509	1338	520	e-147	96	72	(D90906) poly(3-hydroxyalkanoate) synthase [Synecchocystis sp.]	
21752	ENU05546	ANI61C3622:	22-47	803-829	NAP	g538067	1959	143	1.00E-33	38	16	(M77661) putative pol polyprotein [Magnaporthe grisea]	
			1..307										

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Primer Basis	Selection Database	aat	Blast Score	Blast Prob	% id	% cvrg	Description	
21753	ENU05547	ANI61C710I:	38-57	802-829	NAP	g82865	231	99	4.00E-20	28	23	regulatory protein LAC9 - yeast	
21754	ENU05548	ANI61C711I:	102-120	444-471	NAP	g731968	281	100	6.00E-21	47	43	[Kluyveromyces marxianus var. lactis)	
			430...1									hypothetical 35.9 KD protein in HXT8-	
21755	ENU05549	ANI61S878I:	187-206	408-431	NAP	g2494125	468	172	1.00E-48	48	44	[Saccharomyces cerevisiae]	
			.614									(AC02376) Strong similarity to	
21756	ENU05550	ANI61C1047	22-41	772-795	NAP	g2342601	1299	244	5.00E-64	45	5	Cucumis acetyl-CoA acyltransferase	
			2:1..1931									(gb D70895). [Arabidopsis thaliana]	
21757	ENU05551	ANI61C4808:			NAP	g3219304	463	131	3.00E-36	58	26	[Metarhizium anisopliae]	
			1813..2678									(AB009461) MUS38 [Neurospora crassa]	
21758	ENU05552	ANI61C3351:	102-121	437-456	NAP	g2408015	200	73	2.00E-12	36	42	(Z99162) hypothetical protein	
			420..1									[Schizosaccharomyces pombe]	
21759	ENU05553	ANI61C1065	24-51	391-410	NAP	g1363742	442	182	2.00E-45	61	51	probable membrane protein YLR243w	
			5:1469..1894									-yeast (Saccharomyces cerevisiae)	
21760	ENU05554	ANI61S835I:			NAP	g3097062	168	72	4.00E-12	32	50	[Saccharomyces cerevisiae]	
			.787									(Y17145) putative betaine transporter	
21761	ENU05555	ANI61C3157:	111-130	370-397	NAP	g1172532	521	183	4.00E-46	72	39	[Eubacterium acidaminophilum]	
			1..418									Penicillolysine precursor (deuterolysine)	
21762	ENU05556	ANI61C18I:	1..	114-133	716-736	NAP	g2330791	188	83	5.00E-20	32	35	[Penicillium citrinum]
			767									(Z98601) carboxypeptidase s precursor	
21763	ENU05557	ANI61C8494:	22-48	455-479	NAP	g1304227	167	91	5.00E-18	32	44	[Schizosaccharomyces pombe]	
			3514..3060									(D63781) Epoxide hydrolase [Glycine max]	
21764	ENU05558	ANI61C9184:	219-237	382-401	NAP	g129766	316	69	8.00E-19			methylene-fatty-acyl-phospholipid synthase (unsaturated phospholipid methyltransferase) [Saccharomyces cerevisiae]	
			3881..3418										
21765	ENU05559	ANI61C9126:	22-44	765-789	NAP	g127736	1164	141	5.00E-33	28	18	Myosin-2 isoform [Saccharomyces cerevisiae]	
			1..1738									(AL031603) BTB domain and	
21766	ENU05560	ANI61C9707:	22-48	785-811	NAP	g3646452	569	93	2.00E-18	28	19	Ankyrin repeat containing protein.	
			4373..1505									[Schizosaccharomyces pombe]	
21767	ENU05561	ANI61C6194:	60-85	780-802	NAP	g1580818	1021	201	3.00E-98	71	34	(Z69254) alpha-Galactosidase	
			1239..1									[Hypocrealejecorina]	

Seq num	Seq id	Contig source	5 pos	3 pos	Primer Basis	Primer	Selection	Blast aat	Blast Score	Blast Prob	% id	% cvrg	Description
					Database	Hit ncbi gi	g416922	381	100	9.00E-32	53	97	
21768	ENU05562	ANI61C9491:	22-43	570-594	NAP								nucleotidohydrolase (DUTPase) (DUTP pyrophosphatase) (P18)
			2485..1871										[Lycopersicon esculentum] (AL023534) hypothetical protein [Schizosaccharomyces pombe]
21769	ENU05563	ANI61C1103:	118-143	508-527	NAP	g3130037	318	128	3.00E-29	45	45		(L11574) p68 RNA helicase
	1..548	ANI61C4837:	60-79	579-599	NAP	g173419	787	317	5.00E-86	70	38		[Schizosaccharomyces pombe] (AL023594) amino-acid permease
21771	ENU05565	ANI61C1966:	22-46	371-389	NAP	g3150139	181	61	2.00E-19	31	32		bimD protein - <i>Emericella nidulans</i> [Emericella nidulans]
	1..630		291..371			g1078626	3748	328	e-122	97	17		
21772	ENU05566	ANI61C5006:	22-45	782-801	NAP	g1723187	397	116	4.00E-44	46	20		112.3 KD protein in PYK1-SNC1 intergenic region [Saccharomyces cerevisiae]
	1..2511		913..257			g2967448	102	40	0.013	31	13		(AB008683) alpha2(I) collagen [Bos taurus]
21774	ENU05568	ANI61S2718:			NAP	g3978134	779	256	2.00E-67	52	26		(U65409) Sla2p [Yarrowia lipolytica]
	1..561					g1572721	254	50	0.00002	29	19		(U70136) megakaryocyte stimulating factor: MSF [Homo sapiens]
21776	ENU05570	ANI61S4379:			NAP	g4490992	219	61	3.00E-11	31	55		(AL035707) putative salicylate hydroxylase [Streptomyces coelicolor]
	1..1071					g117619	215	56	0.000000	32	38		Choline transport protein [Saccharomyces cerevisiae]
21777	ENU05571	ANI61C7082:	22-41	805-829	NAP	g2494820	518	134	1.00E-45	46	48		Rhamnogalacturonase B precursor (rhamnogalacturonan lyase) (RGASE B) (RHG B) [Aspergillus aculeatus]
	397..1485		1..1242										hypothetical 86.2-KD protein C4G8.04 in chromosome 1
21778	ENU05572	ANI61C5323:	23-42	726-744	NAP	g1351596	221	98	7.00E-20	32	19		[Schizosaccharomyces pombe]
	796..1929												Potential CAAX prenyl protease 1 (prenyl protein-specific endoprotease 1) (PPSEP 1) [Schizosaccharomyces pombe]
21780	ENU05574	ANI61C8098:	22-49	550-575	NAP	g1351596	297	85	1.00E-22	44	36		60S ribosomal protein L27A (L29) (CRP1) [Neurospora crassa]
	1..602												
21781	ENU05575	ANI61C1069			NAP	g1351689							
	5..940..306												
21782	ENU05576	ANI61C1129	23-42	720-739	NAP	g132845	598	137	1.00E-31	78	100		
	9..784..1565												

Seq num	Seq id	Contig source	5' pos	Primer 3 pos	Primer Basis	Selection	aat	Blast	Blast	% id	%
					ncbi gi	Score	Score	Prob	cvrg	Description	
					gl877482	65	53	0.000000	32	(U89271) short-chain alcohol dehydrogenase [Tripsacum dactyloides]	
21784	ENU05578	ANI61C7468:	69-88	776-795	NAP	g2213907	1272	438	e-122	81	93
		ANI61S4063:	1..396	1494..592							
21785	ENU05579	ANI61C1014	102-121	468-494	NAP	g3929649	463	167	6.00E-41	84	36
		0:1..515				g1806234	120	63	6.00E-14	31	61
21787	ENU05581	ANI61C1014	34-61	726-749	NAP	g4185560	3327	571	e-162	99	12
		8:1981..1				g4759160	252	69	5.00E-17		
21788	ENU05582	ANI61C6750:	34-53	625-644	NAP	g4262650	245	98	5.00E-26	38	31
		1851..2553									
21789	ENU05583	ANI61C4308:	117-136	584-603	NAP						
		1..641									
21790	ENU05584	ANI61C1086	43-64	395-422	NAP	g3023956	101	69	2.00E-11	34	9
		1:1263..821									
21791	ENU05585	ANI61C9585:	22-48	502-521	NAP	g1175439	599	258	3.00E-68	57	22
		637..1									
21792	ENU05586	ANI61C4157:	102-127	562-588	NAP	g1723926	248	130	1.00E-29	40	24
		3992..3384									
21793	ENU05587	ANI61C3304:	56-75	699-717	NAP	g729611	371	122	3.00E-27		
		827..1									
21794	ENU05588	ANI61C8348:	22-42	447-472	NAP	g3560147	263	122	2.00E-27	38	24
		1658..2190									
21795	ENU05589	ANI61C700:1	122-141	712-731	NAP	g1580818	1013	312	5.00E-90	64	37
		..887									
21796	ENU05590	ANI61C6928:	25-52	680-707	NAP	g2342691	167	68	8.00E-14	29	33
		775..1									
21797	ENU05591	ANI61C1019	27-46	563-582	NAP	g544013	143	64	7.00E-16	35	28
		2:1383..2024									

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	Score	Score Prob	% id	% cvg	Description	
21798	ENU05592	ANI61C1575:	22-49	594-614	NAP	g3004863	530	214	4.00E-55	54	27	"(AF029354) exo-beta-1,3-glucanase [Ampelomyces quisqualis]"	
21799	ENU05593	ANI61C9237:	64-83	806-825	NAP	g1723929	1819	261	6.00E-69	51	17	hypothetical 171.5 KD helicase in NUT1-ARO2 intergenic region	
21800	ENU05594	ANI61C1582:	22-45	725-748	NAP	g2500542	247	105	4.00E-22	31	19	putative ATP-dependent RNA helicase YMR128W [Saccharomyces cerevisiae]	
21801	ENU05595	ANI61C7665:	69-88	761-780	NAP	g586486	508	178	4.00E-44	37	41	hypothetical 77.3 KD protein in FIG1-GIP1 intergenic region	
21802	ENU05596	ANI61C2116:	1..964		NAP	g2105430	687	216	2.00E-55	48	24	(U97079) U5-116kD [Mus musculus]	
21803	ENU05597	ANI61C3561:	95-114	609-630	NAP	g1437475	194	105	4.00E-22	38	57	"(D86544) hydroxyquinol-1,2-dioxygenase [Ralstonia pickettii]" "(AJ022397) beta-1,3 exoglucanase [Trichoderma harzianum]" "(AC006264) unknown protein [Arabidopsis thaliana]	
21804	ENU05598	ANI61C5947:	58..1380		NAP	g2924313	552	120	1.00E-26	34	25	(Z95620) hypothetical protein [Schizosaccharomyces pombe] (AL032684) zinc finger protein [Schizosaccharomyces pombe] (AF065435) nodulin [Glycine max]	
21805	ENU05599	ANI61C431:8	22-48	452-471	NAP	g4803936	138	80	1.00E-17				
21806	ENU05600	ANI61C374:1	204-223	380-399	NAP	g2117310	70	39	0.032	22	63	(AF00426) fimbriae-associated protein Fap1 [Streptococcus parasanguinis]	
21807	ENU05601	ANI61C6452:	27-54	805-829	NAP	g3810847	471	192	3.00E-48	37	41	(AF043699) similar to a human off (GB:D13642) and human UV-damaged DNA binding factor (GB:U32986) in separate non-overlapping regions [Caenorhabditis elegans]	
21808	ENU05602	ANI61C9353:	22..1176	72-90	496-518	NAP	g3851530	195	59	4.00E-17	41	32	transcriptional regulator Y protein TYRR [Escherichia coli]
21809	ENU05603	ANI61C32:1..	1..539	522-549	NAP	g3929312	145	51	0.000007	34	7	Ammonium transporter MEP3 [Saccharomyces cerevisiae]	
21810	ENU05604	ANI61S133:1.	.407		NAP	g2804455	274	79	3.00E-23	47	10	IAA-amino acid hydrolase [Arabidopsis thaliana]	
21811	ENU05605	ANI61S618:5	73..1	212-232	456-476	NAP	g136600	886	360	3.00E-99			
21812	ENU05606	ANI61C1008	6:1023..1	70-89	727-746	NAP	g1708982	810	143	4.00E-62	53	54	
21813	ENU05607	ANI61S2221:	308..1			NAP	g1708463	131	78	5.00E-14	28	37	

Seq num	Seq id	Contig source	5 pos	Primer 3 pos	Primer Basis	Selection Database Hit	ncbi gi	aat Score	blast Score	blast Prob	% id	% cvrg	Description
21814	ENU05608	ANI61C6473:	22-46	727-749	NAP	g2408055	154	59	3.00E-11	28	35	(Z99164) hypothetical protein	
21815	ENU05609	ANI61C9354:	898..1		NAP	g2565275	361	146	1.00E-34	68	81	[Schizosaccharomyces pombe] (AF023611) Dm1p homolog [Homo sapiens]	
21816	ENU05610	ANI61C5269:	37-58	712-730	NAP	g550452	766	154	1.00E-65	57	39	"(U08469) 3-methylcrotonyl-CoA carboxylase, biotin-carrier domain [Glycine max]"	
21817	ENU05611	ANI61C8323:	164-183	361-386	NAP	g1084969	612	190	2.00E-58	94	23	sulfate adenylyltransferase (EC 2.7.7.4) - <i>Emericella nidulans</i> [ <i>Emericella nidulans</i> ]	
21818	ENU05612	ANI61C3094:	98-125	805-829	NAP	g1652620	459	96	1.00E-47	55	45	(D90907) pyridine nucleotide transhydrogenase beta subunit [Synechocystis sp.] (Z32683) similar to RNA binding domain; cDNA EST EMBL:D74891 comes from this gene; cDNA EST EMBL:D75208 comes from this gene; cDNA EST EMBL:D72347 comes from this gene; cDNA EST EMBL:D7552 comes from this gene; cDNA EST EMBL:D... [] (AL049498) hypothetical rho1 gdp-gtp exchange protein	
21819	ENU05613	ANI61C2132:	22-41	425-446	NAP	g3878950	252	80	2.00E-23	44	98	[Schizosaccharomyces pombe] hypothetical 51.7 KD protein in CTP1-SUL2 intergenic region [Saccharomyces cerevisiae] (L10328) o197 [Escherichia coli]	
21820	ENU05614	ANI61C8419:	28-46	805-827	NAP	g4539278	553	81	2.00E-15			(Z97208) hypothetical protein [Schizosaccharomyces pombe] proline-rich protein MP3 - mouse (fragment) [] DNA-directed RNA polymerase II largest subunit (B220) [Saccharomyces cerevisiae] (AL031262) hypothetical protein [Schizosaccharomyces pombe]	
21821	ENU05615	ANI61S2455:	33-52	413-438	NAP	g586361	127	62	0.000000	30	32		
21822	ENU05616	ANI61S2364:	61-87	427-452	NAP	g290544	730	234	1.00E-74	98	72		
21823	ENU05617	ANI61C1143	5:351..1918	22-47	803-829	NAP	g2239185	1187	253	1.00E-66	45	(Z97208) hypothetical protein [Schizosaccharomyces pombe]	
21824	ENU05618	ANI61S4374:	1..547		NAP	g91210	117	61	0.000000	30	73	proline-rich protein MP3 - mouse (fragment) [] DNA-directed RNA polymerase II largest subunit (B220) [Saccharomyces cerevisiae] (AL031262) hypothetical protein [Schizosaccharomyces pombe]	
21825	ENU05619	ANI61C6626:	1..2628	22-48	780-807	NAP	g2507347	1984	48	0.00008	56	14	
21826	ENU05620	ANI61C7149:	28-50	770-790	NAP	g3417430	359	90	1.00E-17	31	30		
			320..3018										

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	blast Score	blast Prob	% id	% cvrg	Description
21827	ENU05621	ANI61C2318:	1..1219	NAP	g2267008	195	112	4.00E-24	32	10	(AF006827) adenylate cyclase	[Magnaporthe grisea]	
21828	ENU05622	ANI61C1143	88-108	368-390	NAP	g3978466	217	103	5.00E-22	42	19	(AF086822) dihydroxyacetone synthase	[Candida boidinii]
21829	ENU05623	ANI61C1455:	122-143	491-510	NAP	g3738169	289	92	3.00E-18	41	41	(AL031856) putative mitochondrial protein import protein - DNAJ protein	[Schizosaccharomyces pombe]
21830	ENU05624	ANI61C1069:	23-46	590-612	NAP	g2967835	661	214	1.00E-61	66	54	(AF052061) polygalacturonase [Ophistoma novo-ulmi]	
21831	ENU05625	ANI61C4657:	3615..6275	NAP	g1703456	1367	231	3.00E-68	53	23	Cation-transporting ATPase PAT1	[Dictyostelium discoideum]	
21832	ENU05626	ANI61C1004	51-71	641-660	NAP	g1352388	377	173	1.00E-42	38	32	"Lanosterol synthase (oxidosqualene--lanosterol cyclase) (2,3-epoxysqualene-lanosterol cyclase) (OSC)"	[Rattus rattus]
21833	ENU05627	ANI61C1035:	118-138	381-400	NAP	g4150918	263	109	7.00E-24	51	55	(Z50728) putative acetyltransferase	[Schizosaccharomyces pombe]
21834	ENU05628	ANI61C9868:	29-49	805-824	NAP	g2133268	1616	457	e-128	91	32	DNA-binding protein amdA-Emericella nidulans	[Emericella nidulans]
21835	ENU05629	ANI61C9030:	22-45	720-739	NAP	g2414578	251	68	2.00E-20	39	60	(Z99292) hypothetical protein	[Schizosaccharomyces pombe]
21836	ENU05630	ANI61C1122	116-142	423-448	NAP	g84160	98	64	8.00E-10	32	40	fragmin - slime mold (Physarum polycephalum) (fragments)	[Fusarium solani]
21837	ENU05631	ANI61C1120	25-48	808-828	NAP	g2133293	814	154	8.00E-84	72	98	"(AL031852) putative cleavage and polyadenylation specificity factor subunit, yeast pre-mRNA 3'-end processing factor CF II homolog	[Schizosaccharomyces pombe]
21838	ENU05632	ANI61C5075:	22-49	720-745	NAP	g3738146	528	75	7.00E-13			(AL049522) WD repeat protein	[Schizosaccharomyces pombe]
21839	ENU05633	ANI61C5115:	60-85	727-750	NAP	g4539609	279	101	9.00E-21	39	100	"(Z99164) hypothetical protein	[Schizosaccharomyces pombe]
21840	ENU05634	ANI61C7762:	24-45	540-561	NAP	g2408044	695	287	5.00E-77	65	24	"(AB015510) FIL-CMCCase"	[Aspergillus aculeatus]
21841	ENU05635	ANI61C6096:	202-223	454-479	NAP	g3242653	155	55	0.000000	45	26		
			368..710										

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit ncbi gi	Score	Score	Blast Prob	% id	% cvrg	Description
21842	ENU05636	ANi61C3621:	22-45	419-440	NAP	g2664240	476	199	1.00E-50	59	47	(AL009227) electron transfer flavoprotein alpha-subunit precursor
21843	ENU05637	ANi61C2544:	22-43	805-824	NAP	g3287941	210	101	5.00E-21	45	26	[Schizosaccharomyces pombe] hypothetical GTP-binding protein in SEH1-PRP20 intergenic region C25H2.15 in chromosome II
21844	ENU05638	ANi61C6113:	44-71	806-826	NAP	g1723894	806	238	6.00E-67	56	40	[Saccharomyces cerevisiae] [Schizosaccharomyces pombe]
21845	ENU05639	ANi61C2481:	22-42	581-600	NAP	g1787798	482	206	2.00E-52	43	91	[AE000249] putative enzyme [Escherichia coli]
21846	ENU05640	ANi61C8019:	38-58	485-507	NAP	g4106657	466	189	2.00E-47	57	46	(AL035064) activator 1 subunit (replication factor subunit)
21847	ENU05641	ANi61C8982:	22-42	762-780	NAP	g1346661	337	74	1.00E-12	47	10	[Saccharomyces pombe] NAM9 protein precursor
21848	ENU05642	ANi61C1079	24-45	775-794	NAP	g3133101	832	215	1.00E-64	56	72	(AL023554) conserved hypothetical protein. [Schizosaccharomyces pombe]
21849	ENU05643	ANi61C1061	43-62	709-734	NAP	g2133034	385	151	7.00E-36	26	45	probable membrane protein YPR156c-yeast (Saccharomyces cerevisiae) [Saccharomyces cerevisiae]
21850	ENU05644	ANi61C1799:	40-67	464-489	NAP	g1524045	165	63	1.00E-12	39	37	(X96643)
21851	ENU05645	ANi61S1588:	339-1098		NAP	g340613	112	41	0.007	25	68	Geranylgeranylpyrophosphate Synthetase [Gibberella fujikuroi] (L07545) A 'c' was inserted after nt 369 (=nt 10459 in genomic sequence (M10126)) to correct -1 frameshift probably due to gel compression [Leishmania tarentolae] (Z99091) putative exocyst complex component [Schizosaccharomyces pombe]
21852	ENU05646	ANi61C1255:	22-45	297-321	NAP	g4867840	299	137	5.00E-32			hypothetical 29.7 KD protein in RPL1-CPDB intergenic region (F286) [Escherichia coli]
21853	ENU05647	ANi61C1043	119-136	453-479	NAP	g732284	99	52	0.000002	30	31	(AL049495) putative synaptobrevin-type protein transport protein [Schizosaccharomyces pombe]
21854	ENU05648	ANi61S2100:	81-100	388-405	NAP	g4539261	197	61	0.000000	42	66	
			482..1				006					

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	blastn gi	aat	Blast Score	Blast Prob	% id	% cvrg	Description	
21855	ENU05649	ANT05C5945:	221-240	373-396	NAP	g1827509	203	100	9.00E-21	33	24	(D83993) similar to pir: S52731 (23.4% identity in 273 aa overlap)	NADH-cytochrome B5 reductase precursor (P344P32) [Saccharomyces cerevisiae]	
21856	ENU05650	ANI05C1909:	71-92	504-525	NAP	g2494052	138	57	0.000000 09	41	45	[Schizosaccharomyces pombe] purine nucleoside phosphorylase (inosine phosphorylase) (PNP) [Bacillus stearothermophilus] ARP2/3 complex 16 KD subunit (P16-ARC) [Homo sapiens]		
21857	ENU05651	ANI05C1058	62-81	470-487	NAP	g3121767	72	49	0.00003	31	99	hypothetical protein YDR398w - yeast (Saccharomyces cerevisiae) [Saccharomyces cerevisiae]		
21858	ENU05652	ANI05C5888:	22-44	731-750	NAP	g2131466	205	55	5.00E-10	30	35	(Z98529) putative ma polymerase ii transcription factor b subunit [Schizosaccharomyces pombe] tannase (EC 3.1.1.20) - Aspergillus oryzae [Aspergillus oryzae] (Z37980) ORF14 [Escherichia coli]		
21859	ENU05653	ANI05C7786:	222-244	795-822	NAP	g2330699	356	104	2.00E-28	39	53	(AF000232) protein mannosyltransferase 1 [Candida albicans]		
21860	ENU05654	ANI05C4503:	777..1		NAP	g1351919	189	85	4.00E-16	28	98	Copper amine oxidase precursor (MAOX) [Arthrobacter sp.]		
21861	ENU05655	ANI05C4705:	22-40	792-811	NAP	g4757882	344	167	8.00E-41			bystin-like [Homo sapiens]		
21862	ENU05656	ANI05C1133:	1..1508	756-783	NAP	g3411013	412	97	1.00E-37	46	27	hypothetical 66.7 KD protein in EGD2-SUN1 intergenic region [Saccharomyces cerevisiae]		
21863	ENU05657	ANI05C1141:	6948..6145	1350..2351	NAP	g1351919	184	103	9.00E-22	37	24	D1 (SNRNP core protein D1) (SM-D1) (SM-D autoantigen) [Mus musculus] (AL022117) asparagine synthetase [Schizosaccharomyces pombe] (D63703) isobutene-forming enzyme and benzoate 4-hydroxylase [Rhodotorula minuta]		
21864	ENU05658	ANI05C1090	35-57	436-460	NAP	g731763	318	109	8.00E-32	47	27			
21865	ENU05659	ANI05C1834:	1:1..499		NAP									
21866	ENU05660	ANI05C6155:	107-130	504-527	NAP									
21867	ENU05661	ANI05C1098	4:96..1386		NAP									
21868	ENU05662	ANI05C7744:	8689..8335	24-44	313-334	NAP	g2959371	315	95	2.00E-29	63	18		
21869	ENU05663	ANI05C6500:	632..1	41-60	495-512	NAP	g1020413	120	57	8.00E-11	32	33		

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit ncbi gi	Blast Score	Blast Score	% id	% cvrg	Description		
21870	ENU05664	ANi61C6591:	34..52	808..827	NAP	g2132842	532	237	6.00E-62	51	87	probable membrane protein YOL077c - yeast [Saccharomyces cerevisiae]	
21871	ENU05665	ANi61C112	117..136	670..697	NAP	g3859709	344	176	2.00E-43	37	44	(AL033497) nucleotide phosphodiesterase [Candida albicans] probable reverse transcriptase Mars1 (clone pCGC20) - fungus (Ascobolus immersus) (fragment) [Ascobolus immersus]	
21872	ENU05666	ANi61C213:	43..62	715..742	NAP	g2133333	215	50	9.00E-17	27	37	(AF093142) aconitase [Aspergillus terreus]	
21873	ENU05667	ANi61C1105	50..69	755..781	NAP	g2293196	397	176	2.00E-43	34	65	(AF083220) YteT [Bacillus subtilis]	
21874	ENU05668	ANi61C3631:	7..851..1		NAP	g2244802	208	101	5.00E-21	33	16	(Z97336) retrovirus-related polyprotein homolog [Arabidopsis thaliana] (D90914) hypothetical protein [Synechocystis sp.]	
21875	ENU05669	ANi61C4225:	1..879	71..90	437..456	NAP	g1653493	403	153	2.00E-40	63	66	(X89442) peptide synthetase [Metarhizium anisopliae]
21876	ENU05670	ANi61C8023:	1..1115	40..66	738..765	NAP	g2342601	463	168	6.00E-41	33	5	[Saccharomyces cerevisiae] hypothetical protein YOR021c - yeast [Saccharomyces cerevisiae]
21877	ENU05671	ANi61C6494:	22..44	787..813	NAP	g1078030	294	79	2.00E-30	42	94	mitochondrial carrier protein RIM2 [Saccharomyces cerevisiae]	
21878	ENU05672	ANi61C246:7	23..44	723..750	NAP	g585856	415	164	8.00E-40	43	60	tannase (EC 3.1.1.20) - Aspergillus oryzae [Aspergillus oryzae] ("AF038596) beta-1,3-glucanoyltransferase [Aspergillus fumigatus]" hydroxyproline-rich glycoprotein - perennial teosinte [Zea diploperennis] (AL034353) putative major facilitator family multi-drug resistance protein [Schizosaccharomyces pombe] Arginase [Emeticella nidulans]	
21879	ENU05673	ANi61C6363:	1281..1	23..42	718..737	NAP	g2133259	1584	467	e-131	78	48	oryzae [Aspergillus oryzae]
21880	ENU05674	ANi61C7430:	3318..2845	36..62	430..453	NAP	g2967691	453	108	5.00E-46	68	45	furnigatus]
21881	ENU05675	ANi61S1195:	1..938		NAP	g283032	192	64	0.000000	27	78	perennial teosinte [Zea diploperennis] (AL034353) putative major facilitator family multi-drug resistance protein [Schizosaccharomyces pombe] Arginase [Emeticella nidulans]	
21882	ENU05676	ANi61C8808:	3399..4931	22..48	809..829	NAP	g3925779	177	42	0.005	24	48	TOR2(DRR2) gene [Saccharomyces cerevisiae]
21883	ENU05677	ANi61C9823:			NAP	g2492940	1531	200	e-127	95	77	(AF093142) aconitase [Aspergillus terreus]	
21884	ENU05678	ANi61C8194:	1..2472	24..48	779..801	NAP	g742559	1859	200	1.00E-50	41	10	
21885	ENU05679	ANi61C3566:	2989..526	48..67	805..829	NAP	g3661614	1985	242	2.00E-63	50	35	

Sq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit ncbi gi	aat Score	Blast Score	Prob	% id	% cvrg	Description	
21886	ENU05680	ANI61C1218:	28-55	601-621	NAP	g1339938	428	185	2.00E-46	51	25	(D50430) glycerol-3-phosphate dehydrogenase [Mus musculus]	
21887	ENU05681	ANI61S2611:	1644..1003	1..368	27-46	244-261	NAP	g2500536	283	79	5.00E-26	50	20 probable ATP-dependent RNA helicase DBP9 [Saccharomyces cerevisiae]
21888	ENU05682	ANI61C6784:	3114..2036	1..857	61-80	792-811	NAP	g1168351	198	49	0.00005	29	76 Alcohol dehydrogenase (ADH) [Bacillus stearothermophilus] (AF031886) erythrocyte binding protein [Plasmodium yoelii yoelii]
21889	ENU05683	ANI61S1114:	1477..1			NAP	g2947228	184	39	0.054	25	16 hypothetical protein [Plasmodium yoelii yoelii] FPR1-TOM22 intergenic region	
21890	ENU05684	ANI61C4594:	22-41	1..382	804-824	NAP	g1730777	1772	367	e-109	72	26 [Saccharomyces cerevisiae]	
21891	ENU05685	ANI61C4238:	102-125	335-361	NAP	g2132680	166	81	3.00E-15	40	3	probable membrane protein YLR087c-yeast [Saccharomyces cerevisiae]	
21892	ENU05686	ANI61C1030	22-49	2:484..2062	801-828	NAP	g4007758	666	139	2.00E-32	53	55 [Saccharomyces cerevisiae] (AL034433) conserved hypothetical protein [Schizosaccharomyces pombe] (Z95397) unknown	
21893	ENU05687	ANI61C6614:	1648..159	23-44	784-803	NAP	g2104465	627	87	2.00E-16		[Schizosaccharomyces pombe] hypothetical 24.6 KD protein in MCK1-RP55B intergenic region	
21894	ENU05688	ANI61C1031	5:1412..1739	22-47	457-479	NAP	g1353100	176	91	4.00E-18	43	45 [Saccharomyces cerevisiae] delta-1-pyrroline-5-carboxylate dehydrogenase precursor (P5C dehydrogenase) [Saccharomyces cerevisiae]	
21895	ENU05689	ANI61C6286:	706..1089	27-46	450-477	NAP	g730430	239	116	1.00E-25	49	22 alpha-amylase (EC 3.2.1.1) 3 precursor - Aspergillus oryzae [Aspergillus oryzae]	
21896	ENU05690	ANI61C2164:	68..1154	22-41	772-799	NAP	g67385	673	114	4.00E-66	45	55 alpha-amylase (EC 3.2.1.1) 3 precursor - Aspergillus oryzae [Aspergillus oryzae]	
21897	ENU05691	ANI61C1147	3:1..1399	22-47	792-819	NAP	g2493479	1035	201	4.00E-51	36	21 "dynactin, 150 KD isoform (150 KD dynein-associated polypeptide) (DP-150) (DAP-150) (P150-glued) [Neurospora crassa]" (Y10542) homologous to 40KD subunit of RNA-polymerase I and III [Cricetulus griseus]	
21898	ENU05692	ANI61C8423:	2330..1180	22-49	768-787	NAP	g1914859	814	282	2.00E-75	56	75 putative sterigmatocystin biosynthesis protein STCQ [Emericella nidulans] (Y17332) proline-rich protein [Zea mays]	
21899	ENU05693	ANI61C7771:	4940..5391			NAP	g2498970	539	202	6.00E-52	78	54	
21900	ENU05694	ANI61S4257:	1..892			NAP	g4138732	194	55	0.000000	23	71	
							5						

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit ncbi gi	aat Score	Blast Prob	% id	% cvrg	Description
21901	ENU05695	ANI61C7923:	23-44	456-483	NAP	g1805251	184	61	0.00000	31	36 (U58946) transposase [Aspergillus awamori]
21902	ENU05696	ANI61C8749:	122-141	352-371	NAP	g3135990	365	157	4.00E-38	53	27 (AL023589) membrane transporter [Schizosaccharomyces pombe]
21903	ENU05697	ANI61C1122	35-62	537-564	NAP	g3925779	138	68	7.00E-11	32	27 (AL034353) putative major facilitator family multi-drug resistance protein [Schizosaccharomyces pombe]
21904	ENU05698	ANI61C1033	23-42	786-813	NAP	g4583552	1171	327	e-103	74	75 "(AJ012316) arabinogalactan endo-1,4-beta-galactosidase [Aspergillus tubingensis]"
21905	ENU05699	ANI61C7064:	22-43	720-743	NAP	g113314	4318	575	e-163	98	7 delta-(L-alpha-aminoacidyl)-L-cysteinyl-D-valine synthetase (ACV synthetase) (ACVS) [Emericella nidulans]
21906	ENU05700	ANI61C9189:	75-98	426-449	NAP	g1174433	146	78	4.00E-14	42	40 Signal recognition particle 19 KD protein homolog [Yarrowia lipolytica]
21907	ENU05701	ANI61C3701:	27-46	446-465	NAP	g3219956	168	44	0.0008	45	98 hypothetical protein C57A7.01 in chromosome I [Schizosaccharomyces pombe]
21908	ENU05702	ANI61C1058	36-63	531-556	NAP	g4160397	299	134	5.00E-31	39	53 (AL035210) halotolerance protein [Schizosaccharomyces pombe]
21909	ENU05703	ANI61C7089:	22-42	320-347	NAP	g2501094	96	52	0.000001	24	48 Syntaxin 6 [Rattus norvegicus]
21910	ENU05704	ANI61C908:1	22-42	363-382	NAP	g1085674	414	135	2.00E-31	75	79 blasticidin S deaminase - Aspergillus terreus [Aspergillus terreus]
21911	ENU05705	ANI61C1584:	92-111	391-413	NAP	g730406	106	46	0.0001	36	84 Profilin []
21912	ENU05706	ANI61C5748:	46-65	448-467	NAP	g3293344	150	77	7.00E-14	29	16 (AF059614) transportin; TRN [Xenopus laevis]
21913	ENU05707	ANI61C8295:	22-48	775-802	NAP	g2342601	436	92	8.00E-30	31	5 (X89442) peptide synthetase [Metarhizium anisopliae]
21914	ENU05708	ANI61C9805:	1.1117	2499-885	NAP	g4512702	567	121	7.00E-27	30	41 (AC006569) hypothetical protein [Arabidopsis thaliana]
21915	ENU05709	ANI61C8160:	1976..3983		NAP	g3885836	414	69	8.00E-19	30	34 (AF091042) putative cercosporin transporter [Cercospora kikuchii]
21916	ENU05710	ANI61C615:	74-93	660-679	NAP	g4499837	276	88	2.00E-27	30	57 (AJ011963) dimethyl-allyl-tryptphan-synthase [Claviceps purpurea]
21917	ENU05711	ANI61C6187:	734..1516	35-54	NAP	g585965	1184	371	e-102	67	37 Vesicular-fusion protein SEC18 [Saccharomyces cerevisiae]
			1366..1								

Seq num	Seq id	Contig source	5 pos	3 pos	Primer Basis	Primer Selection	Database	Hit ncbi	gi	Score	Score	Blast Prob	Blast % id	% cvrg	Description
21918	ENU05712	ANI61C8757:	121-140	332-351	NAP		g3560215	203	77	5.00E-14	36	28	"(AL031536) yeast reduced viability upon starvation protein rvs167 homolog, SH3 domain containing [Schizosaccharomyces pombe]"		
21919	ENU05713	ANI61C1104	24-43	802-821	NAP		g84176546	284	50	0.00003			(AL035259) possible RanBP7-importin-beta-Cse1p superfamily [Schizosaccharomyces pombe] (X96767) U1 snRNP-specific protein C		
21920	ENU05714	ANI61C26556:	2041..2589		NAP		g1360017	117	70	1.00E-11	45	62	[Mus musculus]		
21921	ENU05715	ANI61S3099:	1..507		NAP		g82698	220	36	0.14	36	49	hydroxyproline-rich glycoprotein precursor - maize [Zea mays]		
21922	ENU05716	ANI61C8555:	42-66	284-310	NAP		g1707880	154	84	3.00E-16			aminomethyltransferase precursor (glycine cleavage system T protein) [Saccharomyces cerevisiae] ("U93872) ORF 73, contains large complex repeat CR 73 [Kaposi's sarcoma-associated herpesvirus]" hypothetical 138.8 KD protein C11D3.14C in chromosome I		
21923	ENU05717	ANI61S1431:	1..746		NAP		g2246532	170	46	0.0002	21	22	[Schizosaccharomyces pombe] (X81635) RAD26 [Saccharomyces cerevisiae]		
21924	ENU05718	ANI61C3881:	96-115	681-698	NAP		g1351710	415	203	2.00E-51	43	18	[Mus musculus]		
21925	ENU05719	ANI61S2549:	73..645		NAP		g91206	110	60	0.000000	29	96	HXT5-NRK1 intergenic region [Saccharomyces cerevisiae] (AF112473) PyrABCN [Emeicella nidulans]		
21926	ENU05720	ANI61C4525:	102-127	605-631	NAP		g550429	592	233	9.00E-61	53	20	[Arthrobacter sp.] beta-galactosidase (lactase)		
21927	ENU05721	ANI61C5834:	64-83	785-804	NAP		g731689	1635	491	e-138	61	7	(AL031740) putative calcium dependant serine-threonine protein kinase. [Schizosaccharomyces pombe] (AL023777) coenzyme a synthetase [Schizosaccharomyces pombe] (AL023634) hypothetical protein [Schizosaccharomyces pombe]		
21928	ENU05722	ANI61C117:1	23-45	722-749	NAP		g4185560	1852	534	e-151	97	12			
21929	ENU05723	ANI61C9675:	24-43	786-813	NAP		g3913155	1105	101	5.00E-21	30	22			
21930	ENU05724	ANI61C4143:	86-111	693-712	NAP		g3650382	253	115	5.00E-25	30	26			
21931	ENU05725	ANI61C1116	22-43	807-829	NAP		g3184098	1329	173	1.00E-85	64	50			
21932	ENU05726	ANI61C4422:	3:21..1728	26-45	720-739	NAP	g3150262	167	58	2.00E-14	31	65			
			1470..2350												

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	Score	Score Prob	% id	% cvrg	Description
21933	ENU05727	ANI61C2800:	94-113	420-445	NAP	g2909783	511	187	1.00E-46	33	17	(AL049489) conserved hypothetical TBC domain-containing protein [Schizosaccharomyces pombe] (AF020289) MgATP-energized glutathione S-conjugate pump [Arabidopsis thaliana] (AL023389) putative aminotransferase [Schizosaccharomyces pombe]
21934	ENU05728	ANI61C8872:	22-43	760-780	NAP	g3850091	199	73	1.00E-15	30	46	[Arabidopsis thaliana] (AL023389) putative aminotransferase [Schizosaccharomyces pombe] delta-1-pyrroline-5-carboxylate dehydrogenase precursor (P5C dehydrogenase) [Agaricus bisporus] "serine/threonine protein phosphatase PP2A-beta, catalytic subunit [Sus scrofa]"
21935	ENU05729	ANI61C1089	33-54	728-747	NAP	g2494072	256	127	4.00E-29	42	32	[Arabidopsis thaliana] (AL023389) putative aminotransferase [Schizosaccharomyces pombe] delta-1-pyrroline-5-carboxylate dehydrogenase precursor (P5C dehydrogenase) [Agaricus bisporus] "serine/threonine protein phosphatase PP2A-beta, catalytic subunit [Sus scrofa]"
21936	ENU05730	ANI61C283:5	22-44	460-479	NAP	g1352666	963	333	7.00E-98	82	83	Biotin-protein ligase (biotin apoprotein ligase) (biotin-[Saccharomyces cerevisiae] proline-specific permease (proline transport protein) [Emericella nidulans]
21937	ENU05731	ANI61C9677:	202-223	804-829	NAP	g1345625	423	61	5.00E-14			Biotin-protein ligase (biotin apoprotein ligase) (biotin-[Saccharomyces cerevisiae] proline-specific permease (proline transport protein) [Emericella nidulans]
21938	ENU05732	ANI61C9325:	22-43	729-749	NAP	g3929399	1088	185	1.00E-67	46	51	CA11 protein [Saccharomyces cerevisiae]
21939	ENU05733	ANI61C7546:	47-66	784-807	NAP	g729007	358	56	3.00E-14	43	49	dTDP kinase (EC 2.7.4.9) - human. [Homo sapiens] (U97573) peptidyl-prolyl cis-trans isomerase [Treponema pallidum] Pectate lyase precursor [Emericella nidulans]
21940	ENU05734	ANI61C9605:	27-46	723-742	NAP	g284071	175	83	7.00E-16	41	56	KEX1 protease precursor [Kluyveromyces lactis] (AF029523) heat shock protein 60 [Paracoccidioides brasiliensis] (AF128394) contains similarity to Petunia PTTA' (GB:AF009516) [Arabidopsis thaliana] (D11392) UV-endonuclease [Neurospora crassa] (X89442) peptide synthetase [Metarrhizium anisopliae]
21941	ENU05735	ANI61C601:6	63-84	294-314	NAP	g2988417	43	46	0.0002	39	43	
21942	ENU05736	ANI61S645:1.	39-62	287-314	NAP	g3914273	448	96	1.00E-34	49	65	
21943	ENU05737	ANI61C678:8	27-46	729-747	NAP	g125348	1078	76	3.00E-19	33	31	
21944	ENU05738	ANI61C8413:	30-49	797-816	NAP	g3088571	1869	485	e-136	86	47	
21945	ENU05739	ANI61C2004:	54-73	740-759	NAP	g4325349	302	86	1.00E-24	52	43	
21946	ENU05740	ANI61S2337:1..550										
21947	ENU05741	ANI61C5790:1..434	104-121	361-381	NAP	g4210461	260	87	8.00E-17	49	20	(D11392) UV-endonuclease [Neurospora crassa]
21948	ENU05742	ANI61C4064:1..828	204-227	788-807	NAP	g2342601	301	116	2.00E-32	35	4	(X89442) peptide synthetase [Metarrhizium anisopliae]

Seq num	Seq id	Contig source	5 pos	Primer 3 pos	Primer Basis	Selection Database Hit	aat ncbi gi	Score	Score Prob	% id	% cvrg	Description	
21949	ENU05743	ANI61C8506:	22-44	720-746	NAP	g3136057	427	153	1.00E-36	38	58	(AL023592) actin-like protein	
21950	ENU05744	ANI61C7482:	22-47	752-771	NAP	g2388975	336	67	2.00E-25	44	69	[Schizosaccharomyces pombe] (Z98980) phosphotyrosyl phosphatase activator [Schizosaccharomyces pombe]	
21951	ENU05745	ANI61S2702:	1..589	NAP	g3157413	113	44	0.0008	26	25	(AJ001386) catalase [Claviceps purpurea]		
21952	ENU05746	ANI61C1084	2..460..1	NAP	g731385	112	46	0.0002	33	49	hypothetical 33.7 KD protein in ISC10 3'region [Saccharomyces cerevisiae] (AF052391) heat shock protein 70 [Trichophyton rubrum]		
21953	ENU05747	ANI61C1087	22-45	806-825	NAP	g4176751	2421	443	e-130	92	43	[Z98974] hypothetical protein [Schizosaccharomyces pombe]	
21954	ENU05748	ANI61C5200:	22-42	780-799	NAP	g2388905	459	188	5.00E-47	48	59	hypothetical protein YPL235w - yeast (Saccharomyces cerevisiae) [Saccharomyces cerevisiae]	
21955	ENU05749	ANI61C21:96	37-56	728-749	NAP	5..1	1203	379	e-104	81	56	"nitrite reductase (NADH) (EC 1.6.6.4), short form - <i>Emericella nidulans</i> [ ]"	
21956	ENU05750	ANI61C7402:	22-44	720-740	NAP	1..1593	g83711	2184	314	e-135	94	34	immunoreactive protein - <i>Coccidioides immitis</i> [Coccidioides immitis] (AL035065) putative urea active transporter [Schizosaccharomyces pombe]
21957	ENU05751	ANI61C7966:	25-44	700-723	NAP	3747..3004	g2133240	196	50	8.00E-11	34	100	exonuclease II (exo II) (P140) [Schizosaccharomyces pombe] (AL023592) rna binding protein [Schizosaccharomyces pombe]
21958	ENU05752	ANI61C8144:	22-48	715-734	NAP	449..2530	g4106690	946	104	6.00E-48	42	36	probable membrane protein YLR418c - yeast (Saccharomyces cerevisiae) [Saccharomyces cerevisiae]
21959	ENU05753	ANI61C9575:	22-41	749-769	NAP	4706..8327	g729456	2757	227	7.00E-59	44	21	Mbp1 From <i>Saccharomyces Cerevisiae</i> [ ]
21960	ENU05754	ANI61C7591:	22-43	666-687	NAP	1015..1722	g3136047	385	169	1.00E-41	44	53	putative ATP-dependent RNA helicase CDC28 [Schizosaccharomyces pombe] (AL031261) putative transport protein [Schizosaccharomyces pombe]
21961	ENU05755	ANI61C1370:			NAP	533..4	g1363749	151	89	2.00E-17	38	35	probable membrane protein YLR418c - yeast (Saccharomyces cerevisiae) [Saccharomyces cerevisiae]
21962	ENU05756	ANI61C7297:	22-44	375-402	NAP	576..1016	g3402004	273	94	6.00E-19	58	78	putative ATP-dependent RNA helicase CDC28 [Schizosaccharomyces pombe] [Schizosaccharomyces pombe]
21963	ENU05757	ANI61C543:1	34-61	628-651	NAP	..1874	g3913210	1707	324	e-117	73	29	[Schizosaccharomyces pombe] (AL031261) putative transport protein [Schizosaccharomyces pombe]
21964	ENU05758	ANI61C811:1	22-43	756-781	NAP	..1042	g3417424	410	180	1.00E-44	38	10	HIR1 protein - yeast (Saccharomyces cerevisiae) [Saccharomyces cerevisiae]
21965	ENU05759	ANI61C1079	28-48	806-828	NAP	5..2047..3775	g626178	834	204	6.00E-52	42	28	

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit ncbi gi	aat Score	Blast Score	Prob	% id	% cvrg	Description	
21966	ENU05760	ANI61C9078:	22-45	668-694	NAP	g2492604	2285	157	9.00E-38	37	15	[Candida albicans] multidrug resistance protein CDR2	
21967	ENU05761	ANI61C1585:	42-68	448-470	NAP	g2144467	267	120	6.00E-27	43	22	alpha-amylase (EC 3.2.1.1) precursor - yeast (Lipomyces kononenkiae) [Schizosaccharomyces pombe] (AL021837) hypothetical protein	
21968	ENU05762	ANI61C1208:	22-44	810-829	NAP	g2894293	295	101	7.00E-21	24	54	(AL033505) hypothetical protein SC1E6.19c [Streptomyces coelicolor] (Z99126) putative dna helicases.	
21969	ENU05763	ANI61C7167:	41-64	424-444	NAP	g3861442	255	83	1.00E-15	50	41	[Schizosaccharomyces pombe] mitochondrial carrier protein RIM2 [Saccharomyces cerevisiae]	
21970	ENU05764	ANI61C3924:	22-46	719-738	NAP	g2656007	782	183	1.00E-77	50	44	(AL034353) putative major facilitator family multi-drug resistance protein [Schizosaccharomyces pombe] RAS-related protein RAB23V [Beta vulgaris]	
21971	ENU05765	ANI61C4789:	118-137	307-326	NAP	g585856	211	96	2.00E-19	40	32	"phosphate cytidylyltransferase 2, ethanolamine [Homo sapiens]" putative glucosyltransferase C17C9.07 [Schizosaccharomyces pombe] (Z82019) sepin [Agaricus bisporus]	
21972	ENU05766	ANI61C1039	35-54	803-829	NAP	g3925779	282	55	4.00E-10	23	45	fatty acid synthase alpha subunit [Emericella nidulans]	
21973	ENU05767	ANI61S3461:	28-53	272-298	NAP	g3024528	435	176	5.00E-44	80	50	Glucose Oxidase (E.C.1.1.3.4) [Hsp90 chaperones]	
21974	ENU05768	ANI61C4749:	22-42	780-801	NAP	g4505651	524	54	8.00E-12	36	59	probable membrane protein YOR109w - yeast (Saccharomyces cerevisiae)	
21975	ENU05769	ANI61C1954:	2526..4013		NAP	g1722566	534	196	3.00E-56	52	43	[Saccharomyces cerevisiae]	
21976	ENU05770	ANI61C4887:	105-123	396-415	NAP	g2244629	415	120	6.00E-32	58	94	(Z82019) sepin [Agaricus bisporus]	
21977	ENU05771	ANI61C1913:	31-50	806-829	NAP	g2492657	4813	558	e-158	98	18	putative sterigmatocystin biosynthesis fatty acid synthase alpha subunit [Emericella nidulans]	
21978	ENU05772	ANI61S1288:	47-70	350-369	NAP	g442927	133	54	0.000000	33	28	Glucose Oxidase (E.C.1.1.3.4) [Hsp90 chaperones]	
21979	ENU05773	ANI61C7281:	1246..1	716-735	NAP	g4539286	849	213	9.00E-55	44	47	(AL049498) activator of Hsp70 and [Schizosaccharomyces pombe]	
21980	ENU05774	ANI61C243:3	23-50	692-712	NAP	g2132889	228	163	1.00E-39	32	22	probable membrane protein YOR109w - yeast (Saccharomyces cerevisiae)	
21981	ENU05775	ANI61C7816:	1..546	46-65	498-525	NAP	g4502887	198	94	9.00E-19	40	28	[Saccharomyces cerevisiae] "ceroid-lipofuscinosis, neuronal 2, late infantile (Jansky-Bielschowsky disease) [Homo sapiens]"

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database	Hit ncbi gi	Score	Score	Prob	% id	% cvrg	Description
21982	ENU05776	ANI61C525:7	22-47	799-818	NAP		g1077042	3207	122	9.00E-54	61	14	cadmium resistance protein YCF1 - yeast [Saccharomyces cerevisiae)
21983	ENU05777	ANI61C1705:	22-45	802-829	NAP		g586361	733	153	2.00E-36	45	54	hypothetical 51.7 KD protein in CTP1-SUL2 intergenic region
21984	ENU05778	ANI61S4513:	35-57	317-334	NAP		g136232	115	68	6.00E-11	30	18	[Saccharomyces cerevisiae] "potassium transport protein, low-affinity [Saccharomyces cerevisiae]"
21985	ENU05779	ANI61C1142	48-67	784-803	NAP		g171124	411	101	7.00E-21	25	48	(M20319) aminotriazole resistance protein [Saccharomyces cerevisiae]
21986	ENU05780	ANI61C9782:	49-70	446-465	NAP		g2131764	128	73	9.00E-13	33	40	hypothetical protein YLR063w - yeast (Saccharomyces cerevisiae)
21987	ENU05781	ANI61C5615:	1694..1		NAP		g3021303	2839	531	e-150	95	12	[Saccharomyces cerevisiae] (Y15996) acetyl-CoA carboxylase [Emericella nidulans]
21988	ENU05782	ANI61C8296:	24-43	804-828	NAP		g3417424	791	39	0.000000	5		(AL031261) putative transport protein [Schizosaccharomyces pombe]
21989	ENU05783	ANI61C8795:	22-47	807-826	NAP		g1175379	428	151	7.00E-36	30	36	hypothetical 88.2 KD protein C2F7.18C in chromosome II
21990	ENU05784	ANI61C3558:	1067..1		NAP		g1709924	491	214	5.00E-55	50	15	phosphoribosylformylglycaminidine synthase (FGAM synthase) (formylglycaminamide ribonide amidotransferase) (FGARAT)
21991	ENU05785	ANI61C4915:	39-58	711-731	NAP		g2104421	1647	139	2.00E-32	34	23	[Saccharomyces cerevisiae] (Z95395) putative taf; transcription factor TFIID complex component
21992	ENU05786	ANI61C2010:	29-50	720-744	NAP		g2493011	732	254	8.00E-67	47	17	[Schizosaccharomyces pombe] probable calcium-transporting ATPase 8 [Saccharomyces cerevisiae]
21993	ENU05787	ANI61C6994:	1..1196	563-590	NAP		g4584493	174	101	4.00E-21	35	58	(AL049587) putative transcriptional regulator [Streptomyces coelicolor]
21994	ENU05788	ANI61S1378:	783..1393	41-59	219-239	NAP	g243989	474	192	5.00E-49	90	5	"sodium channel alpha subunit [human, skeletal muscle, Peptide, 1..327 aa]"
21995	ENU05789	ANI61C385:4	608..4993	30-57	808-829	NAP	g1723752	242	91	2.00E-23	35	99	hypothetical 25.6 KD protein in SMI-1 PHO81 intergenic region
21996	ENU05790	ANI61C4905:	1..545		NAP		g4107343	436	175	1.00E-43	62	23	[Saccharomyces cerevisiae] (AJ224922) ATP citrate lyase [Sordaria macrospora]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database	Hit	ncbi gi	Score	Score	Blast Prob	% id	% cvrg	Description
21997	ENU05791	ANi61C3311:	103-124	388-407	NAP	g4680709	322	97	3.00E-32					(AF132969) CGI-35 protein [Homo sapiens]
21998	ENU05792	ANi61C7708:	22-43	802-821	NAP	g3005587	326	33	2.3	30	30	33		(AF048977) Ser/Arg-related nuclear matrix protein [Homo sapiens]
21999	ENU05793	ANi61C8066:	41-60	715-742	NAP	g1710663	1183	111	5.00E-69	58	22			putative DNA-directed RNA polymerase III 130 KD polypeptide (RNA polymerase III subunit 2)
22000	ENU05794	ANi61C8202:	34-53	724-743	NAP	g553118	646	132	2.00E-54	38	53			[Schizosaccharomyces pombe] (M27081) alkane hydroxylating cytochrome P-450 [Candida maltosa]
22001	ENU05795	ANi61C1091	43-62	780-799	NAP	g3024986	265	142	3.00E-33					hypothetical zinc-type alcohol dehydrogenase-like protein in AHFF-RNK intergenic region [Escherichia coli]
22002	ENU05796	ANi61C3211:	22-43	714-733	NAP	g3183035	1559	159	1.00E-41	41	27			importin beta-1 subunit (karyopherin beta-1 subunit) (importin 95) [Schizosaccharomyces pombe]
22003	ENU05797	ANi61C1633:	22-46	442-463	NAP	g1706221	211	62	3.00E-17	43	100			cytochrome B5 [Saccharomyces cerevisiae]
22004	ENU05798	ANi61C8674:	102-125	263-290	NAP	g409547	127	66	8.00E-11	33	19			(L07492) sugar transport protein [Saccharomyces cerevisiae]
22005	ENU05799	ANi61C1106	67-94	500-527	NAP	g2131422	184	83	2.00E-15	34	38			hypothetical protein YDR306c - yeast (Saccharomyces cerevisiae)
			7:1..558											[Saccharomyces cerevisiae]
22006	ENU05800	ANi61C5670:			NAP	g83726	714	280	4.00E-75	97	42			hypothetical nox2 protein - Emericella nidulans mitochondrial (SGC3)
		1..428												[Emericella nidulans]
22007	ENU05801	ANi61C7760:	29-56	306-331	NAP	g631806	233	104	3.00E-22	41	26			"beta-chimerin, cerebellar - rat (fragment) I"
22008	ENU05802	ANi61C6462:	1..352	804-824	NAP	g1805251	924	159	6.00E-60	44	50			(U58946) transposase [Aspergillus awamori]
22009	ENU05803	ANi61C7280:	1..1190	5582-4737	NAP	g2956768	400	122	4.00E-27	37	71			(AL022103) transmembrane transporter liz1p. [Schizosaccharomyces pombe]
22010	ENU05804	ANi61C4923:	1..1107	804-823	NAP	g2507441	1041	135	4.00E-80	63	53			"T-complex protein 1, delta subunit (TCP-1-delta) (CCT-delta)
22011	ENU05805	ANi61C2862:	105-124	580-602	NAP	g4158188	147	74	1.00E-12	37	49			[Saccharomyces cerevisiae]" (AL035206) putative alcohol dehydrogenase [Streptomyces coelicolor]
		706..1												

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database	Hit ncbi gi	Score	Score Prob	% id	% cvrg	Description
22012	ENU05806	ANI61C1129	119-146	443-465	NAP	g2408082	398	169	8.00E-42	52	17	(Z99167) putative helicase
22013	ENU05807	ANI61C9103:	32-50	776-802	NAP	g2673955	1266	357	6.00E-98	87	32	[Schizosaccharomyces pombe] (U62935) multidrug resistance protein
22014	ENU05808	ANI61C6282:	112-135	711-738	NAP	g731262	220	125	4.00E-28	24	23	2 [Aspergillus fumigatus] vacuolar protein sorting-associated protein VPS8 [Saccharomyces cerevisiae]
22015	ENU05809	ANI61C6738:	57-76	810-829	NAP	g731597	300	94	2.00E-18	31	70	hypothetical 36.1 KD protein in YLF2-PRPS4 intergenic region
22016	ENU05810	ANI61C1129	23-47	788-808	NAP	g1352980	778	300	1.00E-85	64	24	[Saccharomyces cerevisiae] ATP-dependent RNA helicase DOB1 (mRNA transport regulator MTR4)
22017	ENU05811	ANI61C850:7	22-46	601-626	NAP	g1706480	212	87	8.00E-18	34	19	[Saccharomyces cerevisiae] DNA ligase I (polydeoxyribonucleotide synthase (ATP)) [Xenopus laevis]
22018	ENU05812	ANI61C3634:	1..3043	804-823	NAP	g1546072	1105	147	8.00E-35	32	11	(U68040) polyketide synthase [Cochliobolus heterostrophus]
22019	ENU05813	ANI61C5125:	22-47	770-797	NAP	g731899	947	280	6.00E-75	49	18	putative membrane glycoprotein in SDL1 5'region precursor [Saccharomyces cerevisiae]
22020	ENU05814	ANI61C5245:	31-58	604-631	NAP	g3738163	347	94	1.00E-18	38	99	(AL031856) putative DNA J domain containing protein [Schizosaccharomyces pombe]
22021	ENU05815	ANI61S1152:	118-145	505-524	NAP	g2498506	271	85	3.00E-25	42	26	proline-rich protein LAS17 [Saccharomyces cerevisiae]
22022	ENU05816	ANI61C1643:	78-97	720-740	NAP	g1261823	684	229	1.00E-59	48	25	(L77234) glycine rich protein [Neurospora crassa]
22023	ENU05817	ANI61S3304:	1060..1	52-71	NAP	g4097158	162	94	6.00E-19	37	7	(U46488) NtPs [Proteus mirabilis]
22024	ENU05818	ANI61C8526:	1..522	4623..5636	NAP	g3004634	798	113	6.00E-53	59	81	(U96385) GATA transcription factor [Penicillium chrysogenum]
22025	ENU05819	ANI61C4111:	1..1163	27-46	NAP	g1076802	134	38	0.12			extensin-like protein - maize [Zea mays]
22026	ENU05820	ANI61C3323:	483..1136	32-59	NAP	g401335	526	114	1.00E-42	77	99	vacuolar ATP synthase 16 KD proteolipid subunit [Neurospora crassa]
22027	ENU05821	ANI61C1225:	594..1	190-211	NAP	g131768	217	87	1.00E-16	41	31	quinate permease (quinate transporter) [Emericella nidulans]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description	
22028	ENU05822	ANI61C9283:	107-126	444-463	NAP	g871830	113	39	0.017	35	60	(D30747) mini-collagen [Acropora donei]	
22029	ENU05823	ANI61C2431:	325..1	325..1	NAP	g3319315	977	290	7.00E-78	54	33	[Thielavia heterothallica]	
22030	ENU05824	ANI61C1512:	1336..1	1336..1	NAP	g3929395	2040	328	4.00E-89	67	32	vacuolar ATP synthase 98 KD subunit (vacuolar ATPase 98 KD subunit)	
22031	ENU05825	ANI61C5551:	1.1788	22-48	785-809	NAP	g2120666	724	241	6.00E-63	42	48	"2,4-chlorocatechol 1,2-dioxygenase (EC 1.13.11.-) tfdB - Pseudomonas putida [Pseudomonas putida]" (AL022071) hypothetical protein
22032	ENU05826	ANI61S2863:	505..1	36-55	436-454	NAP	g2950458	228	88	3.00E-17	29	19	[Schizosaccharomyces pombe] (AF019254) DNA polymerase epsilon homolog [Emericella nidulans] (AJ223459) PmA protein [Emericella nidulans]
22033	ENU05827	ANI61C5475:	1735..7652	22-46	792-812	NAP	g4102990	9834	578	e-164	98	12	[Schizosaccharomyces pombe] (AF019254) DNA polymerase epsilon homolog [Emericella nidulans] (AJ223459) PmA protein [Emericella nidulans]
22034	ENU05828	ANI61C4262:	3239..864	22-47	806-828	NAP	g2808662	854	122	3.00E-27	30	33	"glucan (1,4-alpha-), branching enzyme 1 (glycogen branching enzyme) [Homo sapiens]" (U07187) Mlh1p [Saccharomyces cerevisiae]
22035	ENU05829	ANI61C2219:	1..1025	42-65	613-638	NAP	g4557619	1082	161	1.00E-87	66	35	protein kinase (EC 2.7.1.37) - fission yeast (Schizosaccharomyces pombe) [Schizosaccharomyces pombe]
22036	ENU05830	ANI61C8552:	10563..10144	NAP	g460627	92	53	0.000000	31	15	hypothetical 143.7 KD protein C11D3.15 in chromosome I [Schizosaccharomyces pombe]		
22037	ENU05831	ANI61C1129	1:683..1	112-136	548-567	NAP	g2130466	719	290	7.00E-78	62	51	hypothetical 89.4 KD TRP-ASP repeats containing protein in PMT6-PCT1 intergenic region [Saccharomyces cerevisiae]
22038	ENU05832	ANI61C4402:	2025..280	27-48	622-649	NAP	g1351711	1351	311	4.00E-88	66	18	hypothetical 89.4 KD TRP-ASP repeats containing protein in PMT6-PCT1 intergenic region [Saccharomyces cerevisiae]
22039	ENU05833	ANI61C1064	1:1763..3872	22-41	671-695	NAP	g1176045	1101	286	2.00E-76	50	35	(AL049485) probable zinc-binding alcohol dehydrogenase [Streptomyces coelicolor] (AF027687) beta glucosidase homolog [Cochliobolus heterostrophus]
22040	ENU05834	ANI61C1036	1:6952..7642	77-96	564-590	NAP	g4539186	228	102	7.00E-23	45	51	chitin synthase 2 (chitin-UDP acetyl-glucosaminyl transferase 2) [Emericella nidulans]
22041	ENU05835	ANI61C9204:	1333..324	59-78	805-829	NAP	g2598192	900	375	e-103	67	30	
22042	ENU05836	ANI61C5575:	402..1	NAP	g1705828	123	63	0.000000	32	16			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat	Blast Score	Blast Prob	% id	% cvrg	Description
22043	ENU05837	ANI61C1100:	22-49	616-638	NAP	g3695005	256	115	3.00E-25	37	49	(AF038586) pyruvate dehydrogenase kinase isoform 2; PDK2 [Zea mays]	
22044	ENU05838	ANI61S37:44	6..1	72-91	NAP	g1881271	210	78	4.00E-14	35	73	"(AB01488) function unknown, similar product in H. influenzae and	
22045	ENU05839	ANI61C1145	102-124	455-479	NAP	g4760360	115	76	1.00E-13			synechocystis. [Bacillus subtilis]" "(AL035213) predicted using hexExon; L3291.5, Hypothetical protein, len: 300	
22046	ENU05840	ANI61S2374:	66-86	257-276	NAP	g78837	517	205	9.00E-53	95	38	aa [Leishmania major]" [Escherichia coli]	
22047	ENU05841	ANI61C7587:	33-55	294-313	NAP	g729611	286	126	5.00E-29			rimK protein - Escherichia coli Vanadate resistance protein GOG5vVRG4/VAN2 [Saccharomyces cerevisiae]	
22048	ENU05842	ANI61C8467:	189-208	367-388	NAP	g3059184	147	79	1.00E-14	33	40	(D8014) homologous to HpcE (HHD isomerase) protein of E. coli	
22049	ENU05843	ANI61C5479:	28-49	802-829	NAP	g114878	379	147	8.00E-35	37	83	[Rhodococcus erythropolis] carboxyvinyl-carboxyphosphonate phosphorylmutase (carboxyphosphonoenoatepyruvate phosphonomutase) (CPEP hygroscopicus) [Streptomyces hygroscopicus]	
22050	ENU05844	ANI61C1078	102-124	354-373	NAP	g4249409	111	63	4.00E-13	33	29	(AC06072) putative sugar transporter [Arabidopsis thaliana]	
22051	ENU05845	ANI61C4441:	6:1..423	22-48	633-659	NAP	g1351645	869	324	6.00E-88	55	52	hypothetical amino-acid permease C8A4.11 [Schizosaccharomyces pombe]
22052	ENU05846	ANI61C1134	6:1472..493	32-51	774-793	NAP	g4583351	380	185	4.00E-46	41	47	(AF14167) lysosomal peptidase insensitive protease [Canis familiaris]
22053	ENU05847	ANI61C2920:	387..1499	37-56	790-809	NAP	g1723578	381	102	1.00E-38	36	78	probable oxidoreductase C26F1.07 in chromosome I [Schizosaccharomyces pombe]
22054	ENU05848	ANI61C7166:	267..653	50-69	442-461	NAP	g3136036	128	82	2.00E-15	40	48	(AL023590) Glutathione S-transferase [Schizosaccharomyces pombe]
22055	ENU05849	ANI61C2437:	2082..3715	25-52	725-751	NAP	g728771	639	101	5.00E-42	52	23	Alanine/arginine aminopeptidase [Saccharomyces cerevisiae]
22056	ENU05850	ANI61C6823:	576..1	53-73	530-549	NAP	g2226425	124	71	6.00E-12	25	10	(Z97204) hypothetical protein [Schizosaccharomyces pombe]

Seq num	Seq id	Contig source	5 pos	3 pos	Primer Basis	Primer Selection	aat	Blast Score	Blast Prob	% id	% cvrg	Description
22057	ENU05851	ANI61C2391:	24-43	634-654	NAP	g3800835	205	67	2.00E-10	38	4	(AF079138) type I polyketide synthase
22058	ENU05852	ANI61S1602:	49-76	439-466	NAP	g2909465	110	56	0.000000	34	38	PikAII [Streptomyces venezuelae] (AL021930) hypothetical protein
22059	ENU05853	ANI61C7205:	49-71	414-434	NAP	g1588283	463	205	2.00E-52	61	12	Rv0276 [Mycobacterium tuberculosis] MSH6 gene [Saccharomyces cerevisiae]
22060	ENU05854	ANI61C4233:	101-126	791-813	NAP	g600810	228	90	2.00E-17	39	99	(Z46921) unknown [Saccharomyces cerevisiae]
22061	ENU05855	ANI61C9182	54-73	770-789	NAP	g731502	351	153	1.00E-36	32	25	importin beta-4 subunit (karyopherin beta-4 subunit) (fan binding protein YRB4) [Saccharomyces cerevisiae]
22062	ENU05856	ANI61C8801:	165-182	469-488	NAP	g130582	196	97	1.00E-19	35	12	Retrovirus-related pol polyprotein from transposon TNT-1.94 [Nicotiana tabacum]
22063	ENU05857	ANI61C3205:	23-44	649-668	NAP	g3288709	1601	291	6.00E-78	52	19	(AB010442) PMR1 [Penicillium digitatum]
22064	ENU05858	ANI61C4172:	89-108	681-700	NAP	g3413518	506	231	5.00E-60	41	16	(AB010810) phospholipase D
22065	ENU05859	ANI61C3591:	29-48	793-811	NAP	g3116147	329	64	7.00E-17	30	47	[Candida albicans] (AL023290) amino acid permease [Schizosaccharomyces pombe]
22066	ENU05860	ANI61C5426:	43-63	522-549	NAP	g1731075	306	178	4.00E-44	43	53	probable NADH-dependent flavin oxidoreductase YQJM [Bacillus subtilis]
22067	ENU05861	ANI61C1073	22-48	778-796	NAP	g3393022	397	176	2.00E-43	38	38	[AL031174] hypothetical protein [Schizosaccharomyces pombe]
22068	ENU05862	ANI61C7940:	127-145	642-664	NAP	g2498701	94	71	1.00E-11	26	46	sterigmatocystin 7-O-methyltransferase precursor [Aspergillus flavus]
22069	ENU05863	ANI61C3966:	918-16	24-46	NAP	g4539255	359	129	3.00E-29			[AL049495] hypothetical protein [Schizosaccharomyces pombe]
22070	ENU05864	ANI61S4253:	1..822		NAP	g3153821	160	47	0.0001	23	30	(AF062655) plenty-of-prolines-101; POP101; SH3-philo-protein [Mus musculus]
22071	ENU05865	ANI61C9594:	1..503		NAP	g3282229	293	78	3.00E-14			(U68722) BcLHH [Boryotinia fuckeliana]
22072	ENU05866	ANI61C8675:	92-111	368-387	NAP	g1749656	105	73	2.00E-12	35	38	(D89224) similar to Saccharomyces cerevisiae ORF YCR028 [Schizosaccharomyces pombe]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat	Blast Score	Blast Score	% id	% cvg	Description	
22073	ENU05867	ANI61C4988:	36-58	483-510	NAP	gl351666	316	119	4.00E-27	50	30	C1F7.02C	[Schizosaccharomyces pombe] [putative ATP-dependent RNA helicase]	
22074	ENU05868	ANI61C5515:	115-134	391-410	NAP	g2501339	327	148	2.00E-35	44	24	niger]	[Aspergillus niger] [tryptophan dimethylallyltransferase (EC 2.5.1.34) - ergot fungus]	
22075	ENU05869	ANI61C7746:	22-49	615-635	NAP	g2133285	298	129	3.00E-29			[Claviceps purpurea]	[Leucyl-tRNA synthetase, cytoplasmic [Neurospora crassa]]	
22076	ENU05870	ANI61C1105:	1..787		NAP	g135140	570	219	9.00E-63	54	22	[Leucyl-tRNA synthetase, cytoplasmic [Neurospora crassa]]	[Leucyl-tRNA synthetase, cytoplasmic (leucine--tRNA ligase) (LEURS)]	
22077	ENU05871	ANI61C6132:			NAP	g1730744	352	136	1.00E-31	56	45	[MSK1 intergenic region [Saccharomyces cerevisiae]]	[MSK1 intergenic region in MKS1- (U35661) colony 1 [Ophiostoma ulmij]]	
22078	ENU05872	ANI61C1070	42-61	806-828	NAP	g998355	455	71	2.00E-22	31	31	[Schizosaccharomyces pombe]	[Schizosaccharomyces pombe] [Ophiostoma ulmij]	
22079	ENU05873	ANI61C2660:	25-44	709-736	NAP	g2145937	415	57	7.00E-17	33	12	[Mycobacterium leprae]	[Mycobacterium leprae] [AB016221] SSL1	
22080	ENU05874	ANI61S2794:	113-139	459-486	NAP	g3327882	453	205	1.00E-52	54	43	[Schizosaccharomyces pombe]	[Schizosaccharomyces pombe] [U58884] SH3P7 [Mus musculus]	
22081	ENU05875	ANI61C8962:	31-58	754-773	NAP	g1407655	179	46	0.0003			[Sordaria macrospora]	[Sordaria macrospora] [AJ224922] ATP citrate lyase	
22082	ENU05876	ANI61C8475:	28-47	793-812	NAP	g4107343	1137	243	e-111	91	36	[C56F8.17C in chromosome I [Schizosaccharomyces pombe]]	[hypothetical protein C56F8.17C in chromosome I [Schizosaccharomyces pombe]]	
22083	ENU05877	ANI61C5331:	117-134	425-444	NAP	g1723448	339	124	9.00E-31	46	28	[Metarhizium anisopliae]	[Metarhizium anisopliae] [Dihydrodipicolinate synthase (DHDPs)]	
22084	ENU05878	ANI61S813:1			NAP	g2635194	425	173	9.00E-43	47	99	[Corynebacterium glutamicum]	[Corynebacterium glutamicum]	
22085	ENU05879	ANI61S617:6	216-235	527-546	NAP	g4091929	422	185	2.00E-46	47	50	[Candida albicans]	[Candida albicans] [AF069752] C5,6 desaturase	
22086	ENU05880	ANI61S564:5	51..1		NAP	g2635812	276	125	1.00E-28	46	70	[Z99120] similar to hypothetical proteins [Bacillus subtilis]	[Z99120] similar to hypothetical proteins [Bacillus subtilis] (X89442) peptide synthetase	
22087	ENU05881	ANI61C5372:	22-48	790-817	NAP	g2342601	820	242	3.00E-63	48	5	[Dihydrodipicolinate synthase (DHDPs)]	[Dihydrodipicolinate synthase (DHDPs)]	
22088	ENU05882	ANI61C4407:	1805...3381	26-45	584-606	NAP	g118239	131	42	0.000000	31	71		
			732..1									002		

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Primer Database Hit	aat ncbi gi	Blast Score	Blast Prob	% id	cvg	Description
22089	ENU05883	ANI61C4408:	22-44	633-652	NAP	g3116018	679	134	1.00E-46	44	53	(Y13067) vanillin: NAD+ oxidoreductase [Pseudomonas fluorescens]
22090	ENU05884	ANI61C1974:	133-152	494-517	NAP	g83673	183	96	3.00E-19	36	34	amidase (EC 3.5.1.4) - Aspergillus oryzae [Aspergillus oryzae]
22091	ENU05885	ANI61C409:1	29-48	761-780	NAP	g114971	1192	181	6.00E-45	37	33	beta-glucosidase precursor (genitobiase) (cellobiase) (beta-D-glucoside glucohydrolase) [Kluyveromyces marxianus] (AL034382) putative Trp-Asp repeat protein [Schizosaccharomyces pombe]
22092	ENU05886	ANI61C9938:	183-204	430-453	NAP	g3947883	172	68	3.00E-11	31	31	ATP-dependent bile acid permease [Saccharomyces cerevisiae] (Y12527) HMWP1 protein [Yersinia enterocolitica]
22093	ENU05887	ANI61C1941:	22-43	792-819	NAP	g3915963	1019	192	2.00E-48	45	14	probable membrane protein YPL183c - yeast [Saccharomyces cerevisiae] [Saccharomyces cerevisiae] (AL022580) putative protein [Arabidopsis thaliana]
22094	ENU05888	ANI61C9360:	23-47	522-545	NAP	g2765195	214	101	7.00E-21	33	6	(AL021841) amiB [Mycobacterium tuberculosis]
22095	ENU05889	ANI61C7355:	22-43	727-746	NAP	g2132992	120	104	9.00E-22	34	21	diphospho-N-acetylglucosamine:polypeptide beta-N-acetylglucosaminyl transferase (uridine diphospho-N-acetylglucosamine:polypeptide beta-N-acetylglucosaminyl transferase) [Homo sapiens]
22096	ENU05890	ANI61C7856:	24-43	485-504	NAP	g3080368	162	91	6.00E-18	34	24	(AL022580) putative protein [Arabidopsis thaliana]
22097	ENU05891	ANI61S1700:	36-63	387-413	NAP	g2894215	104	71	6.00E-12	29	38	(AL021841) amiB [Mycobacterium tuberculosis]
22098	ENU05892	ANI61C2695:	58-83	404-425	NAP	g4505499	213	119	1.00E-26	40	18	O-GlcNAc transferase (uridine acetylglucosamine:polypeptide beta-N-acetylglucosaminyl transferase) [Homo sapiens]
22099	ENU05893	ANI61C2136:	115-134	805-829	NAP	g266448	648	252	3.00E-66			long-chain-fatty-acid-CoA ligase 1 (long-chain acyl-CoA synthetase 1) (fatty acid activator 1) [Saccharomyces cerevisiae]
22100	ENU05894	ANI61C1060	153-176	654-679	NAP	g2499125	458	196	2.00E-49	37	8	vacuolar protein sorting-associated protein VPS13 [Saccharomyces cerevisiae]
22101	ENU05895	ANI61C7807:	22-46	804-829	NAP	g3220205	166	55	0.000000			(AF054613) peroxin [Yarrowia lipolytica]
22102	ENU05896	ANI61C3104:	61-80	807-826	NAP	g4007757	1872	368	e-126	72	51	(AL034433) glucose-6-phosphate isomerase [Schizosaccharomyces pombe]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database	Hit ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
22103	ENU05897	ANI61C6457:	22-47	801-826	NAP	g2052244	324	92	3.00E-18	37	52	(Y12561) Cdc1 protein	
22104	ENU05898	ANI61C477:1	24-45	535-560	NAP	g3879684	151	85	4.00E-16	36	49	[Schizosaccharomyces pombe] (Z74042) predicted using Genefinder; Similarity to <i>Haemophilus</i> 3-oxoacyl-(acyl)-carrier protein reductase (SW:FABG_HAEIN); cDNA EST	
			194...1787									yk470b2.3 comes from this gene; cDNA EST yk470b2.5 comes from this gene [Caenorhabditis elegans] (AB010274) fatty acid synthetase [Schizosaccharomyces pombe]	
22105	ENU05899	ANI61C9467:	22-42	796-819	NAP	g4115480	1564	122	2.00E-43	42	12	[Schizosaccharomyces pombe] cell division-associated protein BIMB	
			3514...72			g416716	917	254	3.00E-67	92	10	[] (AF0820217) acetoacetyl-CoA synthetase; acetoacetyl-CoA ligase; acyl-activating enzyme	
22106	ENU05900	ANI61C9162:	27-49	434-456	NAP	g3769519	982	209	2.00E-53	45	41	[Schizosaccharomyces pombe] (D90912) hypothetical protein	
			1823...2453									[Synechocystis sp.] (AL031741) putative membrane transporter [Schizosaccharomyces pombe]	
22107	ENU05901	ANI61C1100	50-69	795-814	NAP	g1653242	390	91	1.00E-23	32	58	[Sinorhizobium meliloti] (L10127) ORF17 [Molluscum contagiosum virus type 1]	
			4:4254..2142			g3650370	299	116	1.00E-25	37	41	(AL031739) putative dna primase large subunit [Schizosaccharomyces pombe] (AF009415) choline dehydrogenase [Staphylococcus xylosus] (AB004534) cdc2 kinase homologue [Schizosaccharomyces pombe] (AL023706) hypothetical protein [Schizosaccharomyces pombe] (U70136) megakaryocyte stimulating factor; MSF [Homo sapiens] putative RAS-related protein C1B3.11C [Schizosaccharomyces pombe] (AF082072) ABC transporter protein Atc [Emericella nidulans]	
22108	ENU05902	ANI61C4407:	34-54	707-730	NAP	g3650405	960	216	2.00E-55	49	53		
			4252...5353			g4574121	402	100	2.00E-20	36	27		
22109	ENU05903	ANI61C1871:	22-49	640-660	NAP	g2257494	737	122	4.00E-27	45	41		
			684...1			g3169091	1112	199	4.00E-81	59	46		
22110	ENU05904	ANI61C1015	37-54	764-790	NAP	g462768	85	41	0.008				
			2:1..1341										
22111	ENU05905	ANI61C9626:	22-48	802-829	NAP								
			607..2155										
22112	ENU05906	ANI61C9067:	26-49	806-825	NAP								
			3953...1900										
22113	ENU05907	ANI61C7016:	25-48	806-825	NAP								
			4685...3207										
22114	ENU05908	ANI61C7570:	24-50	803-822	NAP								
			1..1423										
22115	ENU05909	ANI61S1726:	1..791		NAP	g1572721	130	45	0.0008	25	18		
			2707...3778			g3219964	455	158	4.00E-38	46	87		
22117	ENU05911	ANI61C7639:	22-49	807-829	NAP	g4587971	3918	501	e-141	99	20		
			2584..1										

Seq num	Seq id	Contig source	5 pos	Primer 3 pos	Primer Basis	Selection Database	Hit ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
22118	ENU05912	ANJ61C2128:	22-41	725..746	NAP	g1709029	1120	295	2.00E-79	56	27	MIC1 protein	[Saccharomyces cerevisiae]
22119	ENU05913	ANJ61C1267:	22-42	786..805	NAP	g2133039	685	218	4.00E-56	45	17	probable membrane protein	YPR184w - yeast [Saccharomyces cerevisiae)
22120	ENU05914	ANJ61S4277:	69-88	527..547	NAP	g4733981	345	57	4.00E-18			(AC007268) putative serine carboxypeptidase	[Arabidopsis thaliana]
22121	ENU05915	ANJ61S4437:	204-225	414..436	NAP	g2414610	170	53	4.00E-13	43	48	"(Z99295) oxidoreducatase, possible sorbitol utilization	
22122	ENU05916	ANJ61C7381:	34-61	686..713	NAP	g1666269	430	90	6.00E-36	40	97	[Schizosaccharomyces pombe]" (Z82021) cytochrome P450	[Agaricus bisporus]
22123	ENU05917	ANJ61C2718:	50-76	457..479	NAP	g229530	193	75	5.00E-20	43	97	cytochrome b2	1-103 [Saccharomycetales]
22124	ENU05918	ANJ61S3976:	136..520		NAP	g547782	162	73	1.00E-12	36	47	"aminoglycoside 3'-phosphotransferase (kanamycin kinase, type I) (neomycin-kanamycin phosphotransferase, type I) (APH(3')I) (Plasmid NTP16)"	
22125	ENU05919	ANJ61C775:2	24-51	682..709	NAP	g1730771	602	172	3.00E-42	55	25	hypothetical 110.9 KD protein in SPC98-TOM70 intergenic region	
22126	ENU05920	ANJ61C2389:	72-93	375..401	NAP	g1351972	666	153	7.00E-37	95	16	[Saccharomyces cerevisiae]	
22127	ENU05921	ANJ61C1098	91-110	738..756	NAP	g3914054	447	131	5.00E-30	32	35	Nitrogen regulatory protein area [Emericella nidulans]	
22128	ENU05922	ANJ61C3268:	22-44	802..829	NAP	g2132229	149	47	0.0002	31	94	MUTS protein homolog 1 [Schizosaccharomyces pombe]	
22129	ENU05923	ANJ61C1371:	112-133	640..667	NAP	g3702646	135	72	5.00E-12	26	38	hypothetical protein YPL199c - yeast (Saccharomyces cerevisiae) [Saccharomyces cerevisiae]	
22130	ENU05924	ANJ61C6060:	22-47	597..624	NAP	g4495124	436	174	5.00E-43	43	62	(AL035675) WD repeat protein; human U5 SNRNP-specific-like	
22131	ENU05925	ANJ61C679:2	22-45	721..748	NAP	g2131263	2782	396	e-109	66	13	[Schizosaccharomyces pombe] GLT1 protein - yeast (Saccharomyces cerevisiae) [Saccharomyces cerevisiae]	
			506..1										

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database	nebi gi	Score	Score Prob	aat	Blast	Blast	% id	cvg	Description
22132	ENU05926	ANI61C1134:	52-71	781-800	NAP	g2132124	1978	445	e-124	75	25	hypothetical protein YOR304w - yeast			
22133	ENU05927	ANI61C2187:	24-47	680-702	NAP	g2144167	351	70	7.00E-26	32	34	[Saccharomyces cerevisiae]			
			1719..1									(Candida molischiana) [Pichia capsulata]			
22134	ENU05928	ANI61C7216:	22-48	793-815	NAP	g4033486	238	56	6.00E-20	33	51	putative tartrate transporter			
			214..1063									[Agrobacterium vitis]			
22135	ENU05929	ANI61C247.1	29-48	797-816	NAP	g3133104	154	61	0.000000	34	74	(AL023554) conserved hypothetical protein			
			250..2139									[Schizosaccharomyces pombe]			
22136	ENU05930	ANI61C8055:	22-47	765-784	NAP	g117298	1073	194	9.00E-49			cytochrome P450(BM-3) / NADPH-cytochrome P450 reductase			
			2141..227									[Bacillus megaterium]			
22137	ENU05931	ANI61C8057:	91-110	417-444	NAP	g586797	112	61	0.000000	26	28	hypothetical 59.1 KD protein ZK637.1			
			1..467									in chromosome III []			
22138	ENU05932	ANI61S1712:	22-41	395-420	NAP	g114971	415	173	5.00E-43	53	17	beta-glucosidase precursor			
			1..453									(gentiobiase) (cellobiase) (beta-D-glucoside glucohydrolase)			
22139	ENU05933	ANI61C7085:	26-45	803-829	NAP	g1352079	1500	357	e-126	77	32	[Kluyveromyces marxianus] beta-glucosidase 1 precursor			
			2078..3434									(gentiobiase) (cellobiase) (beta-D-glucoside glucohydrolase) [Aspergillus aculeatus]			
22140	ENU05934	ANI61S2736:			NAP	g786117	236	48	0.0001	19	55	(L41834) nuclear protein [Ensis minor]			
22141	ENU05935	ANI61C3233:3	22-49	803-829	NAP	g2956768	907	242	3.00E-63	47	67	(AL022103) transmembrane transporter			
22142	ENU05936	ANI61S1621:	67-85	320-344	NAP	g3925755	110	62	0.000000	30	21	lizlp. [Schizosaccharomyces pombe] (AL024352) putative phosphodiesterase-nucleotide pyrophosphatase precursor			
			365..1									[Schizosaccharomyces pombe]			
22143	ENU05937	ANI61C978:8	22-48	718-737	NAP	g2132846	275	113	2.00E-24	31	48	probable membrane protein YOL119c - yeast			
			38..1									[Saccharomyces cerevisiae]			
22144	ENU05938	ANI61C1138	26-48	442-461	NAP	g731462	179	94	9.00E-19	40	22	hypothetical 74.0 KD protein in CAI1-HOM3 intergenic region			
			7..1..552									[Saccharomyces cerevisiae]			

Seq num	Seq id	Contig source	5 pos	Primer 3 pos	Primer Basis	Selection	Blast aat	Blast Blast	% id	% cvrg	Description
						Database Hit	ncbi gi	Score	Prob		
22145	ENU05939	ANI61C1146	22-45	714-732	NAP	g3810838	429	88	7.00E-17	37	38
			7.3408..4913								
22146	ENU05940	ANI61C1098	26-45	721-743	NAP	g3451448	195	80	3.00E-14	35	80
			8..1704..2552								
22147	ENU05941	ANI61C1053	22-43	710-734	NAP	g3914984	1047	72	4.00E-12	22	7
			1..3372..1								
22148	ENU05942	ANI61C9561:	32-51	758-785	NAP	g2342601	674	128	6.00E-43	39	5
			288..1649								
22149	ENU05943	ANI61C2459:	22-49	788-812	NAP	g101795	1373	406	e-112	98	51
			3409..4341								
22150	ENU05944	ANI61C1143	24-46	735-756	NAP	g3869276	296	138	4.00E-32	33	97
			6..5110..4334								
22151	ENU05945	ANI61S973:1..511			NAP	g631954	402	145	2.00E-34	53	18
22152	ENU05946	ANI61C8446:	34-53	480-506	NAP	g3850084	308	105	2.00E-29	44	52
			608...1								
22153	ENU05947	ANI61C6254:	58-77	768-787	NAP	g2501339	541	161	2.00E-47	49	37
			1232..2582								
22154	ENU05948	ANI61C3968:	22-42	712-739	NAP	g470731	1194	269	e-126	97	60
			789..1								
22155	ENU05949	ANI61S75..52	215-232	463-482	NAP	g3915105	430	189	9.00E-48	55	31
			7..1								
22156	ENU05950	ANI61C6610:	30-50	577-601	NAP	g2559008	345	131	1.00E-32	57	30
			702..1								
22157	ENU05951	ANI61S3152:	122-146	437-463	NAP	g1546698	456	111	3.00E-24	93	34
			590..107								
22158	ENU05952	ANI61C9158:	22-43	446-464	NAP	g1708464	689	171	2.00E-62	73	31
			1..560								
22159	ENU05953	ANI61C5582:	103-128	683-706	NAP	g1351078	107	76	3.00E-13	25	26
			1..745								
22160	ENU05954	ANI61S2588:	205-232	343-370	NAP	g128192	514	209	8.00E-54	82	15
			580..188								

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	Score	Score Prob	% id	% cvg	Description
22161	ENU05955	ANJ61S4224:	997..549	NAP		g3329623	130	30	8.7	28	44	(AF078790) No definition line found [Caenorhabditis elegans]
22162	ENU05956	ANJ61C6104:	22-49	810-829	NAP	g2499716	755	217	8.00E-56	46	59	"exopolygalacturonase precursor (exoPG) (galacturan 1,4-alpha-galacturonidase) (poly(1,4-alpha-D-galacturonide)galacturonohydrolase) [Aspergillus tubingensis]"
22163	ENU05957	ANJ61C4643:	72-89	777-796	NAP	g1346380	1126	383	e-105	81	30	Kinesin heavy chain []
22164	ENU05958	ANJ61C9251:	23-45	408-434	NAP	g3130014	63	61	0.000000	29	40	(AL023517) putative lipoprotein [Streptomyces coelicolor]
22165	ENU05959	ANJ61C1307:	25-44	808-829	NAP	g114275	698	223	1.00E-57	46	80	L-Asparaginase precursor (L-asparagine amidohydrolase) [Erwinia chrysanthemi]
22166	ENU05960	ANJ61S4270:	610..1	NAP		g3738194	192	59	0.000000	41	26	(AL031854) hypothetical protein [Schizosaccharomyces pombe]
22167	ENU05961	ANJ61C1126	24-43	394-421	NAP	g464369	108	64	5.00E-10	32	18	Phenol 2-monoxygenase (phenol hydroxylase) [Trichosporon cutaneum]
22168	ENU05962	ANJ61C1110	46-65	723-744	NAP	g3650376	720	216	1.00E-55	44	30	(AL031740) dna ligase protein [Schizosaccharomyces pombe]
22169	ENU05963	ANJ61C2411:	22-41	803-829	NAP	g3395556	724	146	1.00E-63	58	70	(AL031180) putative 2-hydroxyacid dehydrogenase [Schizosaccharomyces pombe]
22170	ENU05964	ANJ61C2118:	51-70	763-780	NAP	g2388904	528	173	8.00E-55	51	39	(Z98974) hypothetical protein [Schizosaccharomyces pombe]
22171	ENU05965	ANJ61C3180:	23-42	436-455	NAP	g3036901	89	55	0.000000	28	55	(AJ22715) DapA [Sinorhizobium meliloti]
22172	ENU05966	ANJ61C1061	94-113	732-749	NAP	g461623	522	155	4.00E-37	38	25	beta:galactosidase precursor (lactase) [Aspergillus niger]
22173	ENU05967	ANJ61C5650:	56-78	702-725	NAP	g227874	482	98	1.00E-41	50	28	Extracellular beta glucosidase [Trichoderma reesei]
22174	ENU05968	ANJ61C8513:	65-86	658-677	NAP	g1498245	324	151	6.00E-36	38	29	"(X99960) putative, YGL139w [Saccharomyces cerevisiae]"
22175	ENU05969	ANJ61C3470:	22-49	806-829	NAP	g217326	396	82	3.00E-32	40	42	(D13332) Ca2+-calmodulin-dependent protein kinase II [Drosophila sp.]
22176	ENU05970	ANJ61C4698:	92-119	375-398	NAP	g3913326	173	88	3.00E-17	31	31	Cytochrome P450 52A9 (CYPLIIA9) (alkane-inducible P450-ALK5-A)
			1522..1924									[Candida malosa]

Seq num	Seq id	Contig source	5 pos	3 pos	Primer Basis	Primer Selection	aat	Blast	Blast	%	
					Database	Hit	ncbi gi	Score	Prob	id	cvg
22177	ENU05971	ANI61C7088:	108-127	719-738	NAP	g2407970	666	209	2.00E-53	63	38
			928..1								(Y14750) TOM70 [Podospora anserina]
22178	ENU05972	ANI61C8560:	60-87	519-546	NAP	g640053	144	50	2.00E-12	41	35
			1528..936								(U19714) 3'-phosphoserine aminotransferase [Saccharomyces cerevisiae]
22179	ENU05973	ANI61C8579:	22-47	793-820	NAP	g4586928	449	155	5.00E-37	39	5
			1699..344								(AB017641) polyketide synthase [Micromonospora griseorubida]
22180	ENU05974	ANI61C1021	22-48	710-732	NAP	g3087842	624	152	8.00E-53	48	55
			5:1152..1								(Y08841) core protein II [Neurospora crassa]
22181	ENU05975	ANI61S557:1.			NAP	g2213913	92	53	8.00E-10	21	9
			.750								(AF004884) neuronal calcium channel alpha 1A subunit isoform A-1 [Homo sapiens]
22182	ENU05976	ANI61C9522:	22-43	646-669	NAP	g4104764	293	119	2.00E-26	40	54
			1062..1831								(AF039534) salicylate hydroxylase [Pseudomonas stutzeri]
22183	ENU05977	ANI61S3702:			NAP	g125462	90	38	0.046		
			140..527								"aminoglycoside 3'-phosphotransferase (kanamycin kinase, type I) (neomycin-kanamycin phosphotransferase, type I) (APH(3')I) [Cloning vector pHIND2.2]"
22184	ENU05978	ANI61C7393:	22-41	568-595	NAP	g113701	332	128	5.00E-33	48	36
			715..1								Acetamidase [Emericella nidulans]
22185	ENU05979	ANI61C4935:	40-59	499-521	NAP	g4803681	131	73	2.00E-12		
			591..1								(AL049819) putative AraC-family transcriptional regulator [Streptomyces coelicolor]
22186	ENU05980	ANI61C5316:	47-65	533-552	NAP	g4008543	98	61	0.000000	29	62
			1..593				009				(AL034492) putative deacetylase [Streptomyces coelicolor]
22187	ENU05981	ANI61C1030	22-45	633-660	NAP	g1708808	550	213	2.00E-59	47	79
			1:5850..6911								Lactoylglutathione lyase (methylglyoxalase) (aldoketonutase) (glyoxalase I) (GLX I) (ketone-aldehyde mutase) (S-D-lactoylglutathione methylglyoxal lyase)
22188	ENU05982	ANI61C1103	102-127	453-479	NAP	g3860373	466	171	4.00E-42	57	47
			2:476..1								[Saccharomyces cerevisiae] (A012668) tomatinase [Fusarium oxysporum f. sp. lycopersici]
22189	ENU05983	ANI61C2278:	39-66	721-748	NAP	g2275095	185	109	2.00E-23	26	24
			879..1								(X86179) phosphoprotein [Schizosaccharomyces pombe]
22190	ENU05984	ANI61S2170:	30-49	334-361	NAP	g3183329	297	126	6.00E-29	53	26
			543..159								Hypothetical aminotransferase C6B12.04C [Schizosaccharomyces pombe]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit ncbi gi	Score	Score	Blast Prob	% id	% cvrg	Description
22191	ENU05985	ANI61C2482: 1..703	102-125	653-680	NAP	g3850151	437	115	4.00E-44	58	70	[Candida albicans] (AL033396) rehydrin-like protein
22192	ENU05986	ANI61C1048 7:6940..8616	43-70	807-829	NAP	g1805251	1078	131	4.00E-43	41	50	[U58946] transposase [Aspergillus awamori]
22193	ENU05987	ANI61C1147: 22-45 2911..4181	22-45	705-730	NAP	g1749410	711	183	5.00E-59	59	41	"(D89101) similar to <i>Saccharomyces cerevisiae</i> Asparagine synthetase(glutamine-hydrolyzing)2, SWISS-PROT Accession Number P49060 [Schizosaccharomyces pombe]"
22194	ENU05988	ANI61C2507: 144-171 1229..391	796-818	NAP	g2896707	511	138	4.00E-51	52	90	(AL021897) echa8 [Mycobacterium tuberculosis]	
22195	ENU05989	ANI61S3763: 1..619	33-52	385-410	NAP	g4263063	213	98	7.00E-20	34	28	(AC005142) hypothetical protein [Arabidopsis thaliana]
22196	ENU05990	ANI61S1588: 1..487			NAP	g2500356	357	157	6.00E-38	54	69	60S ribosomal protein L10 (QM protein homolog) (SPQMD)
22197	ENU05991	ANI61C1133 2:493..1	105-125	379-398	NAP	g1749480	179	82	3.00E-15	43	26	[Schizosaccharomyces pombe] ("D89136) similar to <i>Saccharomyces cerevisiae</i> BCS1 protein, SWISS-PROT Accession Number P32839
22198	ENU05992	ANI61C4764: 971..2614	22-46	723-744	NAP	g1711623	1646	372	e-102	67	29	[Schizosaccharomyces pombe] "alanyl-tRNA synthetase, cytoplasmic (alanine—tRNA ligase) (ALARS) [Saccharomyces cerevisiae]" (AL022103) transmembrane transporter lizlp [Schizosaccharomyces pombe] (AL033389) alcohol dehydrogenase [Schizosaccharomyces pombe] hypothetical zinc-type alcohol dehydrogenase-like protein in GDH3-CNE1 intergenic region
22199	ENU05993	ANI61C8670: 1371..215	35-54	793-815	NAP	g2956768	384	80	3.00E-14	27	61	[Gibberella fujikuroi] "pyruvate dehydrogenase E1 component, beta subunit precursor (PDHE1-B) [Schizosaccharomyces pombe]"
22200	ENU05994	ANI61C1074 6:1750..1442	53-78	261-288	NAP	g3850084	134	54	0.000000	36	30	
22201	ENU05995	ANI61C487:6 04..1	114-136	474-493	NAP	g731294	247	79	3.00E-14	37	43	
22202	ENU05996	ANI61C9976: 2078..412	23-50	809-828	NAP	g3549899	332	78	6.00E-14			
22203	ENU05997	ANI61C7223: 6158..5046	23-49	794-813	NAP	g1171890	885	261	3.00E-71			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database	Hit ncbi gi	Score	Score	Blast Prob	% id	% cvrg	Description
22204	ENU05998	ANI61C553:2	27-46	342-361	NAP		g3378446	112	48	0.00005	30	63	(AF079317) 4-hydroxy-2-oxovalerate aldolase [Sphingomonas aromaticivorans]
22205	ENU05999	ANI61S2740: 1..354		NAP		g4218005	122	39	0.014	31	16	(AC006135) putative vicilin storage protein (globulin-like) [Arabidopsis thaliana]	
22206	ENU06000	ANI61C9901: 3907..4488		NAP		g2131340	358	127	8.00E-29	47	61	hypothetical protein YDL119c - yeast [Saccharomyces cerevisiae] probable membrane protein YLR359w - yeast [Saccharomyces cerevisiae]	
22207	ENU06001	ANI61C9014: 105-128	453-474	NAP		g1077357	232	99	4.00E-23	42	31	[Saccharomyces cerevisiae] (AJ242551) 12-oxophytodienoate reductase [Lycopersicon esculentum]	
22208	ENU06002	ANI61C3570: 71-90	331..1656	NAP		g4894182	652	183	2.00E-45			Nitrate reductase [Synecchococcus sp.]	
22209	ENU06003	ANI61C7889: 49-70	1..837	NAP		g730115	395	158	4.00E-38	38	35	Calcium binding mitochondrial carrier superfamily member Aralar [Homo sapiens]	
22210	ENU06004	ANI61C9695: 37-56	892..1	NAP		g4507007	267	128	6.00E-29	31	37	"(L76169) reverse transcriptase, RnaseH [Glomerella cingulata]" Probable serine/threonine-protein kinase YKL116C [Saccharomyces cerevisiae]	
22211	ENU06005	ANI61C1230: 22-45	4470..1314	NAP		g1166378	1020	101	5.00E-21			Extensin precursor (cell wall hydroxyproline-rich glycoprotein) [Nicotiana tabacum]	
22212	ENU06006	ANI61C2256: 22-43	1842..633	NAP		g140965	346	173	1.00E-42	40	48	3-oxoacyl- [Cuphea lanceolata]	
22213	ENU06007	ANI61S1491: 1..981		NAP		g119714	466	36	0.38	41	43	(AF038568) negative regulator Moe1 [Schizosaccharomyces pombe]	
22214	ENU06008	ANI61C4969: 22-41	1048..17	NAP		g4176721	683	196	1.00E-49	52	46	(AF006000) unknown [Bordetella pertussis]	
22215	ENU06009	ANI61C1471: 38-61	1005..1	NAP		g2290999	409	163	2.00E-43	42	85	(U64852) W01A11.2 gene product [Caenorhabditis elegans]	
22216	ENU06010	ANI61C9067: 114..1174	5:1444..2508	NAP		g1465804	295	143	1.00E-33	32	77	fructose-bisphosphate aldolase [Saccharomyces cerevisiae]	
22217	ENU06011	ANI61C1087	25-52	NAP		g113626	612	185	9.00E-56			Allantoin permease (allantoin transport protein) [Saccharomyces cerevisiae]	
22218	ENU06012	ANI61C5251: 672..1	23-45	NAP		g416875	353	116	6.00E-30	35	41		
22219	ENU06013	ANI61C1972: 1260..386		NAP									

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	Score	Score Prob	% id	cvg	Description
22220	ENU06014	ANI61C1013	4:1072..1		NAP	g2500936	447	196	2.00E-49	40	36	High-affinity glucose transporter RGT2 [Saccharomyces cerevisiae]
22221	ENU06015	ANI61C4401:	38-57	672-693	NAP	g549689	352	129	9.00E-32	51	99	Hypothetical 19.7 kD protein in LHS1-NUP100 intergenic region [Saccharomyces cerevisiae]
22222	ENU06016	ANI61C6292:	22-45	745-765	NAP	g3015626	1262	227	e-119	98	68	(AF041976) nitrogen metabolite repression regulator NmrA [Emericella nidulans]
22223	ENU06017	ANI61C2265:	72-91	623-645	NAP	g4758416	489	201	5.00E-51			golgi-specific brefeldin A-resistance factor 1 [Homo sapiens]
22224	ENU06018	ANI61C1241:	42-61	764-783	NAP	g1078633	5787	123	2.00E-69	97	21	myosin I myoA - Emericella nidulans [Emericella nidulans]
22225	ENU06019	ANI61C8228:	23-42	716-734	NAP	g2293233	152	76	3.00E-13	26	49	(AF008220) YfcJ [Bacillus subtilis]
22226	ENU06020	ANI61C9644:	40-59	725-749	NAP	g1546072	1051	144	9.00E-34	38	10	(U68040) polyketide synthase [Cochliobolus heterostrophus]
22227	ENU06021	ANI61C1915:	22-47	642-667	NAP	g462683	320	137	7.00E-32			putative N-acetylglucosamine-6-phosphate deacetylase (GLCNAC 6-P deacetylase) [Caenorhabditis elegans] (Z99111) similar to formylmethionine deformylase [Bacillus subtilis] (AB003111) actin [Humicola grisea var. thermoidea]
22228	ENU06022	ANI61S4147:	62-81	310-329	NAP	g2633827	408	165	1.00E-40	63	65	(AL031535) putative n-terminal acetyltransferase complex su bunit [Schizosaccharomyces pombe] Octapeptide-repeat protein T2 [Mus musculus]
22229	ENU06023	ANI61S2660:	1..360		NAP	g4249564	206	61	0.000000	48	30	(AB003111) actin [Humicola grisea var. thermoidea]
22230	ENU06024	ANI61C8071:	27-46	447-474	NAP	g3560266	248	63	6.00E-20	44	72	(AL031535) putative n-terminal acetyltransferase complex su bunit [Schizosaccharomyces pombe]
22231	ENU06025	ANI61S4267:	399..892		NAP	g730888	138	50	0.00001	31	85	Octapeptide-repeat protein T2 [Mus musculus]
22232	ENU06026	ANI61C1090:	197-223	417-443	NAP	g585965	230	104	5.00E-22	37	19	Vesicular-fusion protein SEC18 [Saccharomyces cerevisiae]
22233	ENU06027	ANI61C4878:	1..464		NAP	g3202046	117	80	2.00E-14	30	9	(AF069525) 190 kDa ankyrin isoform; AnkG190 [Rattus norvegicus] (AT012408) citrate synthase [Anabaena PCC7120]
22234	ENU06028	ANI61C6400:	1..496	433-460	NAP	g3819717	165	52	1.00E-13	31	42	[Anabaena PCC7120]
22235	ENU06029	ANI61C532:6	105..6538		NAP	g3023956	178	80	5.00E-15	34	11	Vegetable incompatibility/protein HET-E-1 [Podospora anserina] (Z68905) ATP-binding cassette multidrug transporter [Emericella nidulans]
22236	ENU06030	ANI61C3032:	84-103	720-738	NAP	g1834342	800	292	2.00E-79	54	19	
			885..1									

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Basis	Selection	Database	Hit	ncbi gi	aat	Blast Score	Blast Prob	% id	% cvrg	Description
22237	ENU06031	ANI61C1134	104-131	483-510	NAP		g1711561	177	67	5.00E-17	47	18	Sugar transporter STL1		[Saccharomyces cerevisiae]
22238	ENU06032	ANI61C4015:	24-51	341-365	NAP		g1255425	86	46	0.0001	21	42	(U53154) No definition line found		[Caenorhabditis elegans]
22239	ENU06033	ANI61C8048:	43-62	804-829	NAP		g3184558	290	82	4.00E-15	31	77	(AF052290) unknown [Synechococcus PCC7002]		
22240	ENU06034	ANI61S3246:	169..616		NAP		g4204304	259	129	2.00E-29	42	24	(AC003027) lcl prt_seq No definition line found [Arabidopsis thaliana]		
22241	ENU06035	ANI61C1043	22-45	774-801	NAP		g1743374	143	69	5.00E-19	28	36	(Y10034) 1-aminocyclopropane-1-carboxylic acid oxidase [Rumex palustris]		
22242	ENU06036	ANI61C1041	22-41	803-827	NAP		g3738182	1083	287	5.00E-77	63	47	"(AL031854) probable t-complex protein 1, theta subunit [Schizosaccharomyces pombe]"		
22243	ENU06037	ANI61S1333:	1..588		NAP		g3153821	140	45	0.0006	22	21	(AF062655) plenty-of-prolines-101; POP101; SH3-philo-protein [Mus musculus]		
22244	ENU06038	ANI61C6363:	24-43	809-828	NAP		g1890776	157	68	9.00E-11			(U88574) syringomycin biosynthesis enzyme [Pseudomonas syringae pv. syringae]		
22245	ENU06039	ANI61C6186:	23-50	802-829	NAP		g418150	726	157	7.00E-38			GABA-specific permease (GABA-specific transport protein)		
22246	ENU06040	ANI61C5013:	193-220	784-808	NAP		g731276	967	314	6.00E-91	71	65	[Saccharomyces cerevisiae] hypothetical 40.7 KD protein in PYKL-SNC1 intergenic region		
22247	ENU06041	ANI61C5574:	53-72	371-394	NAP		g115943	334	103	4.00E-30	41	58	[Saccharomyces cerevisiae] cytochrome C heme lyase (CCHL) (holecytocochrome-C synthase) [Neurospora crassa]		
22248	ENU06042	ANI61C9267:	56-82	455-474	NAP		g1890290	51	42	0.003	25	17	(U89999) Ski2 [Xenopus laevis]		
22249	ENU06043	ANI61S2314:	65-84	392-411	NAP		g3891714	155	84	9.00E-16	32	38	Gal6 (Yeast Bleomycin Hydrolase) Mutant C73a □		
22250	ENU06044	ANI61C7278:	29-48	444-463	NAP		g267125	511	154	1.00E-46	98	99	"Thioredoxin [Aspergillus nidulans, Peptide, 109 aa]", hypothetical calcium-binding protein C18B11.04 in chromosome 1 [Schizosaccharomyces pombe]		
22251	ENU06045	ANI61C382:3	22-41	650-675	NAP		g1171671	688	166	1.00E-71	74	100			

Seq num	Seq id	Contig source	5 pos	3 pos	Primer Basis	Selection	Database	Hit	ncbi gi	aat	Blast Score	Prob	% id	% cvrg	Description
22252	ENU06046	ANI61C9568:	37-56	639-658	NAP		g3999112		1005	242	4.00E-76	48	27		[Kluyveromyces lactis] beta-galactosidase (lactase)
22253	ENU06047	ANI61C1019	1..1387	5..1..1249	NAP		g1166378		376	72	4.00E-12	34	23		"(L76169) reverse transcriptase, RNaseH [Glomerella cingulata]"
22254	ENU06048	ANI61C431:4	203-222	491-510	NAP		g2388991		206	69	2.00E-11	35	64		[Schizosaccharomyces pombe] (Z98980) hypothetical protein
22255	ENU06049	ANI61C4184:	22-45	723-741	NAP		g3850071		405	170	1.00E-41	37	54		[Schizosaccharomyces pombe] (AL033385) cadmium resistance protein [Schizosaccharomyces pombe] putative mitochondrial ATP-dependent protease precursor
22256	ENU06050	ANI61C7503:	37-56	617-634	NAP	1..2346	g1170811		2349	302	2.00E-81	53	25		[Schizosaccharomyces pombe] (AB011836) alkyl hydroperoxide reductase large subunit [Bacillus halodurans]
22257	ENU06051	ANI61C3397:	29-48	780-807	NAP		g4512354		202	71	1.00E-11				[Schizosaccharomyces pombe] (AL031852) putative cleavage and polyadenylation specificity factor
22258	ENU06052	ANI61C3251:	39-58	804-824	NAP	1943..3165	g3738153		237	69	5.00E-23	39	25		[Schizosaccharomyces pombe] (Z97193) hypothetical protein Rv1877
22259	ENU06053	ANI61C9170:	22-47	806-829	NAP	2863..1253	g2225983		414	34	1				[Mycobacterium tuberculosis] (Z98951) hypothetical protein
22260	ENU06054	ANI61C2103:	111-130	456-480	NAP	1..579	g2370466		374	165	2.00E-40	46	3		[Schizosaccharomyces pombe] vacuolar ATP synthase subunit E (V-ATPase E subunit) (V-ATPase 26 KD subunit) [Neurospora crassa]
22261	ENU06055	ANI61C5199:	102-129	418-437	NAP	1587..1130	g2493134		299	50	4.00E-13	48	58		ST14-associating protein SAP190 [Saccharomyces cerevisiae]
22262	ENU06056	ANI61C3111:	102-123	660-686	NAP	1..720	g1710848		428	138	3.00E-45	45	21		(AL035064) hypothetical protein
22263	ENU06057	ANI61C466:9	22-49	797-816	NAP	50..3127	g4106672		57	37	0.16				[Schizosaccharomyces pombe] (AL031534) ribosomal processing, rna binding, nucleolar protein
22264	ENU06058	ANI61C5033:	22-46	724-749	NAP	1..1089	g3560147		522	117	1.00E-40	35	41		[Schizosaccharomyces pombe] (U58946) transposase [Aspergillus awamori]
22265	ENU06059	ANI61S4450:	26-51	338-359	NAP	1..472	g1805251		275	79	2.00E-14	39	28		(AB015509) beta-mannosidase [Aspergillus aculeatus]
22266	ENU06060	ANI61C3498:	98-119	591-613	NAP	714..1	g3242651		554	187	2.00E-58	59	20		(Z96072) hypothetical protein Rv2715 [Mycobacterium tuberculosis]
22267	ENU06061	ANI61C7525:	36-63	542-569	NAP	1536..2125	g2182006		76	56	0.000000	32	49		60S ribosomal protein YL6 (L5) (RP8) [Saccharomyces cerevisiae]
22268	ENU06062	ANI61C6205:	66-85	794-813	NAP	2201..1216	g730569		888	238	4.00E-91	73	92		

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit ncbi gi	aat Score	Blast Prob Score	% id	% cvrg	Description	
22269	ENU06063	ANI61C9151:	22-48	703-727	NAP	g2497499	482	125	8.00E-54	52	Guanylate kinase (GMP kinase) [Mus musculus]	
22270	ENU06064	ANI61C1564:	50-69	711-730	NAP	g1730729	441	79	4.00E-27	30	39	hypothetical 74.8 KD protein in ALG11-YIP3 intergenic region [Saccharomyces cerevisiae]
22271	ENU06065	ANI61C7241:	27-46	722-748	NAP	g3006142	339	116	2.00E-25	36	43	(AL022299) hypothetical protein [Schizosaccharomyces pombe]
22272	ENU06066	ANI61C498:7	207-226	360-379	NAP	g1526987	117	66	3.00E-13	36	52	(U13050) pectate lyase D [Fusarium solani f. sp. pisiformis]
22273	ENU06067	ANI61C4158:	22-49	799-818	NAP	g1764018	622	108	2.00E-43	44	66	(Z83760) COS41.18 [Ciona intestinalis]
22274	ENU06068	ANI61C7648:	22-48	373-398	NAP	g4886445	209	34	0.59			(AL050269) hypothetical protein [Homo sapiens]
22275	ENU06069	ANI61C3744:	56-78	803-829	NAP	g118498	1074	252	3.00E-66	45	55	aldehyde dehydrogenase (ALDDH) [Emericella nidulans]
22276	ENU06070	ANI61C4669:	111-130	736-758	NAP	g3114719	1141	336	1.00E-91	64	18	(Z68906) ATP-binding multidrug cassette transporter [Botryotinia fuckeliana]
22277	ENU06071	ANI61C867:1	40-60	808-829	NAP	g1438951	581	115	4.00E-25	46	51	(U61842) cutinase negative acting protein [Fusarium solani f. sp. pisiformis] (Z82080) cDNA EST EMBL:D66071
22278	ENU06072	ANI61C1057	22-44	805-829	NAP	g3880602	127	74	1.00E-12			comes from this gene; cDNA EST yK274a10.3 comes from this gene; cDNA EST yK274a10.3 comes from this gene; cDNA EST yK289f12.3 comes from this gene; cDNA EST yK289f12.5 comes from this gene; cDNA EST yK274a10.5 comes from this gene; cDNA EST... [Escherichia coli]
22279	ENU06073	ANI61C1041	22-39	413-432	NAP	g140338	258	106	2.00E-22			hypothetical 23.1 KD protein in DSMC-PFLA intergenic region [Escherichia coli]
22280	ENU06074	ANI61C2627:	31-50	724-743	NAP	g2995341	190	66	4.00E-10	25	46	(AL022244) hypothetical protein [Schizosaccharomyces pombe]
22281	ENU06075	ANI61C1049	1104..1		NAP	g1705915	2051	309	2.00E-83	51	16	Clathrin heavy chain [Bos taurus]
22282	ENU06076	ANI61C1002:	23-42	604-631	NAP	g3130036	389	125	4.00E-28	50	49	(AL023534) putative methionine aminopeptidase 1 [Schizosaccharomyces pombe]
		732..1										

Seq num	Seq id	Contig source	5 pos	Primer 3 pos	Primer Basis	Selection Database	Hit ncbi gi	Score	Score Prob	% id	% cvrg	Description
22283	ENU06077	ANI61C3365:	23-49	721-740	NAP	g2290770	668	78	5.00E-37	45	21	(AF002163) delta-adaptin [Homo sapiens]
22284	ENU06078	ANI61C3696:	113-132	561-581	NAP	g3874563	276	115	1.00E-32			
			1..671									
22285	ENU06079	ANI61C6044:	203-222	701-720	NAP	g4165293	583	245	2.00E-64	59	22	(Z81042) similar to Yeast hypothetical protein YEV6 like; cDNA EST yk206h5.3 comes from this gene; cDNA EST yk303h1.3 comes from this gene; cDNA EST yk303h1.5 comes from this gene; cDNA ... [X58824] cdc21 protein
22286	ENU06080	ANI61C3840:	102-119	599-618	NAP	g2500535	206	97	1.00E-19	37	20	[Schizosaccharomyces pombe] putative ATP-dependent RNA helicase YDL031W [Saccharomyces cerevisiae]
22287	ENU06081	ANI61C1933:	64-84	472-499	NAP	g3850093	135	76	1.00E-13	28	33	(AL033389) putative allantotripeptidase [Schizosaccharomyces pombe]
22288	ENU06082	ANI61C6667:	1271..434		NAP	g3136096	1016	406	e-112	83	69	(AF032988) spindle assembly checkpoint protein SLDB [Emericella nidulans]
22289	ENU06083	ANI61C130:1 ..788	197-215	624-648	NAP	g4206286	702	239	2.00E-62	63	24	(AF043332) plasma membrane H(+)-ATPase [Emericella nidulans] ("UT5347) fatty acid synthase, alpha subunit [Emericella nidulans]" (AL04583) related to yeast zds family proteins [Schizosaccharomyces pombe]
22290	ENU06084	ANI61C1055 5:1..5216	22-46	773-792	NAP	g1805261	8541	284	e-121	95	14	(AL04583) ABC transporter [Schizosaccharomyces pombe]
22291	ENU06085	ANI61C3890: 1104..1	32-52	623-646	NAP	g4056558	104	85	8.00E-16	30	28	(AL023780) PyrABCN [Emericella nidulans]
22292	ENU06086	ANI61C6567: 691..1	51-78	603-630	NAP	g3184109	673	259	2.00E-71	81	28	(AF112473) ABC transporter [Schizosaccharomyces pombe]
22293	ENU06087	ANI61C6142: 1290..1	35-54	790-809	NAP	g4185560	2042	460	e-147	99	12	(AF112473) PyrABCN [Emericella nidulans]
22294	ENU06088	ANI61C4368: 2711..1864	119-138	802-827	NAP	g1723766	415	158	5.00E-38	40	57	ubiquinone biosynthesis monooxygenase COQ6 [Saccharomyces cerevisiae]
22295	ENU06089	ANI61C1060 2:1542..1	22-46	718-738	NAP	g3929290	727	190	1.00E-69	54	51	(AF094507) B-type cyclin [Candida albicans]
22296	ENU06090	ANI61C8408: 3444..1	57-76	711-730	NAP	g1597721	1958	110	1.00E-23	36	18	(X99021) putative helicase [Schizosaccharomyces pombe]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database	Hit ncbi	gi	aat Score	Blast Score	Prob	% id	% cvrg	Description
22297	ENU06091	ANI61C1987:	30-57	477-504	NAP	g1813523	124	45	0.0005	28	28	(U67763) PbTRAP [Plasmodium berghei]		
22298	ENU06092	ANI61C9063:	22-42	800-827	NAP	g2266911	600	156	3.00E-46	39	78	(AE001274) L4171.5 [Leishmania major]		
22299	ENU06093	ANI61C9187:	29-50	522-544	NAP	g1346405	303	88	4.00E-30	39	28	Laccase precursor (benzenediol:oxygen oxidoreductase) (urishiol oxidase)		
22300	ENU06094	ANI61C1765:	22-45	779-801	NAP	g543923	692	203	9.00E-61			[Schizosaccharomyces pombe] (Z98529) putative cytoskeleton assembly control protein		
22301	ENU06095	ANI61C6158:	22-42	803-826	NAP	g2330690	184	69	3.00E-11	31	18	[Schizosaccharomyces pombe] (M59288) ferrocelatase [Mus musculus]		
22302	ENU06096	ANI61C8249:	22-49	621-646	NAP	g193271	752	213	2.00E-65	61	62	C-24(28) sterol reductase		
22303	ENU06097	ANI61C9171:	58-76	797-816	NAP	g1706692	1173	189	3.00E-58	50	50	[Saccharomyces cerevisiae] vacuolar ATP synthase 98 KD subunit (vacuolar ATPase 98 KD subunit)		
22304	ENU06098	ANI61C8836:	24-45	784-803	NAP	g3929395	1129	195	1.00E-85	61	31	[Neurospora crassa]		
22305	ENU06099	ANI61C3681:			NAP	g2492863	2264	409	e-124	98	58	Ornithine aminotransferase (ornithine-oxo-acid aminotransferase)		
			285..1751									[Emericella nidulans]		
22306	ENU06100	ANI61C9107:	39-58	777-796	NAP	g1027486	805	73	3.00E-25	36	43	(D49538) dihydrogeodin oxidase		
22307	ENU06101	ANI61C5317:	114-133	281-300	NAP	g3660_5661						[Aspergillus terreus]		
22308	ENU06102	ANI61C7469:	115-142	725-744	NAP	1..395						carboxypeptidase S1 [Penicillium janthinellum]		
22309	ENU06103	ANI61C8631:	22-49	799-826	NAP	1114..1						carboxypeptidase S1 [Penicillium janthinellum]		
22310	ENU06104	ANI61C8596:	22-41	773-793	NAP	4266..2596						(AL035592) hypothetical protein		
			2017..1									[Schizosaccharomyces pombe]		
												putative glycine dehydrogenase (decarboxylating) precursor (glycine decarboxylase) (glycine cleavage system P-protein)		
22311	ENU06105	ANI61C2944:	212-231	500-524	NAP	1..545						[Schizosaccharomyces pombe]		
												Rhamnogalacturonan lyase (RGASE B) (RHG B) [Aspergillus aculeatus]		

Seq num	Seq id	Contig source	5 pos	3 pos	Basis	Database	Hit	ncbi gi	Score	Score	Blast Prob	% id	% cvrg	Description
22312	ENU06106	ANi61C6952:	99-118	652-673	NAP		g3549877	116	67	1.00E-10	32	37	(Y15902) repression-(nmr)-responsible protein	
22313	ENU06107	ANi61C8294:	22-46	611-630	NAP		g131618	1083	259	1.00E-86			[Gibberella fujikuroi]	
			1154...1										phosphoribosylamine-glycine ligase (GARS) (glycinamide RIBONucleotide synthetase)	
													(phosphoribosyl)glycinate synthetase) / phosphoribosylformylglycynamidine cyclo-ligase (AIRS) (phosphoribosylaminoimidazole synthetase) ...	
22314	ENU06108	ANi61C83529:	26-45	517-536	NAP		g30293956	369	166	8.00E-41	45	13	[Schizosaccharomyces pombe] Vegetable incompatibility protein HET-E-1 [Podospora anserina]	
22315	ENU06109	ANi61C3904:	35-54	714-735	NAP		g1352399	370	146	2.00E-34			"glucan 1,3-beta-glucosidase precursor (exo-beta 1,3 glucanase) (1,3-beta-D-glucanohydrolase) [Cochliobolus carbonum]" (Z99759) rna binding protein	
			2002...1										[Schizosaccharomyces pombe] (Z68905) ATP-binding cassette multidrug transporter [Emericella nidulans]	
22316	ENU06110	ANi61C60:18	40-59	586-605	NAP		g2467274	466	127	6.00E-36	66	100	(AL03548) meu14, ring zinc finger [Schizosaccharomyces pombe] (D88302) ydhJ [Bacillus subtilis]	
22317	ENU06111	ANi61C1057	24-45	774-797	NAP	1:1..3158	g1834342	1828	232	3.00E-60	70	15	nidulans]	
22318	ENU06112	ANi61C43884:	64-91	451-478	NAP	481..1	g4456818	183	112	1.00E-24	27	47	(tyrosyl-tRNA synthetase, cytoplasmic (tyrosyl-tRNA ligase) (TYRRS) [Saccharomyces cerevisiae]" hypothetical 41.8 KD protein (ORFm)	
22319	ENU06113	ANi61C4660:	52-78	444-464	NAP	506..1	g1945094	317	126	1.00E-28	42	51	[Saccharomyces cerevisiae]" hypothetical 103.6 KD protein in COX5B-PFK26 intergenic region [Saccharomyces cerevisiae] (AF098669) pantothenate kinase [Emericella nidulans]	
22320	ENU06114	ANi61C344:1	22-49	786-805	NAP	726..475	g549037	845	103	4.00E-42	44	63	(Z99759) hypothetical protein [Schizosaccharomyces pombe]	
22321	ENU06115	ANi61C7626:	22-48	595-617	NAP	1362..2185	g2828499	226	117	8.00E-26	28	64	[1]	
22322	ENU06116	ANi61C2105:	22-41	656-675	NAP	257..1047	g731857	267	118	4.00E-26	37	26	hypothetical 103.6 KD protein in COX5B-PFK26 intergenic region [Saccharomyces cerevisiae] (AF098669) pantothenate kinase [Emericella nidulans]	
22323	ENU06117	ANi61C346:4	106-123	623-642	NAP	053..3380	g4191500	1045	199	2.00E-50	97	49	(Z99759) hypothetical protein [Schizosaccharomyces pombe]	
22324	ENU06118	ANi61S4392:			NAP	1..741	g2467272	701	275	3.00E-73	61	31		

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database	Hit ncbi gi	Score	Score Prob	% id	% cvrg	Description	
22325	ENU06119	ANi61C1002	102-121	499-526	NAP	g585377	550	220	2.00E-57	51	39	[Saccharomyces cerevisiae] probable mannosyltransferase KTR4	
22326	ENU06120	ANi61C9979:	82-101	394-418	NAP	g280164	63	62	0.000000	22	43	probable dehydrogenase (EC 1.-.-.) - <i>Vibrio cholerae</i> [Vibrio cholerae]	
22327	ENU06121	ANi61C1079	22-46	766-789	NAP	g135100	1254	276	8.00E-84			"aspartyl-TRNA synthetase, cytoplasmic (aspartate--TRNA ligase) (ASPRS) [Saccharomyces cerevisiae]"	
22328	ENU06122	ANi61C9357:	30-57	810-829	NAP	g1176581	1120	300	7.00E-81	53	31	hypothetical 101.7 KD protein in EGT2-KRE1 intergenic region	
			6603..5322										
22329	ENU06123	ANi61S3452:	59-86	462-489	NAP	g807674	327	99	4.00E-24	45	21	[Saccharomyces cerevisiae] (M23385) pol protein [Simian sarcoma virus]	
22330	ENU06124	ANi61C1040	115-134	777-796	NAP	g3183028	370	159	2.00E-38	35	77	probable histidinol-phosphatase [Schizosaccharomyces pombe] (AF022789) ubiquitin hydrolyzing enzyme I [Homo sapiens]	
22331	ENU06125	ANi61C5831:	57-84	262-289	NAP	g3220154	235	107	3.00E-23	47	28		
22332	ENU06126	ANi61C6438:	102-129	620-642	NAP	g1709240	518	175	4.00E-43	48	31	cell division control protein NDA4 []	
22333	ENU06127	ANi61C8710:	57-77	802-829	NAP	g2132227	364	96	2.00E-31	42	76	hypothetical protein YPL196w - yeast ( <i>Saccharomyces cerevisiae</i> )	
			389..1493										
22334	ENU06128	ANi61C3623:	211-238	448-467	NAP	g1169590	164	89	3.00E-17	37	43	[ <i>Saccharomyces cerevisiae</i> ] Malonyl COA-acyl carrier protein transacylase (MCT) [Haemophilus influenzae Rd]	
22335	ENU06129	ANi61C4966:	22-49	657-684	NAP	g83673	503	78	1.00E-34	37	45	amidase (EC 3.5.1.4) - <i>Aspergillus</i> oryzae [Aspergillus oryzae] (Z97204) hypothetical protein	
22336	ENU06130	ANi61C6896:	43-62	652-671	NAP	g2226418	178	75	5.00E-13	34	53	[ <i>Schizosaccharomyces pombe</i> (AL035637) glycoprotein endopeptidase-like protein.	
22337	ENU06131	ANi61C3102:	115-137	514-533	NAP	g4481949	581	226	1.00E-58	67	51	[ <i>Schizosaccharomyces pombe</i> hypothetical 58.0 KD peptidase in PTP3-II V1 intergenic region	
22338	ENU06132	ANi61C7249:	22-42	810-829	NAP	g731481	500	114	1.00E-24	44	42	[ <i>Saccharomyces cerevisiae</i> ] [Homo sapiens]	
22339	ENU06133	ANi61C651:1	23-43	730-755	NAP	g4507711	119	49	0.00003	36	62	(AL031825) rna binding protein - putative pre mRNA splicing factor [ <i>Schizosaccharomyces pombe</i> ]	
22340	ENU06134	ANi61C9781:	825..1050	95-116	403-422	NAP	g3702642	285	97	8.00E-20	52	36	
			1060..606										

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Primer Basis	Selection	Blast aat	Blast Blast	%	
						Database Hit	ncbi gi	Score Score	Prob % id	cvg Description
22341	ENU06135	ANI61C1861:	22-43	802-829	NAP	g1762781	1324	129	3.00E-29	44 (U65685) phosphoinositide-specific phospholipase C [Botryotinia fuckeliana]
22342	ENU06136	ANI61S2460:	1..574		NAP	g913016	107	79	2.00E-14	27 12 (S76267) Snp2 homolog=bfr1 [Schizosaccharomyces pombe] bicolor]
22343	ENU06137	ANI61C6319:	34-53	806-825	NAP	g4539662	252	74	8.00E-22	31 27 (AF061282) polyprotein [Sorghum bicolor]
22344	ENU06138	ANI61C9871:	22-41	790-810	NAP	g141051	419	81	6.00E-32	43 53 hypothetical protein in MMSB 3'region (ORF1) [Pseudomonas aeruginosa] (U09782) myosin heavy chain [Argopecten irradians]
22345	ENU06139	ANI61C591:7	27..1	644-662	NAP	g497653	70	38	0.058	19 11 (U38416) ferulate-5-hydroxylase [Arabidopsis thaliana] (M94131) mucin [Homo sapiens]
22346	ENU06140	ANI61C4843:	625..11	514-538	NAP	g1488255	96	75	3.00E-13	26 32 (M94131)
22347	ENU06141	ANI61S2985:	1..591		NAP	g186396	135	38	0.058	33 15 (Homo sapiens)
22348	ENU06142	ANI61C8111:	42-61	631-648	NAP	g2494820	1626	125	1.00E-55	85 36 Rhamnogalacturonase B precursor (rhhamnogalacturonan lyase) (RGASE B) (RHGB) [Aspergillus aculeatus]
22349	ENU06143	ANI61C1024	24-51	806-829	NAP	g1723685	925	180	4.00E-62	56 78 hypothetical 38.3 KD protein in RPL16B-PDC6 intergenic region [Saccharomyces cerevisiae]
22350	ENU06144	ANI61S3184:	1..431		NAP	g539218	149	41	0.003	25 26 hypothetical protein YKL201c - yeast (Saccharomyces cerevisiae) []
22351	ENU06145	ANI61C2805:	68-87	465-484	NAP	g2131533	167	83	5.00E-16	32 29 hypothetical protein YDR501w - yeast (Saccharomyces cerevisiae) [Saccharomyces cerevisiae]
22352	ENU06146	ANI61C8818:	69-88	440-459	NAP	g2492821	330	143	6.00E-34	48 100 Augmenter of liver regeneration (HERV1 protein) [Homo sapiens] putative tartrate transporter [Agrobacterium vitis]
22353	ENU06147	ANI61C2583:	118-137	645-663	NAP	g4033486	270	122	2.00E-27	30 58 [Trichoderma harzianum] (AF023156) carnitine acetyltransferase FacC [Emericella nidulans]
22354	ENU06148	ANI61C1112	8..173	69-88	NAP	g2492491	971	167	5.00E-84	86 87 DNA-directed RNA polymerase III 25 KD polypeptide (C25) [Saccharomyces cerevisiae]
22355	ENU06149	ANI61C4678:	78..716	67-86	NAP	g2511761	938	215	4.00E-97	97 23
22356	ENU06150	ANI61C3182:	27-54	805-829	NAP	g549722	199	51	1.00E-20	
			1847..2710							

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit ncbi gi	Score	Score Prob	% id	% cvrg	Description
22357	ENU06151	ANI61C7398:	78-97	445-464	NAP	g3417421	266	126	8.00E-29	52	40 (AL031261) forkhead nuclear signalling domain protein
22358	ENU06152	ANI61C476:4	92-119	330-354	NAP	g4377374	113	.43	0.000000	26	35 (AE001684) Adenosylmethionine-8-Amino-7-Oxononanoate Aminotransferase [Chlamydia pneumoniae]
			55..1						0.09		
22359	ENU06153	ANI61C4149:	25-44	581-601	NAP	g2497670	43	.49	0.00003	39	15 Homeobox protein LIM-1 [Danio rerio]
22360	ENU06154	ANI61C9601:	30-54	620-644	NAP	g2494036	218	60	7.00E-13		D-amino acid oxidase (DAMOX) (DAO) (DAO) [Trigonopsis variabilis]
22361	ENU06155	ANI61C8113:	25-47	657-684	NAP	g729467	564	206	1.00E-52	42	48 purine-cytosine permease (PCP) (cytosine/purine transport protein)
22362	ENU06156	ANI61C4412:	59-86	807-829	NAP	g529564	532	115	4.00E-32	36	65 [Saccharomyces cerevisiae] "L35343) 2,3-butenediol dehydrogenase [Pseudomonas putida]"
22363	ENU06157	ANI61C3596:	102-124	490-515	NAP	g1703372	126	83	1.00E-15	27	35 Probable sterol O-acyltransferase (sterol-ester synthase)
22364	ENU06158	ANI61C1165:	22-49	786-811	NAP	g1346405	736	181	5.00E-45	34	46 [Schizosaccharomyces pombe] Laccase precursor (benzenediol:oxygen oxidoreductase) (urishiol oxidase)
22365	ENU06159	ANI61C508:2	22-47	806-829	NAP	g2497175	396	92	4.00E-32	39	92 (laccase I) [Emericella nidulans] hypothetical 31.1 KD protein in SIP18-SPT21 intergenic region
22366	ENU06160	ANI61C6718:	110-129	477-496	NAP	g1020413	84	.55	0.000000	30	22 [Saccharomyces cerevisiae] (D63703) isobutene-forming enzyme and benzoate 4-hydroxylase
			1..527						002		
22367	ENU06161	ANI61C1080	24-43	684-703	NAP	g1723910	818	321	4.00E-87	66	33 [Rhodotorula minuta] Pre-mRNA splicing factor RNA helicase PRP43 (helicase JAI)
22368	ENU06162	ANI61C9004:	95-114	423-442	NAP	g1834322	347	92	1.00E-29	45	52 [Saccharomyces cerevisiae] (D50661) RNA polymerase II subunit 3
22369	ENU06163	ANI61C4804:	22-49	725-749	NAP	g4102636	2457	555	e-159	99	43 [Schizosaccharomyces pombe] (AF04812) G/S regulator
22370	ENU06164	ANI61C9461:	38-57	576-603	NAP	g586919	198	80	1.00E-14	37	71 [Emericella nidulans] YSA1 protein [Saccharomyces cerevisiae]
			1625..2292								

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22371	ENU06165	ANI61C5506:	27-46	791-816	NAP	g1723769	261	134	6.00E-31	28	51	putative transporter YGR260W	
22372	ENU06166	ANI61C8552:	23-46	803-829	NAP	g2132019	392	70	2.00E-11			[Saccharomyces cerevisiae] hypothetical protein YOL141w - yeast (Saccharomyces cerevisiae)	
22373	ENU06167	ANI61C5975:	67-90	554-572	NAP	g3649751	421	174	5.00E-43	44	54	[Saccharomyces cerevisiae] (Z15137) esterase A [Streptomyces chrysomallus]	
22374	ENU06168	ANI61C103:1	70-89	562-582	NAP	g2414601	250	63	3.00E-21	51	20	[Schizosaccharomyces pombe] (Z99295) phosphatidyl synthase [Schizosaccharomyces pombe] Dolichyl-diphosphooligosaccharide--protein glycosyltransferase beta subunit precursor (oligosaccharyl transferase beta subunit) [Saccharomyces cerevisiae]	
22375	ENU06169	ANI61C5302:	46-66	802-829	NAP	g465480	283	145	3.00E-34				
22376	ENU06170	ANI61C1132:	25-44	776-796	NAP	g3136056	1918	85	8.00E-16	32	22	(AL023592) RanBP7/importin-beta/Cse1p superfamily protein [Schizosaccharomyces pombe] (AJ238009) serine threonine protein kinase [Sclerotinia sclerotiorum] hypothetical 47.3 KD protein C17G8.13C in chromosome I [Schizosaccharomyces pombe] (AL031543) putative amino-acid permease [Schizosaccharomyces pombe] (Y13967) alpha-aminoacid reductase large subunit [Penicillium chrysogenum]	
22377	ENU06171	ANI61C3382:	22-44	711-733	NAP	g4584836	913	273	3.00E-99	67	37	(Z229988) Mnt1 protein [Saccharomyces cerevisiae] (Z99258) molybdopterin biosynthesis [Schizosaccharomyces pombe] hypothetical 16.7 KD protein C1F12.10C in chromosome I	
22378	ENU06172	ANI61C2441:	39-58	595-614	NAP	g1723485	403	182	2.00E-45	44	54		
22379	ENU06173	ANI61C9052:	122-142	344-363	NAP	g3581896	89	40	0.000007	34	18		
22380	ENU06174	ANI61C3578:	109-128	300-319	NAP	g3282044	367	159	6.00E-39	66	8		
22381	ENU06175	ANI61C9636:	103-121	521-540	NAP	g454894	354	148	1.00E-43	45	47		
22382	ENU06176	ANI61C1147	7,922..2,445	4730..4145	NAP	g2414593	781	186	2.00E-46	42	52	[Saccharomyces cerevisiae] (Z99258) molybdopterin biosynthesis [Schizosaccharomyces pombe] hypothetical 16.7 KD protein C1F12.10C in chromosome I	
22383	ENU06177	ANI61C1183:	36-55	449-476	NAP	g1723514	180	83	9.00E-16	31	100	[Schizosaccharomyces pombe] probable protein-tyrosine phosphatase CDC14 [Saccharomyces cerevisiae] "myosin heavy chain-B, neuronal - chicken [Gallus gallus]"	
22384	ENU06178	ANI61C7662:	22-44	628-649	NAP	g1168807	485	207	5.00E-53	55	32		
22385	ENU06179	ANI61C6688:	33-60	500-525	NAP	g476389	55	42	0.003	19	9		
			328..873										

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	Score	Score	Blast Prob	% id	% cvrg	Description
22386	ENU06180	ANi61C8735:	24-50	513-532	NAP	g2224699	197	102	2.00E-21	33	23	(AB002377) KIAA0379 [Homo sapiens]	
22387	ENU06181	ANi61C9465:	47-66	776-795	NAP	g3785995	2130	204	6.00E-52	53	18	(AC005499) unknown protein [Arabidopsis thaliana]	
22388	ENU06182	ANi61C6501:	93-115	606-625	NAP	g3915154	142	63	1.00E-10	32	42	P450_58) [Fusarium sporotrichioides] trichodiene oxygenase (cytochrome delta(24)-sterol C-methyltransferase	
22389	ENU06183	ANi61C8122:	1..553	745..1	NAP	g462024	312	91	4.00E-27	42	47	[Saccharomyces cerevisiae] [Thermotoga neapolitana] (AF038586) pyruvate dehydrogenase kinase isoform 2; PDK2 [Zea mays] (AJ007446) hypothetical protein	
22390	ENU06184	ANi61C6703:	206-229	539-561	NAP	g3695005	350	159	2.00E-38	54	47	(AF048977) Ser/Arg-related nuclear matrix protein [Homo sapiens] (Y12314) GTPase	
22391	ENU06185	ANi61C4945:	50-73	396-420	NAP	g3282095	199	93	1.00E-18	37	48	[Schizosaccharomyces pombe] (U16782) chlorophenol monooxygenase [Rastonia eutropha] (AF062655) plenty-of-prolines-101; POP101; SH3-philo-protein [Mus musculus]	
22392	ENU06186	ANi61S920:1.	.784	544..1	NAP	g3005587	180	58	0.000000	21	31	(Z95334) 17i23.15 protein. [Schizosaccharomyces pombe] (Z82098) hypothetical protein Rv3536c shk1 gene [Schizosaccharomyces pombe]	
22393	ENU06187	ANi61C8511:	64-83	409-429	NAP	g1935000	587	190	5.00E-60	80	75	[Mycobacterium tuberculosis] (U16782) chlorophenol monooxygenase [Rastonia eutropha] (AF035075) conserved hypothetical protein [Schizosaccharomyces pombe] (Z68904) ATP-binding cassette multidrug transporter [Emericella nidulans]	
22394	ENU06188	ANi61C7695:	74-93	727-749	NAP	g2094861	234	118	5.00E-26	25	13	D-lactate dehydrogenase (D-LDH) [Escherichia coli]	
22395	ENU06189	ANi61C7316:	22-47	732-759	NAP	g1666124	417	170	1.00E-41	32	100	phenol 2-monooxygenase (EC 1.14.13.7) - jelly fungus (Trichosporon beigei) []	
22396	ENU06190	ANi61C2480:	46-65	781-800	NAP	g1098357	1116	161	4.00E-75	66	43		
22397	ENU06191	ANi61C1054	36-54	804-829	NAP	g1764155	1012	236	1.00E-61	46	46		
22398	ENU06192	ANi61S1352:	0:1370..3393	1..677	NAP	g3153821	118	47	0.0001	24	21		
22399	ENU06193	ANi61C5463:	102-126	539-560	NAP	g4107315	225	116	1.00E-25	42	20		
22400	ENU06194	ANi61C1114	1..622	2:1..1798	NAP	g1834340	1288	93	2.00E-42	59	15		
22401	ENU06195	ANi61C5207:	37-56	799-818	NAP	g1730102	781	294	6.00E-79	53	84		
22402	ENU06196	ANi61C7617:	23-44	714-735	NAP	g423973	536	227	7.00E-59	52	36		
			834..1										

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	Score	Score	Blast Prob	% id	% cvrg	Description	
22403	ENU06197	ANI61C3223:	102-125	514-536	NAP	g2554598	85	62	0.000000	29	31	(AB00508)	poly(3-hydroxybutyrate) depolymerase precursor [Comamonas testosteroni]	
22404	ENU06198	ANI61C6564:	1..1142		NAP	g1351598	408	157	1.00E-37	40	44	[Schizosaccharomyces pombe] C4G8.07C in chromosome I	hypothetical 59.6 KD protein	
22405	ENU06199	ANI61S826:1.	.766		NAP	g134769	518	173	1.00E-46	50	59	[Bacillus subtilis] (U91968) topoisomerase I [Emerichella nidulans]	Stage IV sporulation protein B	
22406	ENU06200	ANI61C7078:	1..466		NAP	g2245428	598	173	5.00E-43	94	15	(AL034463) putative nuclear envelope pore membrane protein		
22407	ENU06201	ANI61C8669:	3636..4884		NAP	g4007795	354	90	3.00E-23			[Schizosaccharomyces pombe] cytochrome C heme lyase (CCHL) (holocytochrome-C synthase)		
22408	ENU06202	ANI61C2274:	100-127	300-327	NAP	g115943	281	128	2.00E-29	51	32	[Neurospora crassa]		
22409	ENU06203	ANI61S42:41	3..1	48-69	277-303	NAP	g466053	164	95	3.00E-19	38	23	[Caenorhabditis elegans]	hypothetical 68.7 KD protein ZK757.1 in chromosome III
22410	ENU06204	ANI61C1077	4:1..1700	49-76	807-826	NAP	g1352619	879	146	5.00E-50	73	40	Dihydrolipoamide succinyltransferase component of 2-oxoglutarate dehydrogenase complex precursor (E2)	
22411	ENU06205	ANI61C3628:	72-91	661-680	NAP	g231717	1359	259	1.00E-86	75	36	[Saccharomyces cerevisiae]	Minichromosome maintenance protein 5 (cell division control protein 46)	
22412	ENU06206	ANI61C2430:	1..480	102-127	430-457	NAP	g3261632	375	152	1.00E-36	45	30	[Saccharomyces cerevisiae] (Z79700) accD2 [Mycobacterium tuberculosis]	
22413	ENU06207	ANI61C5576:	1..1921	49-73	809-829	NAP	g3560142	633	109	2.00E-35	34	45	(AL031534) Major facilitator superfamily protein	
22414	ENU06208	ANI61C8479:	1457..1940		NAP	g347455	187	45	0.0003	39	93	[Schizosaccharomyces pombe] (L22030) hydroxyproline-rich glycoprotein [Glycine max]		
22415	ENU06209	ANI61C7459:	585..1	22-42	528-547	NAP	g4033735	286	156	1.00E-37	50	13	(AF054284) spliceosomal protein SAP155 [Homo sapiens]	
22416	ENU06210	ANI61C1134	1:3734..1823	46-73	807-829	NAP	g1175452	332	107	1.00E-22	30	25	hypothetical 85.7 KD protein C13G6.03 in chromosome I	
												[Schizosaccharomyces pombe]		

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	Score	Score Prob	% id	% cvrg	Description
22417	ENU06211	ANI61S1223:	1..340	NAP		g854065	401	49	0.00001	50	26	(X83413) U88 [Human herpesvirus 6]
22418	ENU06212	ANI61S3220:	157-177	311-331	NAP	g1352438	195	91	5.00E-18	36	38	eukaryotic initiation factor 4A-like protein C1F5.10
22419	ENU06213	ANI61C9889:	102-124	366-385	NAP	g112947	150	84	4.00E-16	38	28	[Schizosaccharomyces pombe] AAC-rich mRNA clone AAC3 protein [Dictyostelium discoideum] H beta 58 homolog [Homo sapiens]
22420	ENU06214	ANI61C8653:	1..409	NAP		g4758510	735	195	4.00E-49			
22421	ENU06215	ANI61C1095	22-48	509-536	NAP	g131782	524	132	1.00E-52	63	13	DNA repair protein RAD50 (153 KD protein) [Saccharomyces cerevisiae] (U00050) similar to enoyl-CoA hydrolases; highest similarity to YKRS_YEAST [Caenorhabditis elegans]
22422	ENU06216	ANI61C8033:	22-47	806-829	NAP	g485111	405	159	8.00E-45	42	58	probable sterigmatocystin biosynthesis P450 monooxygenase STCF (cytochrome P450 60A2) [Emericella nidulans]
22423	ENU06217	ANI61C9123:	46-65	773-800	NAP	g2493389	136	66	3.00E-10	23	55	probable sterigmatocystin biosynthesis P450 monooxygenase STCF (cytochrome P450 60A2) [Emericella nidulans]
22424	ENU06218	ANI61C6123:	22-49	565-585	NAP	g91209	108	43	0.003	38	58	proline-rich protein MP2 - mouse (fragment) [U832489] septin B [Emericella nidulans]
22425	ENU06219	ANI61C6470:	22-46	801-828	NAP	g1791305	2018	420	e-143	98	65	(Z35595) similar to 4-coumarate-coA ligase; cDNA EST yk455e10.3 comes from this gene; cDNA EST yk455e10.5 comes from this gene; cDNA EST yk286h10.3 comes from this gene; cDNA EST yk286h10.5 comes from this gene [Caenorhabditis elegans]
22426	ENU06220	ANI61S4337:	36-56	433-452	NAP	g3873862	182	89	2.00E-17	35	30	(AJ009825) copper amine oxidase [Cicer arietinum]
22427	ENU06221	ANI61S3166:	52-77	481-499	NAP	g3819099	300	127	6.00E-29	51	20	protein kinase C-like [Aspergillus niger]
22428	ENU06222	ANI61C1129	37-56	728-749	NAP	g2499576	1347	176	3.00E-89	85	21	hypothetical 30.6 KD protein F52C9.4 in chromosome III [Caenorhabditis elegans]
22429	ENU06223	ANI61C293:1	..306		NAP	g1353167	126	61	0.000000	31	37	

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit ncbi gi	aat	Blast Score	Blast Score	% id	% cvrg	Description
22430	ENU06224	ANI61C1386:	42-61	445-464	NAP	g1077342	200	66	1.00E-14	37	54	probable membrane protein YLR284c - yeast (Saccharomyces cerevisiae)
22431	ENU06225	ANI61C1975:	23-42	661-685	NAP	g2342601	1548	166	2.00E-40	36	5	[Saccharomyces cerevisiae] (X89442) peptide synthetase [Metarhizium anisopliae]
22432	ENU06226	ANI61C4494:	54-73	524-546	NAP	g3184512	524	150	8.00E-53	73	77	(U79756) GTPase cRac1B [Gallus gallus]
22433	ENU06227	ANI61C3323:	62-89	313-340	NAP	g585175	314	138	2.00E-32	57	33	guanine nucleotide-binding protein alpha-1 subunit (GPI-alpha) [Neurospora crassa] (AF125451) contains similarity to the NIFR3/SMM1 family [Caenorhabditis elegans] (AF031194) S276 [Triticum aestivum]
22434	ENU06228	ANI61C5753:	202-228	457-482	NAP	g4226107	372	110	7.00E-32	50	27	
22435	ENU06229	ANI61S2462:	24-46	345-372	NAP	g4104056	359	140	6.00E-33	40	38	
22436	ENU06230	ANI61C2477:	22-44	799-826	NAP	g120965	2511	473	e-135	99	53	4-aminobutyrate aminotransferase (gamma-amino-N-butyrate transaminase) (GABA transaminase) (GABA aminotransferase) [Emericella nidulans]
22437	ENU06231	ANI61S1069:			NAP	g732387	196	77	3.00E-16			hypothetical LACA/RP1B family protein in SPO1IR-GLYC intergenic region [Bacillus subtilis] (AJ049608) extensin-like protein [Arabidopsis thaliana]
22438	ENU06232	ANI61S769:1	.859		NAP	g4584539	612		49	36		"Citrate synthase, mitochondrial precursor" [Emericella nidulans]" SIS1 intergenic region
22439	ENU06233	ANI61C6152:	51-69	601-620	NAP	g2493725	869	211	1.00E-84	96	39	
22440	ENU06234	ANI61C6829:	1..682	801-828	NAP	g1730706	583	99	5.00E-20	29	55	
22441	ENU06235	ANI61C4535:	22-47	782-800	NAP	g1166378	958	114	7.00E-25	32	23	[Saccharomyces cerevisiae] "L76169" reverse transcriptase, RNaseH [Gliomera cingulata]" (Z98762) SPAC4A8.16c, putative nuclear transport protein, len:639aa, similar e.g. to YMR309C,
22442	ENU06236	ANI61C2280:	24-51	768-795	NAP	g4490654	1064	162	2.00E-72	48	44	NIP1_YEAST, P32497, nuclear transport protein nip1, (812aa), fasta scores, op:t:926, E:0:0, (34.3% identity in 581 aa overlap), ide...[]"
			1536..1									

Sed num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit nebi gi	Score	Prob	% id	% cvg	Description		
22443	ENU06237	ANI61C1032	34-53	561-587	NAP	g1723482	236	125	3.00E-28	37	67	DMA1 protein [Schizosaccharomyces pombe]	
22444	ENU06238	ANI61C1064	1:4721..5355 1:1..671	188-207	624-650	NAP	g1077386	337	82	8.00E-30	40	40	hypothetical protein YLR345w - yeast (Saccharomyces cerevisiae)
22445	ENU06239	ANI61C5085:	23-42 2220..1	716-742	NAP	g730753	1745	249	1.00E-65			[Saccharomyces cerevisiae] chromosome segregation protein SMC2 (DA-BOX protein SMC2)	
22446	ENU06240	ANI61C1135	22-48 2:1939..3246	776-801	NAP	g731834	596	159	2.00E-38	43	60	hypothetical 41.9 KD protein in SDS3-THS1 intergenic region [Saccharomyces cerevisiae]	
22447	ENU06241	ANI61C3285:	1:17-136 1..534	446-465	NAP	g2623295	174	82	2.00E-16	39	42	(AC002409) hypothetical protein [Arabidopsis thaliana]	
22448	ENU06242	ANI61S1082:	722..1		NAP	g1169440	904	309	7.00E-87	81	5	"dynein heavy chain, cytosolic (DYHC) [Emericella nidulans]" hypothetical protein YOR367w - yeast (Saccharomyces cerevisiae)	
22449	ENU06243	ANI61C9181:	27-54 795..1569	728-747	NAP	g2132141	286	80	4.00E-28	43	99	[Saccharomyces cerevisiae]	
22450	ENU06244	ANI61C6586:	24-45 1527..1	723-746	NAP	g2499125	810	150	1.00E-35	28	9	vacuolar protein sorting-associated protein VPS13 [Saccharomyces cerevisiae]	
22451	ENU06245	ANI61C1112	32-51 5..512..10	458-481	NAP	g2879853	248	78	1.00E-20	45	36	(AL021815) arginase family protein [Schizosaccharomyces pombe]	
22452	ENU06246	ANI61C2339:	64-83 801..319	301-328	NAP	g1351629	109	90	1.00E-17			hypothetical 18.5 KD protein C12G12.05C in chromosome I [Schizosaccharomyces pombe] (U32375) tartrate dehydrogenase [Agrobacterium vitis] (AL032681) putative hydroxyacylglycerol thione hydrolase [Schizosaccharomyces pombe] (AF134304) Scar2 [Homo sapiens]	
22453	ENU06247	ANI61C4662:	109-128 623..325	251-278	NAP	g984373	313	134	2.00E-31	65	27		
22454	ENU06248	ANI61S1794:	1..468		NAP	g3810866	78	36	0.00006	42	39		
22455	ENU06249	ANI61C9545:	100-119 1..682	625-644	NAP	g4927212	125	37	0.15				
22456	ENU06250	ANI61C9449:	25-42 7873..6332	803-823	NAP	g128853	1179	273	4.00E-87	70	62	NADH-ubiquinone oxidoreductase 40 KD subunit precursor (complex I-40KD) (CI-40KD) [Neurospora crassa] hypothetical 25.1 KD protein in PM140-PAC2 intergenic region [Saccharomyces cerevisiae]	
22457	ENU06251	ANI61C1021	22-44 7..2609..1809	740-767	NAP	g731434	253	126	2.00E-28	37	97		

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database	Hit ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
22458	ENU06252	ANI61C8628:	102-124	610-637	NAP		g3256848	187	98	8.00E-20	41	78	(AP000002) 219aa long hypothetical protein [Pyrococcus horikoshii]
22459	ENU06253	ANI61C4897:	22-47	636-654	NAP		g1729996	127	62	8.00E-12	32	63	TOXD protein [Cochliobolus carbonum]
22460	ENU06254	ANI61C306:1	22-46	786-810	NAP		g2114323	287	35	0.73	26	32	(D88734) membrane glycoprotein [Equine herpesvirus 1]
22461	ENU06255	ANI61C5208:	31-50	715-738	NAP		g2132688	1499	279	1.00E-74	47	5	probable membrane protein YLR106c - yeast (Saccharomyces cerevisiae)
22462	ENU06256	ANI61C1077	23-42	716-735	NAP		g1945493	1327	109	3.00E-36	44	25	[Saccharomyces cerevisiae] ("U56965) Similar to NAD(P) transhydrogenase, mitochondrial; coded for by C. elegans cDNA yk27c1.5; coded for by C. elegans cDNA yk35b9.5; coded for by C. elegans cDNA yk161c9.3; coded for by C. elegans ... []" (AL031174) t-complex protein 1 gamma subunit homolog
22463	ENU06257	ANI61C8566:	33-60	760-783	NAP		g3393020	965	348	5.00E-95	70	47	[Schizosaccharomyces pombe] (Z69368) unknown
22464	ENU06258	ANI61C9752:	32-59	804-827	NAP		g1182038	583	153	2.00E-36	37	15	[Schizosaccharomyces pombe]
22465	ENU06259	ANI61C7363:	22-46	710-737	NAP		g2501011	986	224	6.00E-58	43	27	Isoleucyl-tRNA synthetase (isoleucine--tRNA ligase) (IERS) [Synchocystis sp.]
22466	ENU06260	ANI61C1027	22-44	608-630	NAP		g2131201	420	155	3.00E-37	42	55	"Ca <sup>2+</sup> /H <sup>+</sup> -exchanging protein, vacuolar - yeast (Saccharomyces cerevisiae)" [Saccharomyces cerevisiae]
22467	ENU06261	ANI61S4372:			NAP		g581280	444	168	5.00E-42	82	85	(Y00618) unidentified reading frame [Escherichia coli]
22468	ENU06262	ANI61C3636:	22-47	717-744	NAP		g4914370	131	66	1.00E-20			(AC007584) putative polyprotein [Arabidopsis thaliana]
22469	ENU06263	ANI61C5734:	51-78	696-716	NAP		g1870209	430	59	2.00E-18	34	50	(AC000133) ORF [Emericella nidulans]
22470	ENU06264	ANI61C7800:	23-42	714-733	NAP		g2133034	228	95	3.00E-24	31	38	probable membrane protein YPR156c - yeast (Saccharomyces cerevisiae)
			1144...1										[Saccharomyces cerevisiae]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database	Hit	ncbi gi	aat	Blast Score	Blast Prob	% id	% cvrg	Description
22471	ENU06265	ANI61C2511:	1537..238	NAP		g1351666	1401	129	6.00E-75	66	42			C1F7.02C [Schizosaccharomyces pombe]
22472	ENU06266	ANI61C6518:	22-49	756-782	NAP		g2440082	235	75	9.00E-23	33	31		[Y14849] putative glucose sensor [Kluyveromyces lactis]
22473	ENU06267	ANI61C5564:	39-59	763-782	NAP		g1346390	334	149	2.00E-35	32	31		[Saccharomyces cerevisiae] serine/threonine-protein kinase CLA4
22474	ENU06268	ANI61C6853:	120-139	496-515	NAP		g1710791	354	118	2.00E-26	48	42		probable mitochondrial 40S ribosomal protein S5 [Schizosaccharomyces pombe]
22475	ENU06269	ANI61C9440:	50-75	295-314	NAP		g416685	145	61	0.000000	36	36		[ATP11 protein precursor [Saccharomyces cerevisiae]]
22476	ENU06270	ANI61C2599:	52-71	512-531	NAP		g3913432	740	214	5.00E-69	78	25		putative pre-mRNA splicing factor ATP-dependent RNA helicase SPBC16H5.10C
22477	ENU06271	ANI61C2216:	102-122	751-777	NAP		g1706440	247	71	1.00E-24	38	39		[Schizosaccharomyces pombe] Spore wall maturation protein DIT1 [Saccharomyces cerevisiae]
22478	ENU06272	ANI61C686:5	22-49	804-827	NAP		g3150262	468	150	2.00E-35	35	80		(AL023634) hypothetical protein [Schizosaccharomyces pombe]
22479	ENU06273	ANI61C1185:	22-47	805-824	NAP		g133356	3156	160	6.00E-75				DNA-directed RNA polymerase III largeST subunit (C160)
22480	ENU06274	ANI61C4836:	62-81	727-749	NAP		g279978	87	80	3.00E-14	24	46		[Saccharomyces cerevisiae] benzoylformate decarboxylase (EC 4.1.1.7) - Pseudomonas putida []
22481	ENU06275	ANI61C3148:	22-42	731-750	NAP		g416574	1638	550	e-156	94	75		probable formate dehydrogenase (NAD-dependent formate dehydrogenase) (FDH) [Emericella nidulans]
22482	ENU06276	ANI61C5449:	22-48	490-517	NAP		g1546072	131	66	2.00E-10	37	5		(U68040) polyketide synthase [Cochliobolus heterostrophus]
22483	ENU06277	ANI61C8576:	1..586	72-91	541-560	NAP	g1705652	369	99	2.00E-34	56	100		20 KD nuclear C.A.P binding protein (NCBP) (CBP20) [Xenopus laevis] (U68040) polyketide synthase [Cochliobolus heterostrophus]
22484	ENU06278	ANI61C1081	2:1510..3776	22-46	763-782	NAP	g1546072	1253	117	8.00E-26	33	11		"dynein heavy chain, cytosolic (DYHC) [Emericella nidulans]"
			8:5637..1											

Sed num	Seq id	Contig source	5 pos	3 pos	Primer Basis	Primer Selection	aat	Blast	Blast	%		
					Database	Hit	ncbi gi	Score	Score Prob	id	cvg	
					g1362615	405	204	6.00E-52	43	22	Description	
22487	ENU06281	ANI61C9941:	107-127	350-371	NAP	g106185	174	83	1.00E-15	42	53	GTP-binding protein Rab2 - human
		1..392				g1934645	174	92	3.00E-18	37	97	[Homo sapiens]
22488	ENU06282	ANI61C1081:	30-48	606-625	NAP	g1790870	380	87	2.00E-29	42	97	(U93876) hypothetical protein YrdC [Bacillus subtilis]
22489	ENU06283	ANI61C6360:	115-136	809-828	NAP	3284..2430						(U32622) toluenesulfonate zinc-independent alcohol dehydrogenase [Comamonas testosteroni]
22490	ENU06284	ANI61C711:1	56-78	373-394	NAP	g2493915	184	90	9.00E-18	41	60	cutinase precursor [Botryotinia fuckeliana]
22491	ENU06285	ANI61S3073:	..415		NAP	g2950476	134	46	0.00009	38	51	(AL022070) vesicle transport v-share protein [Schizosaccharomyces pombe]
22492	ENU06286	ANI61C2684:	114-133	467-487	NAP	g4506123	243	65	4.00E-21	39	44	pre-mRNA splicing factor similar to S. cerevisiae Prp18 [Homo sapiens]
22493	ENU06287	ANI61C4085:	22-49	809-828	NAP	g2649154	275	123	1.00E-27	31	98	(AE001006) membrane protein [Archaeoglobus fulgidus]
22494	ENU06288	ANI61C861:1	22-41	711-730	NAP	g130155	853	162	4.00E-81	56	41	Deoxyribodipyrimidine photolyase (DNA photolyase) (photoreactivating enzyme) [Neurospora crassa]
22495	ENU06289	ANI61C2490:	27-53	807-829	NAP	g3322837	324	51	3.00E-14	31	41	(AE001229) T. pallidum predicted coding region TP0544 [Treponema pallidum]
22496	ENU06290	ANI61C6643:	50-69	802-821	NAP	g2648180	292	98	6.00E-20	34	66	(AE000943) conserved hypothetical protein [Archaeoglobus fulgidus]
22497	ENU06291	ANI61C7691:	22-48	686-708	NAP	g136642	433	131	6.00E-30			Ubiquitin-conjugating enzyme E2-34 KD (ubiquitin-protein ligase) (ubiquitin carrier protein) (cell division control protein 34) [Saccharomyces cerevisiae]
22498	ENU06292	ANI61C6883:	92-111	262-281	NAP	g984373	391	141	2.00E-33	72	31	(U32375) tartrate dehydrogenase [Agrobacterium vitis]
22499	ENU06293	ANI61C4294:	33-52	747-766	NAP	g228477	191					ECLF2 upstream ORF [sainfine herpesvirus 1]
22500	ENU06294	ANI61C7396:	796..1		NAP	g2117306	452	74	1.00E-14	35	39	(Z95620) dna-(apurinic or apyrimidinic site) lyase [Schizosaccharomyces pombe]
		6367..7884										

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat	Blast Score	Blast Prob	% id	% cvrg	Description
22501	ENU06295	ANI61C9984:	126-145	308-330	NAP	g683698	138	74	3.00E-15	29	40	(Z48229) orf1 [Saccharomyces cerevisiae]	
22502	ENU06296	ANI61C316:5	46-65	804-829	NAP	g4499843	327	44	0.001			(AJ011965) oxidoreductase [Claviceps purpurea]	
22503	ENU06297	ANI61C5121:	23-50	453-473	NAP	g3891484	142	37	0.0002	35	34	"Chain B, Co-Crystal Structure Of Protein Farnesyldiphosphate Complexed With A Farnesyl Diphosphate Substrate"	
22504	ENU06298	ANI61C8634:	22-45	796-816	NAP	g538067	2311	123	1.00E-27	33	18	(M77661) putative pol polyprotein [Magnaporthe grisea]	
22505	ENU06299	ANI61C3333:	22-49	705-732	NAP	g3004863	538	113	3.00E-57	50	30	"(AF029354) exo-beta-1,3-glucanase [Ampelomyces quisqualis]"	
22506	ENU06300	ANI61C5808:	22-46	725-747	NAP	g2209087	897	345	2.00E-94	62	41	(AF000309) putative serine/threonine kinase [Colletotrichum lindernuthianum]	
22507	ENU06301	ANI61C343:6	49-76	558-584	NAP	g3914984	143	80	2.00E-14	31	5	Ferrichrome siderophore peptide synthetase [Ustilago maydis]	
22508	ENU06302	ANI61C1742:	72-93	553-577	NAP	g1652017	201	95	3.00E-19	32	65	(D90901) hypothetical protein [Synechocystis spp.]	
22509	ENU06303	ANI61C4320:	22-46	805-829	NAP	g1723435	1087	350	6.00E-96	55	18	hypothetical 170.7 KD protein C56F8.02 in chromosome I	
22510	ENU06304	ANI61C6618:	49-68	677-699	NAP	g3080522	309	153	1.00E-36	39	36	[Schizosaccharomyces pombe] (AL022599) hypothetical protein [Schizosaccharomyces pombe]	
22511	ENU06305	ANI61C4435:	48-69	516-542	NAP	g3913154	319	145	3.00E-34	39	19	beta-galactosidase (lactase) [Enterobacter cloacae]	
22512	ENU06306	ANI61C8171:	23-46	804-828	NAP	g2506360	276	108	5.00E-23	33	34	NPL1 protein (SEC63 protein) [Saccharomyces cerevisiae]	
22513	ENU06307	ANI61C1086	122-141	500-519	NAP	g729747	411	155	3.00E-37	48	45	Flavohemoprotein (haemoglobin-like protein) (flavohemoglobin) [Ralstonia europa]	
22514	ENU06308	ANI61C2206:	222-242	699-719	NAP	g171565	221	113	1.00E-24	35	56	(K01609) gal10 [Saccharomyces carlsbergensis]	
22515	ENU06309	ANI61C1729:	35-54	730-749	NAP	g1703456	496	128	6.00E-29	43	21	Cation-transporting ATPase PAT1 [Dictyostelium discoideum]	
22516	ENU06310	ANI61C9369:	22-43	802-820	NAP	g1551635	462	73	4.00E-23	40	70	hypothetical 35.8 KD protein C12G12.12 in chromosome I [Schizosaccharomyces pombe]	

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	Score	Score Prob	% id	cvg	Description	
22517	ENU06311	ANI61C8401:	36-55	774-797	NAP	g585255	756	277	7.00E-74	56	49	Histidine biosynthesis bifunctional amidotransferase / cyclase [Saccharomyces cerevisiae]	
22518	ENU06312	ANI61S14:62	3..1		NAP	g3114719	542	183	8.00E-57	62	13	(Z68906) ATP-binding multidrug cassette transporter [Botryotinia fuckeliana]	
22519	ENU06313	ANI61C6428:	122-141	691-714	NAP	g1345625	322	153	4.00E-46			Biotin--protein ligase (biotin--protein ligase) (biotin--[Saccharomyces cerevisiae]	
22520	ENU06314	ANI61C8003:	1200..1		NAP	g140464	594	99	5.00E-20	38	22	[Saccharomyces cerevisiae] (D7853) aspartate kinase-homoserine dehydrogenase [Oryza sativa]	
22521	ENU06315	ANI61C1:108	2..760		NAP	g1777375	198	92	1.00E-18	46	11	[Saccharomyces cerevisiae] (L48074) secreted dipeptidyl peptidase [Aspergillus fumigatus]	
22522	ENU06316	ANI61C8875:	24-43	809-829	NAP	g2340046	813	334	4.00E-91	51	39	(X70694) trehalose-6-phosphate phosphatase [Saccharomyces cerevisiae]	
22523	ENU06317	ANI61C796:1	22-42	709-731	NAP	g406769	921	229	2.00E-59	47	31	Coronin-like protein [Saccharomyces cerevisiae]	
22524	ENU06318	ANI61C8121:	22-47	723-740	NAP	g3121873	483	192	3.00E-48	50	32	(AL031786) putative delta-1-pyroline-5-carboxylate dehydrogenase [Schizosaccharomyces pombe]	
22525	ENU06319	ANI61S4368:	1..670		NAP	g3687478	213	104	6.00E-22	34	39	(Z49130) cDNA EST EMBL:D74028 comes from this gene; cDNA EST EMBL:D71354 comes from this gene; cDNA EST EMBL:D76320 comes from this gene; cDNA EST yk486c7.3 comes from this gene; cDNA EST yk486c7.5 comes from this gene; cDNA ES.. [] (AL031536) fnx1p.	
22526	ENU06320	ANI61C7484:	22-42	809-829	NAP	g3879532	213	86	3.00E-16	35	81	[Schizosaccharomyces pombe] (US9503) glucoamylase precursor [Aspergillus awamori]	
22527	ENU06321	ANI61C1043	23-50	803-829	NAP	g3560207	234	58	0.000000	07		(AL022105) hypothetical protein [Schizosaccharomyces pombe]	
22528	ENU06322	ANI61C4967:	756..1	22-48	625-644	NAP	g1389841	559	186	1.00E-58	55	33	
22529	ENU06323	ANI61C1205:	513..1	109-128	391-417	NAP	g2956751	205	105	2.00E-22	31	45	

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit ncbi gi	Score	Score	Blast Prob	% id	% cvrg	Description
22530	ENU06324	ANI61C9687:	69-91	787-808	NAP	g1169870	365	185	3.00E-46	45	56	GCD14 protein [Saccharomyces cerevisiae]
22531	ENU06325	ANI61C8614:	23-48	728-748	NAP	g4557481	325	97	2.00E-23	34	14	Canalicular multispecific organic anion transporter [Homo sapiens] (X53744) 68kDa subunit of signal recognition particle [Canis familiaris]
22532	ENU06326	ANI61C7926:	34-53	808-829	NAP	g932	188	42	0.006			Hypothetical 141.1 KD protein in MET2-SEC2 intergenic region
22533	ENU06327	ANI61C1343:	22-48	755-782	NAP	g1730639	299	136	2.00E-31	31	21	
22534	ENU06328	ANI61C1109	51-70	361-380	NAP	g3914342	175	93	1.00E-18	51	17	[Saccharomyces cerevisiae] 3-phytase B precursor (myo-inositol hexaphosphate 3-phosphohydrolase B) (3 phytase B) (myo-inositol hexakisphosphate phosphohydrolase B) [Emericella nidulans]
22535	ENU06329	ANI61C8939:	22-47	803-829	NAP	g2132443	340	64	0.000000	30	76	probable membrane protein YDL144c - yeast [Saccharomyces cerevisiae] (X94769) choline dehydrogenase [Rattus rattus]
22536	ENU06330	ANI61C1065	23-42	413-437	NAP	g1154950	153	96	2.00E-19	34	37	hypothetical 72.8 KD protein in AGA1-MTR intergenic region (O678) [Escherichia coli]
22537	ENU06331	ANI61S3435:	38-65	496-518	NAP	g1176816	899	176	1.00E-81	95	28	"Ankyrin, brain variant 2 (ankyrin B (ankyrin, nonerythroid) [" AL034463) putative single-strand polynucleotide binding protein [Schizosaccharomyces pombe] (U13049) pectate lyase C [Fusarium solani f. sp. pisi]
22538	ENU06332	ANI61C5381:	33-60	709-728	NAP	g231551	262	83	2.00E-28	31	14	hypothetical 20.1 KD protein in RTFI-CSE1 intergenic region [Saccharomyces cerevisiae]
22539	ENU06333	ANI61C6837:	118-136	454-479	NAP	g4007790	151	73	2.00E-13	39	25	putative ATP-dependent RNA helicase C31A2.07C [Schizosaccharomyces pombe]
22540	ENU06334	ANI61C993:8	66..539		NAP	g595570	151	82	2.00E-15	41	54	
22541	ENU06335	ANI61C4542:	23-42	515-534	NAP	g1723978	212	64	1.00E-19			
22542	ENU06336	ANI61C8821:	45-64	747-766	NAP	g1175401	940	371	e-102	66	33	putative ATP-dependent RNA helicase C31A2.07C [Schizosaccharomyces pombe]
22543	ENU06337	ANI61C7550:	1..352		NAP	g114971	185	85	2.00E-16	40	13	beta-glucosidase precursor (gentiobiose) (celllobiose) (beta-D-glucoside glucohydrolase) [Kluyveromyces marxianus]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database	Hit gi	aat	Blast Score	Blast Prob	% id	% cvrg	Description
22544	ENU06338	ANI61C1577:	102..126	583..602	NAP	g1169546	177	67	7.00E-13	35	82		receptor C28H8.4 [Caenorhabditis elegans]
22545	ENU06339	ANI61C7523:	65..84	378..397	NAP	g2136261	77	62	0.000000	25	31		tetracycline transporter-like protein - human [Homo sapiens]
22546	ENU06340	ANI61S4287:	22..48	446..467	NAP	g3941500	153	66	2.00E-10	36	57		(AF062904) putative transcription factor [Arabidopsis thaliana]
22547	ENU06341	ANI61C1023	22..45	375..399	NAP	g4539247	196	89	5.00E-19	48	64		(AL049489) putative actin polymerisation complex protein [Schizosaccharomyces pombe]
22548	ENU06342	ANI61C5375:	15..134	716..742	NAP	g3929399	896	153	2.00E-36	37	51		proline-specific permease (proline transport protein) [Emericella nidulans]
22549	ENU06343	ANI61C7079:	2167..620		NAP	g549674	832	101	7.00E-42	39	56		hypothetical 49.6 KD protein in ELM1-PR12 intergenic region [Saccharomyces cerevisiae]
22550	ENU06344	ANI61C8750:	29..54	790..809	NAP	g3021303	3668	554	e-157	99	12		(Y15996) acetyl-CoA carboxylase [Emericella nidulans]
22551	ENU06345	ANI61C1034	22..44	644..663	NAP	g1209391	2070	254	4.00E-67	46	31		(D83659) TPR protein [Schizosaccharomyces pombe]
22552	ENU06346	ANI61C6562:	9..5166..8019		NAP	g3282044	1037	377	e-104	70	19		(Y13967) alpha-amino adipate reductase large subunit [Penicillium chrysogenum]
			1021..1										(AL049559) putative short-chain dehydrogenase [Schizosaccharomyces pombe]
22553	ENU06347	ANI61C9317:	22..45	803..829	NAP	g4581525	302	117	8.00E-26	34	47		Early modulin 20 precursor (N-20) [Medicago truncatula]
22554	ENU06348	ANI61C888..4	111..130	412..431	NAP	g3914142	36	38	0.052	25	50		threonine synthase [Schizosaccharomyces pombe]
22555	ENU06349	ANI61C2891:	1..1004		NAP	g2501152	660	222	2.00E-57	53	47		(AL022103) transmembrane transporter lizip. [Schizosaccharomyces pombe] (AF007873) dolichol monophosphate manose synthase [Schizosaccharomyces pombe]
22556	ENU06350	ANI61C5514:	23..42	805..829	NAP	g2256768	664	217	1.00E-55	51	63		- yeast (Saccharomyces cerevisiae)
22557	ENU06351	ANI61S3594:	561..156		NAP	g2258414	119	52	0.000000	38	54		[Saccharomyces cerevisiae]
22558	ENU06352	ANI61C234..1	22..42	612..635	NAP	g1077357	1063	124	1.00E-41	61	39		
			575..1										

Seq num	Seq id	Contig source	5 pos	3 pos	Basis	Database	Hit	ncbi gi	Score	Score	Prob	% id	% cvrg	Description	
22559	ENU06353	ANI61C8537:	40-59	712-731	NAP	g409547	239	86	3.00E-20	29	47	(L07492) sugar transport protein [Saccharomyces cerevisiae]			
22560	ENU06354	ANI61C5810:	843..50		NAP	g544232	610	127	9.00E-29	50	59	elongation factor 1-gamma 2 (EF-1-gamma 2) [Saccharomyces cerevisiae]			
22561	ENU06355	ANI61C8235:	22-49	786-813	NAP	g731465	818	267	9.00E-83	57	87	putative mitochondrial carrier YER053C [Saccharomyces cerevisiae]			
22562	ENU06356	ANI61S1427:	1..719		NAP	g110849	161	52	0.00005	31	83	proline-rich protein - mouse [Mus musculus]			
22563	ENU06357	ANI61C2541:	22-47	741-763	NAP	g2330704	727	249	3.00E-65	49	81	(Z98529) putative transcription initiation factor TFIIB subunit [Schizosaccharomyces pombe]			
22564	ENU06358	ANI61C5404:	24-43	630-650	NAP	g3287946	1040	326	9.00E-89	64	25	putative helicase C6F12.16 in chromosome I [Schizosaccharomyces pombe]			
22565	ENU06359	ANI61C8694:	27-50	639-658	NAP	g3978466	1587	275	2.00E-73	50	37	(AF086822) dihydroxyacetone synthase [Candida boidinii]			
22566	ENU06360	ANI61C9257:	1755..1	22-46	795-815	NAP	g2414649	827	198	6.00E-50	38	9	(Z99296) hypothetical protein [Schizosaccharomyces pombe]		
22567	ENU06361	ANI61C1087	1245..1	22-45	800-819	NAP	g140474	576	76	4.00E-13			hypothetical 69.2 KD protein in HSP30-PMP1 intergenic region		
			3:876..2793												
22568	ENU06362	ANI61C669:1	128..658		NAP	g1722769	225	99	1.00E-20	38	20	[Saccharomyces cerevisiae] Phosphatidylinositol 3-kinase VPS34 (PI3-kinase) (PTDINS-3-kinase) (PI3K) (vacuolar sorting protein 34)			
22569	ENU06363	ANI61C1138	6:949..426	38-64	477-503	NAP	g4106669	323	120	2.00E-31	56	33	[Schizosaccharomyces pombe] (AL035064) protein kinase skp1p		
22570	ENU06364	ANI61C5198:	1013..1	24-43	805-825	NAP	g129592	425	188	4.00E-47	45	35	[Schizosaccharomyces pombe] Phenylalanine ammonia-lyase [Rhodotorula mucilaginosa]		
22571	ENU06365	ANI61C445:1	.1246	44-63	722-740	NAP	g1708850	684	134	1.00E-49	48	33	probable leukotriene A-4 hydrolase (LTA-4 hydrolase) (leukotriene A(4) hydrolase) [Saccharomyces cerevisiae] (X86780) cystathione synthase [Streptomyces hygroscopicus]		
22572	ENU06366	ANI61C7858:	5143..4521	23-44	566-585	NAP	g987116	126	52	0.00003	28	99	(AL031825) putative acetylornithine deacetylase [Schizosaccharomyces pombe]		
22573	ENU06367	ANI61C82:17	60..549	44-63	802-829	NAP	g3702638	416	127	1.00E-28	40	61			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Primer Basis	Selection	Database	Hit ncbi gi	aat	Blast Score	Blast Score	% id	% cvrg	Description
22574	ENU06368	ANI61C1781:	37-64	400-425	NAP		g1077382	275	133	7.00E-31	41	19		- yeast ( <i>Saccharomyces cerevisiae</i> )
			1..537											probable membrane protein YLR335w
22575	ENU06369	ANI61C8774:	35-54	802-829	NAP		g3885836	517	45	0.000002				[ <i>Saccharomyces cerevisiae</i> ]
			290..2421				g2828151	162	88	5.00E-17	39	41		(AF091042) putative cercosporin transporter [Cercospora kikuchii]
22576	ENU06370	ANI61C5355:	40-67	441-468	NAP		g3122326	348	163	8.00E-40	50	33		[ <i>Homo sapiens</i> ] LEC14B protein [Lithospermum erythrorhizon]
			391..1				g3242972	1836	395	e-109	70	39		(AF069523) heat shock protein Hsp88 [Neurospora crassa]
22577	ENU06371	ANI61C1843:	22-49	458-479	NAP		g4521101	1136	289	e-121	79	75		(AB016540) alternative oxidase [Aspergillus niger] (U82218) Ats1 [ <i>Schizosaccharomyces pombe</i> ]
			115..525				g1766062	285	125	2.00E-28	42	99		hypothetical protein YLR348c - yeast ( <i>Saccharomyces cerevisiae</i> )
22578	ENU06372	ANI61C1097	27-54	781-806	NAP		g1077385	325	95	7.00E-19	47	66		[ <i>Saccharomyces cerevisiae</i> ] (L35053) endonuclease [Magnaporthe grisea]
			7..4250..5969				g1929333	186	90	1.00E-17	35	66		(Z93767) ywrF [ <i>Bacillus subtilis</i> ]
22579	ENU06373	ANI61C1070	48-67	791-814	NAP		g4115939	407	176	8.00E-44	66	46		(AF118223) contains similarity to Methanobacterium thermoautotrophicum transcriptional regulator (GB:AE000850)
			1..1037											[ <i>Arabidopsis thaliana</i> ]
22580	ENU06374	ANI61C1096:	52-71	464-483	NAP		g1351702	100	61	0.000000	33	31		hypothetical 61.1 KD protein C11D3.05 in chromosome I
			692..161				g140371	224	104	4.00E-22	36	29		[ <i>Schizosaccharomyces pombe</i> ] hypothetical 58.8 KD protein in GLKI-SR9 intergenic region
22581	ENU06375	ANI61C9004:	22-41	684-705	NAP		g4263825	301	130	5.00E-30	42	12		[ <i>Saccharomyces cerevisiae</i> ] (AC006067) hypothetical protein [Arabidopsis thaliana]
			3221..4026				g585175	452	104	2.00E-43	47	60		guanine nucleotide-binding protein alpha-1 subunit (GPI-alpha) [Neurospora crassa]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database	Hit ncbi gi	aat	Blast Score	Blast Score	Prob	% id	% cvrg	Description
22589	ENU06383	ANI61C1050	1:1298..7124	NAP		g3135013	507	136	1.00E-45	51	26	98	13	"(U51272) 1,3-beta-D-glucan synthase catalytic subunit [Emericella nidulans]"
22590	ENU06384	ANI61C7768:	29-48	633-652	NAP		g1491929	10043	316	e-126	98	13	(AJ005963) 100 kDa protein [Ajellomyces capsulatus]	
22591	ENU06385	ANI61C1085	3164..3929	40-64	422-445	NAP	g1834342	444	175	1.00E-43	60	9	(Z68905) ATP-binding cassette multidrug transporter [Emericella nidulans]	
22592	ENU06386	ANI61C2190:	62-81	722-741	NAP	2788..1	g1351615	1732	235	3.00E-61	41	23	hypothetical protein C23D3.15 in chromosome I [Schizosaccharomyces pombe] (AB010389) ALK2 [Yarrowia lipolytica]	
22593	ENU06387	ANI61C5726:	22-48	728-749	NAP	1..959	g3298291	535	229	9.00E-61	46	52	(AF032443) ABC1 transporter; ABC-type ATPase [Magnaporthe grisea] (Z98596) SMC-family protein [Schizosaccharomyces pombe] (AC002342) putative Cu2+-transporting ATPase [Arabidopsis thaliana] (AF140598) ring-box protein 1 [Homo sapiens]	
22594	ENU06388	ANI61C1262:	45-66	446-465	NAP	524..1	g2625138	275	122	2.00E-27	39	10	[Schizosaccharomyces pombe] (AC002342) putative Cu2+-transporting ATPase [Arabidopsis thaliana] (AF140598) ring-box protein 1 [Homo sapiens]	
22595	ENU06389	ANI61C8354:	22-44	723-743	NAP	1077..1	g3861449	420	108	7.00E-23	25	26	[Schizosaccharomyces pombe] (AC002342) putative Cu2+-transporting ATPase [Arabidopsis thaliana] (AF140598) ring-box protein 1 [Homo sapiens]	
22596	ENU06390	ANI61C5304:	22-49	762-780	NAP	1..1908	g2660670	680	135	4.00E-31	36	22	[Schizosaccharomyces pombe] (AC002342) putative Cu2+-transporting ATPase [Arabidopsis thaliana] (AF140598) ring-box protein 1 [Homo sapiens]	
22597	ENU06391	ANI61C8656:	22-45	470-492	NAP	1944..2456	g4769004	415	74	5.00E-36			[Schizosaccharomyces pombe] (AL049498) myosin ii [Schizosaccharomyces pombe] (AL049498) myosin ii	
22598	ENU06392	ANI61C3866:	87-105	439-458	NAP	497..962	g1352994	132	78	2.00E-16			hypothetical 30.6 KD protein in SCP160-SMC3 intergenic region precursor [Saccharomyces cerevisiae] (AL049498) myosin ii	
22599	ENU06393	ANI61C3152:	NAP			185..3464	g4539277	2340	127	1.00E-28	27	18	hypothetical 61.8 KD protein C16E8..13 in chromosome I [Schizosaccharomyces pombe] (AB009461) MUS38 [Neurospora crassa]	
22600	ENU06394	ANI61C6685:	38-57	717-735	NAP	1..938	g3219947	566	244	5.00E-64	52	45	hypothetical 61.8 KD protein C16E8..13 in chromosome I [Schizosaccharomyces pombe] (AB009461) MUS38 [Neurospora crassa]	
22601	ENU06395	ANI61C1464:	83-108	735-762	NAP	1183..1	g3219304	443	185	4.00E-46	40	30	putative transporter C11D3.18C [Schizosaccharomyces pombe] (Z83833) UDP-glucose:sterol glucosyltransferase [Arabidopsis thaliana] "glycogen (starch) synthase isoform 1 [Saccharomyces cerevisiae]"	
22602	ENU06396	ANI61C8385:	26-45	771-790	NAP	1400..3387	g1351714	483	83	2.00E-15	33	44		
22603	ENU06397	ANI61C1122	22-41	395-421	NAP	5..1..442	g2462931	228	100	5.00E-21	42	20		
22604	ENU06398	ANI61C8571	27-46	591-613	NAP	4..1	g136753	726	303	1.00E-81				

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit ncbi gi	Score	Score Prob	% id	% cvrg	Description
22605	ENU06399	ANI61C5996:	24-45	791-816	NAP	g4126481	196	100	1.00E-20	29	98 (AB015352) Akt2 [Alternaria alternata]
22606	ENU06400	ANI61C1158:	63-82	802-829	NAP	g127277	841	254	1.00E-69		mitochondrial phosphate carrier protein (phosphate transport protein) (mitochondrial import receptor) (P32) [Saccharomyces cerevisiae] (Y14855) tropomyosin [Helix aspersa]
22607	ENU06401	ANI61C1029	22-41	413-432	NAP	g4468224	84	48	0.00004	21	33
22608	ENU06402	ANI61C8089:	31-53	767-784	NAP	g117178	147	86	3.00E-16	24	41 benzoate 4-monoxygenase (benzoate-para-hydroxylase) (cytochrome P450 53) [Aspergillus niger]
22609	ENU06403	ANI61C5229:	22-42	725-744	NAP	g1351684	914	87	2.00E-16		hypothetical 420.8 KD protein C1F5.11C in chromosome I [Schizosaccharomyces pombe]
22610	ENU06404	ANI61C1135:	53-72	596-615	NAP	g586531	379	140	1.00E-32	46	98 hypothetical 21.1 KD protein in YM22-CMD1 intergenic region [Saccharomyces cerevisiae]
22611	ENU06405	ANI61C100:1	22-48	802-829	NAP	g4388818	256	157	7.00E-38		(AC006528) putative pol polyprotein with a Zn-finger CCHC type domain (prosite:QDOC50158) and a DDE integrase signature motif [Arabidopsis thaliana]
22612	ENU06406	ANI61C7675:	24-43	809-829	NAP	g120593	192	57	0.000000		L-fucose permease [Escherichia coli]
22613	ENU06407	ANI61C29:98	38-57	714-733	NAP	g2132238	370	151	7.00E-36	39	21 hypothetical protein YPL226w - yeast (Saccharomyces cerevisiae)
22614	ENU06408	ANI61C7767:	22-46	694-712	NAP	g129072	68	49	0.00003	30	57 [Saccharomyces cerevisiae] pyruvate dehydrogenase protein X component precursor [Saccharomyces cerevisiae]
22615	ENU06409	ANI61C6108:	22-46	780-799	NAP	g2342601	656	100	2.00E-20	25	5 (X89442) peptide synthetase [Metarhizium anisopliae]
22616	ENU06410	ANI61C4919:	59-86	628-648	NAP	g586461	272	112	3.00E-24	32	29 hypothetical 104.7 KD protein in PKC1-RTG3 intergenic region [Saccharomyces cerevisiae]
22617	ENU06411	ANI61C1116	22-48	793-820	NAP	g1279693	740	287	6.00E-77	70	19 (X92971) translocation elongation factor [Saccharomyces cerevisiae]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	Score	Score Prob	% id	% cvrg	Description
22618	ENU06412	ANI61C2633:	66-85	343-362	NAP	g1352941	348	151	3.00E-36	53	36	"branched-chain amino acid aminotransferase, cytosolic (BCAT) (TWT2 protein) [Saccharomyces cerevisiae]"
22619	ENU06413	ANI61C1352:	24-44	298-320	NAP	g1176707	81	52	0.000003	28	51	hypothetical 33.0 KD protein in PROB-PROA intergenic region
22620	ENU06414	ANI61C8273:	22-46	804-829	NAP	g1399532	2420	113	2.00E-42	41	24	[Corynebacterium glutamicum] ("U51118) Neurospora crassa NUC-2 (Nuc-2) gene, complete cds.
22621	ENU06415	ANI61C8911:	22-48	641-660	NAP	g3288709	506	193	1.00E-48	46	16	(AB010442) PMR1 [Penicillium digitatum]
22622	ENU06416	ANI61S1445:	780...1		NAP	g730030	141	63	0.000000	16	44	micronuclear linker histone polyprotein (MC1 LH) [Tetrahymena thermophila]
22623	ENU06417	ANI61C7533:	22-42	800-827	NAP	g418391	823	328	2.00E-89	56	75	ZRT1 protein [Saccharomyces cerevisiae]
22624	ENU06418	ANI61C9971:	25-43	292-310	NAP	g1655675	73	67	7.00E-11	33	32	(Z81368) lipK [Mycobacterium tuberculosis]
22625	ENU06419	ANI61C1064	39-66	557-581	NAP	g4176535	417	122	2.00E-38	41	66	(AL035263) putative TFIIH subunit (transcription-repair fac tor)
22626	ENU06420	ANI61C3805:	102-129	413-437	NAP	g1834342	447	186	7.00E-47	53	10	[Schizosaccharomyces pombe] (Z68905) ATP-binding cassette multidrug transporter [Emericella nidulans]
22627	ENU06421	ANI61C3317:	56-75	397-418	NAP	g3702646	59	41	0.0009	29	27	(AL031825) putative membrane transport protein
22628	ENU06422	ANI61C6551:	22-46	723-749	NAP	g3834294	156	55	0.000000	8	0	[Schizosaccharomyces pombe] (U88646) No definition line found [Caenorhabditis elegans]
22629	ENU06423	ANI61C9287:	30-49	802-829	NAP	g1546072	1848	103	1.00E-21			(U68040) polyketide synthase [Cochliobolus heterostrophus]
22630	ENU06424	ANI61C8021:	51-70	805-829	NAP	g3883836	510	125	4.00E-28	30	43	(AF091042) putative cercosporin transporter [Cercospora kikuchii]
22631	ENU06425	ANI61S2328:	33-52	505-527	NAP	g2497183	573	131	2.00E-60	57	17	hypothetical 126.6 KD protein in RPL39-VT11 intergenic region
22632	ENU06426	ANI61C566:3	22-46	805-828	NAP	g3395556	131	43	0.000001	31	72	[Saccharomyces cerevisiae] (AL031180) putative 2-hydroxyacid dehydrogenase [Schizosaccharomyces pombe]

Sed num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database	Hit ncbi gi	Score	Score	Prob	% id	% cvrg	Description
22633	ENU06427	ANI61C7197:	23-46	781-808	NAP	g1170186	1129	316	2.00E-85	53	36	probable ATP-dependent RNA helicase	
22634	ENU06428	ANI61C6444:	24-51	752-775	NAP	g3668171	894	313	1.00E-95	66	22	DBP4 (helicase CA4) (helicase UFI)	
			1..819									[Saccharomyces cerevisiae] (AB006052) RNA polymerase I second-largest subunit [Neurospora crassa]	
22635	ENU06429	ANI61C362:1 ..1628	22-44	801-828	NAP	g2330871	430	174	2.00E-48	41	29	[Z98603] hypothetical protein	
22636	ENU06430	ANI61C1027	5:2528..4163	67-88	727-746	NAP	g1711561	256	50	0.00002			[Schizosaccharomyces pombe] [Saccharomyces cerevisiae] sugar transporter STL1
22637	ENU06431	ANI61C7202:	1217..1			NAP	g1709181	680	192	3.00E-48	47	46	high affinity methionine permease
22638	ENU06432	ANI61C3971:	34-53	726-749	NAP	g3150253	605	178	6.00E-44	39	23	[Saccharomyces cerevisiae] (AL023634) hypothetical protein	
22639	ENU06433	ANI61C2161:	30-49	802-829	NAP	g3730	1119	197	3.00E-75	54	47	[Schizosaccharomyces pombe] (X53424) glycolipid-anchored surface	
22640	ENU06434	ANI61C1116	4:1595..1	27-46	728-747	NAP	g131768	541	136	2.00E-31	34	46	protein [Saccharomyces cerevisiae] quinate permease (quinate transporter)
22641	ENU06435	ANI61C4297:	1275..1678			NAP	g553045	65	47	0.00009	32	64	[M28651] chloroperoxidase
22642	ENU06436	ANI61C1263:	22-49	696-723	NAP	g3810839	375	150	1.00E-35	41	44	[Caldariomyces fumago] (AL032684) conserved hypothetical	
			1..745									zinc-finger protein	
22643	ENU06437	ANI61C8233:	24-43	750-774	NAP	g3947877	540	91	1.00E-54	53	100	[Schizosaccharomyces pombe] (AL034382) putative mitosis and	
			1688..894									maintenance of ploidy protein	
22644	ENU06438	ANI61C3897:			NAP	g1799532	211	59	7.00E-17	30	66	[Schizosaccharomyces pombe] (AB000564) salicylate hydroxylase	
22645	ENU06439	ANI61C2901:	1212..2040			g33342802	197	87	5.00E-17	30	31	[Sphingomonas sp.] (AF061838) putative cytosolic 6-	
			1060..607									phosphogluconate dehydrogenase [Zea mays]	
22646	ENU06440	ANI61C8881:	22-49	725-749	NAP	g2494411	100	37	0.21	28	16	3-(3-hydroxy-phenyl)propionate	
			1327..1									hydroxylase [Escherichia coli]	
22647	ENU06441	ANI61S4274:	35-62	494-519	NAP	g4733982	693	173	3.00E-61			(AC007268) hypothetical protein	
			1..635									[Arabidopsis thaliana]	
22648	ENU06442	ANI61C8550:	51-78	802-821	NAP	g1166378	743	132	2.00E-30	32	25	"(L76169) reverse transcriptase, RNaseH [Glomerella cingulata]"	
			1..2571										

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Basis	Selection Database Hit	ncbi gi	Score	Prob	% id	cvg	Description
22649	ENU06443	ANI61C9556:	36-55	632-651	NAP	g4106657	653	118	5.00E-61	79	50	(AL035064) activator 1 subunit (replication factor subunit)
22650	ENU06444	ANI61C8783:	122-141	519-538	NAP	g1176982	71	59	0.000000	29	41	[Schizosaccharomyces pombe] hypothetical metabolic transport protein in HTPG-iOLR intergenic region
22651	ENU06445	ANI61C4477:	103-130	659-684	NAP	g3702635	288	135	3.00E-31	32	61	(AL031825) hypothetical protein [Schizosaccharomyces pombe]
22652	ENU06446	ANI61C1099	33-52	616-633	NAP	g78100	336	113	2.00E-24	33	37	cyclohexanone monooxygenase (EC 1.14.13.22) - Acinetobacter sp
22653	ENU06447	ANI61C3891:	22-45	456-476	NAP	g3183364	236	94	6.00E-19	34	30	putative transporter C1B3.16C [Schizosaccharomyces pombe]
22654	ENU06448	ANI61S2827:	1..628		NAP	g3808062	134	57	0.000000	20	25	(AB019195) PV100 [Cucurbita maxima]
22655	ENU06449	ANI61C6432:	23-45	721-741	NAP	g3928166	346	149	3.00E-35	35	42	(AJ010317) Sand [Fugu rubripes]
22656	ENU06450	ANI61C6774:	36-55	789-806	NAP	g461623	350	47	2.00E-10	36	21	beta-galactosidase precursor (lactase) [Aspergillus niger]
22657	ENU06451	ANI61S4263:	1..838		NAP	g4218005	300	45	0.0006	29	38	(AC006135) putative vicilin storage protein (globulin-like) [Arabidopsis thaliana]
22658	ENU06452	ANI61C1061	112-131	535-555	NAP	g4049341	99	35	0.52	38	34	(AL034567) putative protein [Arabidopsis thaliana]
22659	ENU06453	ANI61C3499:	22-41	460-479	NAP	g585899	97	56	0.000000	37	100	mitochondrial 60S ribosomal protein L37 precursor (YML37)
22660	ENU06454	ANI61C4192:	153-178	360-386	NAP	g3913969	146	59	2.00E-11	37	28	[Saccharomyces cerevisiae] kynureninase (L-kynurenicine hydrolase) [Rattus norvegicus]
22661	ENU06455	ANI61C1912:	30-49	785-804	NAP	g1723076	270	80	2.00E-21	35	48	hypothetical 57.3 KD protein GMC-type oxidoreductase CY50.03C [Mycobacterium tuberculosis]
22662	ENU06456	ANI61S1424:	1..649		NAP	g228937	211	37	0.11	34	64	Hyp-rich glycoprotein [Zea mays]
22663	ENU06457	ANI61C3442:	50-69	657-675	NAP	g400924	349	101	7.00E-21	24	26	DNA repair protein RAD3 [Schizosaccharomyces pombe]
22664	ENU06458	ANI61C9247:	22-41	808-829	NAP	g3139137	592	111	8.00E-24	36	31	(AF063864) essential nuclear protein Mcm3p [Schizosaccharomyces pombe]
		1..1208										

Seq num	Seq id	Contig source	5 pos	3 pos	Primer Basis	Selection Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvrg	Description
22665	ENU06459	ANI61C1877:	31-51	716-738	NAP	g3288709	1663	267	8.00E-71	54	17	(AB010442) PMR1 [Penicillium digitatum]	
22666	ENU06460	ANI61C1878:	59-82	314-341	NAP	g3041855	180	85	1.00E-16	34	29	(AC004537) similar to tumor suppressor p33ING1; similar to Af044076 (PID:g2829208) [Homo sapiens]	
22667	ENU06461	ANI61C17121:	35-61	451-478	NAP	g1850540	183	56	0.000000	45	99	(U87806) ribosomal P2 phosphoprotein [Alternaria alternata]	
22668	ENU06462	ANI61C1054:	28-49	700-719	NAP	g3183342	235	73	1 6.00E-28	38	54	hypothetical 44.5 KD protein C14C4.09 in chromosome I	
22669	ENU06463	ANI61C8705:	1..943	NAP	g2213552	369	163	1.00E-39	35	44	[Schizosaccharomyces pombe] (Z97052) hypothetical protein [Schizosaccharomyces pombe]		
22670	ENU06464	ANI61C4350:	1..602	NAP	g1174862	141	52	4.00E-14	41	33	putative ubiquitin carboxyl-terminal hydrolase C13A11.04C (ubiquitin thioesterase) (ubiquitin-specific processing protease) (deubiquitinating enzyme) [Schizosaccharomyces pombe]		
22671	ENU06465	ANI61C7356:	22-48	803-828	NAP	g231993	2396	388	e-107			succinate dehydrogenase (ubiquinone) flavoprotein subunit precursor (FF) (flavoprotein subunit of complex II) [Saccharomyces cerevisiae]	
22672	ENU06466	ANI61C2512:	418..2288	NAP	g2492798	485	179	9.00E-47	48	62	aryl-alcohol dehydrogenase (NADP+) (AAD) [Phanerochaete chrysosporium]		
22673	ENU06467	ANI61S1309:	653..1	NAP	g2959371	670	265	4.00E-72	64	38	(AL022117) asparagine synthetase [Schizosaccharomyces pombe]		
22674	ENU06468	ANI61S3208:	594..267	NAP	g117820	515	132	4.00E-42	96	50	cytochrome B6 [Spinacia oleracea]		
22675	ENU06469	ANI61S5578:	1..612	NAP	g1131489	72	45	0.0005	25	58	"(U42580) Pro-rich protein; PAPK (24X); similar to Triticum PK-rich protein, corresponds to GenBank Accession Number X52472		
22676	ENU06470	ANI61S1366:	1..686	NAP	g283032	153	60	0.000000	33	64	[Paramaecium bursaria Chlorella virus 1]" hydroxyproline-rich glycoprotein - perennial teosinte [Zea diploperennis]		

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database	Hit	ncbi gi	Score	Score	Blast Prob	% id	% cvrg	Description
22677	ENU06471	ANI61C1037	22-48	549-576	NAP		g117619	121	50	5.00E-10	27	28	100	probable peroxisomal membrane protein PMP20 (allergen ASP F 3)
22678	ENU06472	ANI61C5116:	22-45	640-660	NAP		g3219959	290	87	1.00E-16	39	34	[Aspergillus fumigatus] probable zinc metallopeptidase	
22679	ENU06473	ANI61C1063	136-160	541-560	NAP		g2146836	1134	270	7.00E-72	56	32	C17A5.04C precursor [Schizosaccharomyces pombe]	
22680	ENU06474	ANI61C1118	89-108	730-749	NAP		g3929357	223	87	2.00E-16	37	34	[Saccharomyces cerevisiae] hypothetical protein YCL054w - yeast	
22681	ENU06475	ANI61C7956:	22-46	617-644	NAP		g1168351	414	76	2.00E-13	38	71	O-methylsterigmatocystin oxidoreductase (OMST) (cytochrome P450 64) [Aspergillus parasiticus]	
22682	ENU06476	ANI61C8967:	22-48	802-829	NAP		g1723751	446	80	4.00E-28	72	42	[Bacillus stearothermophilus] alcohol dehydrogenase (ADH) hypothetical 34.9 KD protein in SMI-PHO81 intergenic region	
22683	ENU06477	ANI61S4000:	214-231	401-420	NAP	472..1								[Saccharomyces cerevisiae] [Schizosaccharomyces pombe] (AL049769) mitochondrial 60s ribosomal protein I10 precursor (I07492) sugar transport protein [Saccharomyces cerevisiae]
22684	ENU06478	ANI61C6670:	87-106	380-398	NAP	1400..1791		g4760344	167	49	0.00002			[X99340] nucleic acid binding protein [Drosophila melanogaster]
22685	ENU06479	ANI61C2264:	49-68	760-780	NAP	1412..43		g409547	261	56	2.00E-16	29	47	(AB018537) elongation factor 3 (Yarrowia lipolytica) [Yarrowia lipolytica]
22686	ENU06480	ANI61C4164:	52-71	662-683	NAP	1348..2131		g1770212	175	81	1.00E-21	29	59	(AL022304) putative long-chain-fatty-acid--coa ligase [Schizosaccharomyces pombe]
22687	ENU06481	ANI61C1984:	1..1014		NAP		g3776152	873	195	2.00E-84	62	55	dihydrolipoamide dehydrogenase precursor [Saccharomyces cerevisiae] (AC007369) Similar to RNA helicases [Arabidopsis thaliana]	
22688	ENU06482	ANI61C5698:	189-210	786-813	NAP	925..1		g3006179	436	139	2.00E-32	45	32	molybdopterin biosynthesis MOEA protein [Synechococcus sp.]
22689	ENU06483	ANI61C6002:	111-130	295-314	NAP	1831..1443		g118678	462	132	4.00E-46			
22690	ENU06484	ANI61S2737:	1..928		NAP		g4836896	198	63	0.000000	002			
22691	ENU06485	ANI61S4388:	64-83	296-315	NAP	470..1		g2497956	114	71	4.00E-12	27	40	

Seq num	Seq id	Contig source	5 pos	Primer 3 pos	Primer Basis	Selection Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
22692	ENU06486	ANI61C1404:	22-48	629-647	NAP	g729296	180	76	2.00E-13	31	76	[Corynebacterium glutamicum]	dihydodicarboxylate synthase (DHDPS)
22693	ENU06487	ANI61C4023:	37-56	621-640	NAP	g1352956	1303	381	e-105	68	43	[Corynebacterium glutamicum]	hypothetical 75.5 KD protein in CCT3-CCT8 intergenic region
22694	ENU06488	ANI61S3272:	40-67	391-415	NAP	g2257528	597	209	4.00E-55	70	26	[Saccharomyces cerevisiae]	(AB004537) methionyl-tRNA synthetase [Schizosaccharomyces pombe]
22695	ENU06489	ANI61C6841:	22-46	803-829	NAP	g231361	910	308	4.00E-83	58	81	[Pseudomonas sp.]	l-aminoacylcopropane-1-carboxylate deaminase (ACC deaminase)
22696	ENU06490	ANI61S2126:	195-220	405-431	NAP	g1706695	96	34	0.48	26	31	[Saccharomyces cerevisiae]	phosphomevalonate kinase
22697	ENU06491	ANI61C7863:	107-126	725-744	NAP	g1175491	570	129	4.00E-58	51	82	[Schizosaccharomyces pombe]	hypothetical 33.9 KD protein C16C9.02C in chromosome I
22698	ENU06492	ANI61C1117	22-43	360-379	NAP	g1546072	289	118	3.00E-26	40	6	[Cochliobolus heterostrophus]	(U68040) polyketide synthase
22699	ENU06493	ANI61C9611:	22-47	777-804	NAP	g2623175	982	226	2.00E-98	65	67	[AF030425]	pyruvate dehydrogenase E1 component alpha subunit [Pichia stipitis]
22700	ENU06494	ANI61C4200:	22-45	508-531	NAP	g3560136	534	138	4.00E-53	54	32	(AL031534)	2-isopropylmalate synthase. [Schizosaccharomyces pombe]
22701	ENU06495	ANI61C8517:	89-108	412-432	NAP	g128862	354	154	4.00E-37	51	55	[Schizosaccharomyces pombe]	NADH-ubiquinone oxidoreductase 30.4 KD subunit precursor (complex I-30KD) (CI-31KD) [Z98981]
22702	ENU06496	ANI61C2596:	22-44	724-748	NAP	g2388993	693	129	3.00E-29	34	14	[Schizosaccharomyces pombe]	putative sodium channel
22703	ENU06497	ANI61S3056:	1..536		NAP	g228937	164	53	0.000001	34	53	[Zea mays]	Hyp-rich glycoprotein
22704	ENU06498	ANI61C2202:	57-76	770-789	NAP	g3122099	1167	433	e-121	72	81	[Gibberella fujikuroi]	farnesyl pyrophosphate synthetase (FPP synthetase) (FPPS) (farnesyl diphosphate synthetase) (dimethylallyltransferase / geranyltransferase [Gibberella fujikuroi])
22705	ENU06499	ANI61C7060:	43-62	412-435	NAP	g2098616	210	100	7.00E-21	38	25	[U73900)	2-hydroxybiphenyl-3-monoxygenase [Pseudomonas azelaica]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database	Hit	ncbi gi	aat	Blast Score	Blast Prob	% id	% cvrg	Description
22706	ENU06500	ANI61C6470:	40-64	801-824	NAP		g2497989	681	212	4.00E-54	49	65		putative mitochondrial carrier YMR166C [Saccharomyces cerevisiae]
22707	ENU06501	ANI61C4397:	45-66	799-818	NAP		g2408036	655	211	5.00E-54	43	67		(Z99163) putative threonine aldolase [Schizosaccharomyces pombe]
22708	ENU06502	ANI61C7311:	31-52	795-822	NAP		g1345823	910	202	3.00E-51	47	52		nitrate transporter (nitrate permease) [Emericella nidulans]
22709	ENU06503	ANI61C294:4	28-48	808-827	NAP		g225924	273	51	7.00E-14				uracil transport protein [Saccharomyces cerevisiae]
22710	ENU06504	ANI61C7960:	22-45	780-799	LINAP		g728904	1577	261	3.00E-69	50	22		calcium-transferring ATPase 2 (vacuolar CA2+-ATPase); Ca2+-transporting ATPase (EC 3.6.1.38) - yeast [Saccharomyces cerevisiae]; (U03060) calcium ATPase [Saccharomyces cerevisiae]; (Z72528) ORF YGL006w [Saccharomyces cerevisiae]
22711	ENU06505	ANI61C7336:	22-44	790-809	LINAP		g3915140	201	113	2.00E-24	32	45		isotrichodermin C-15 hydroxylase (cytochrome P450 65A1); (AF011355) isotrichodermin C-15 hydroxylase [Fusarium sporotrichioides]
22712	ENU06506	ANI61C3911:	42-61	750-770	LINAP		g464369	220	64	5.00E-16	31	37		phenol 2-monoxygenase (phenol hydroxylase); (L04488) phenol hydroxylase [Trichosporon cutaneum] (AL034353) putative major facilitator family multi-drug resistance protein [Schizosaccharomyces pombe]
22713	ENU06507	ANI61C7950:	22-48	680-699	LINAP		g3925779	125	70	1.00E-11	22	41		hypothetical 102.5 KD protein in YPT52-DBP7 intergenic region; hypothetical protein YKR021w - yeast (Saccharomyces cerevisiae); (Z28246) ORF YKR021w [Saccharomyces cerevisiae]
22714	ENU06508	ANI61C9771:	24-45	451-471	LINAP		g549594	41	54	0.000000	33	15		
22715	ENU06509	ANI61C3160:	22-48	562-581	LINAP		g1582765	59	36	0.31	36	24		YFW1 gene [Saccharomyces cerevisiae]
22716	ENU06510	ANI61C6787:	23-42	671-690	LINAP		g3116145	494	208	3.00E-53	43	41		(AL023290) hypothetical protein [Schizosaccharomyces pombe]
		795..1												

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database	Hit ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
22717	ENU06511	ANI61C7358:	30-49	705-730	LINAP	g124211	772	34	0.98				(M36378) translational initiation factor IF-2; (Z99296) beta-transducin [Schizosaccharomyces pombe]
22718	ENU06512	ANI61C801:8	22-47	752-773	LINAP	g4522004	367	164	5.00E-40	37	46	"(AC007069) putative histidine kinase, sensory transduction [Arabidopsis thaliana]"	
22719	ENU06513	ANI61C3916:	22-46	776-795	LINAP	g2662028	577	166	2.00E-40	35	32	(AL031587) dJ1039K5.2 (similar to monocarboxylate transporter (MCT3)) [Homo sapiens]	
22720	ENU06514	ANI61C6734:	23-45	439-458	LINAP	g4464201	120	66	2.00E-10	30	24	(AL023780) putative mRNA stability protein [Schizosaccharomyces pombe] (AF101074) step II splicing factor SLU7 [Homo sapiens]	
22721	ENU06515	ANI61C7353:	50-69	790-809	LINAP	g3184110	716	87	2.00E-16			[Schizosaccharomyces pombe] (Z98981) putative sodium channel [Schizosaccharomyces pombe] putative importin beta-4 subunit (karyopherin beta-4 subunit); (AL023780) putative importin beta-4 subunit [Schizosaccharomyces pombe] neurofilament triplet H1 protein - rabbit (fragment); (M94315) neurofilament-H [Oryctolagus cuniculus]	
22722	ENU06516	ANI61C9768:	30-57	713-735	LINAP	g4249705	449	215	4.00E-55	38	48	[Schizosaccharomyces pombe] (916..1) (AL035075) conserved hypothetical SH3 domain-containing protein [Schizosaccharomyces pombe]	
22723	ENU06517	ANI61C3176:	32-55	781-800	LINAP	g4107314	191	61	8.00E-18	29	52	(Z98981) putative importin beta-4 subunit [Schizosaccharomyces pombe] putative importin beta-4 subunit (karyopherin beta-4 subunit); (AL023780) putative importin beta-4 subunit [Schizosaccharomyces pombe] neurofilament triplet H1 protein - rabbit (fragment); (M94315) neurofilament-H [Oryctolagus cuniculus]	
22724	ENU06518	ANI61C7404:	114-133	709-730	LINAP	g2388993	644	143	2.00E-33	29	15	[Schizosaccharomyces pombe] (1..1861 1..1337) (U56098) FacB [Aspergillus oryzae]	
22725	ENU06519	ANI61C3918:	28-47	803-829	LINAP	g4033414	905	110	1.00E-23	31	24	[Schizosaccharomyces pombe] putative importin beta-4 subunit (karyopherin beta-4 subunit); (AL023780) putative importin beta-4 subunit [Schizosaccharomyces pombe] neurofilament triplet H1 protein - rabbit (fragment); (M94315) neurofilament-H [Oryctolagus cuniculus]	
22726	ENU06520	ANI61C6734:	22-48	632-654	LINAP	g284667	111	46	0.0002			[Schizosaccharomyces pombe] (4810..5529)	
22727	ENU06521	ANI61C3180:	50-69	798-817	LINAP	g2262189	91	64	0.000000			[Schizosaccharomyces pombe] (1499..2664)	
22728	ENU06522	ANI61C6786:	22-45	314-340	LINAP	g2132273	99	59	0.000000			[Saccharomyces cerevisiae]; (U51033) P9513.3 gene product [Saccharomyces cerevisiae]	
22729	ENU06523	ANI61C7390:	31-50	809-828	LINAP	g2388994	1466	235	2.00E-62	54	46	[Schizosaccharomyces pombe] (Z98981) hypothetical gtp-binding protein associated	
			313..1205									[Schizosaccharomyces pombe] (229753) hypothetical protein [Schizosaccharomyces pombe] (3207..1743)	

Sed num	Seq id	Contig source	5 pos	Primer 3 pos	Primer Basis	Selection Database	aat ncbi gi	Score	Score Prob	% id	% cvg	Description
22731	ENU06525	ANI61C378:4	22-46	550-569	LINAP	g2271503	90	57	0.000000	26	46	(AF009672) unknown [Acinetobacter sp. ADP1]
22732	ENU06526	ANI61C679:0:	567..5166		LINAP	g2688966	748	275	2.00E-73	51	46	[Magnaporthe grisea] "glucoamylase S1/S2 precursor (glucan glucohydrolase) ; glucan 1,4-alpha-glucosidase (EC 3.2.1.3) - yeast (Saccharomyces cerevisiae) ; (Z38061) mal5, stal, len: 1367, CAI: 0.3, AMYH_YEAST P08640 glucoamylase S1 (EC 3.2.1.3) [Saccharomyces cerevisiae] ; (U30626) glucoamylase [Saccharomyces cerevisiae var. diastaticus]"
22733	ENU06527	ANI61C741:6	38-57	805-829	LINAP	g728850	107	53	0.000003			
			1..979									
22734	ENU06528	ANI61C739:3	22-46	785-804	LINAP	g547769	561	177	7.00E-44	44	54	KES1 protein ; KES1 protein - yeast (Saccharomyces cerevisiae) ; (U03913) Kes1p [Saccharomyces cerevisiae] ; (U43703) Kes1p [Saccharomyces cerevisiae] ; (Z73501) ORF YPL145c [Saccharomyces cerevisiae] ; (X96770) P2614 product [Saccharomyces cerevisiae]
22735	ENU06529	ANI61C979:8	22-45	734-761	LINAP	g522302	1289	182	3.00E-45	40	23	(L35053) endonuclease [Magnaporthe grisea]
22736	ENU06530	ANI61C3204:	22-42	679-706	LINAP	g1169871	1040	120	4.00E-65	65	29	GCN20 protein ; GCN20 protein - yeast (Saccharomyces cerevisiae) ; (U19971) Gen20p [Saccharomyces cerevisiae] ; (D50617) YFR009W [Saccharomyces cerevisiae]
22737	ENU06531	ANI61C680:7	22-45	727-748	LINAP	g4499840	209	93	2.00E-18	33	7	(AJ011964) d-l-xyerugly-peptide-synthetase [Claviceps purpurea] (AL031852) conserved protein-PHD-finger family [Schizosaccharomyces pombe]
22738	ENU06532	ANI61C979:2	22-45	762-781	LINAP	g3738149	190	36	0.27			
			1991..1121									

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	Score	Score Prob	% id	% cvrg	Description	
22739	ENU06533	ANI61C6772:	54-73	627-647	LINAP	g3877858	68	51	0.000007			(Z34801) Similarity with drosophila MSP-300 protein (PIR acc. no. S30431) [Caenorhabditis elegans]; (Z66514) Similarity with drosophila MSP-300 protein (PIR acc. no. S30431) [Caenorhabditis elegans] (AB010810) phospholipase D [Candida albicans]	
22740	ENU06534	ANI61C8028:	113-132	569-588	LINAP	g3413518	711	291	4.00E-78	68	11	(U89352) lysophospholipase I [Mus musculus]; (U97148) calcium-independent phospholipase A2 isoform 2 [Oryctolagus cuniculus]	
22741	ENU06535	ANI61C8042:	23-42	775-794	LINAP	g1864159	214	85	7.00E-19	33	91	[hypothetical 30.9 KD protein K07C11.7 in chromosome V; (U53336) coded for by C. elegans cDNA cm12g2; coded for by C. elegans cDNA yk56a6.5; coded for by C. elegans cDNA yk70a12.5; coded for by C. elegans cDNA cm11d9; coded for by C. elegans cDNA yk102d1.5; coded for by C. elegans cDNA yk102d1.3;....]	
22742	ENU06536	ANI61C3954:	102-128	421-440	LINAP	g3025256	118	67	1.00E-10	37	39	(AL031743) conserved hypothetical protein [Schizosaccharomyces pombe] (Z99165) protein kinase [Schizosaccharomyces pombe] (Z99568) putative regulatory protein; zinc finger [Schizosaccharomyces pombe] (U23517) similar to ubiquitin conjugating enzyme [Caenorhabditis elegans] (AL035076) putative allantate permease [Schizosaccharomyces pombe]	
22743	ENU06537	ANI61C8012:	48-67	456-479	LINAP	g3650394	77	52	0.000003	30	61		
22744	ENU06538	ANI61C7420:	3101..2742	1040..48	LINAP	g2408067	860	280	8.00E-75	50	44		
22745	ENU06539	ANI61C805:8	22-42	803-829	LINAP	g2462679	138	66	4.00E-10	24	26		
22746	ENU06540	ANI61C7418:	1135..1594	105-124	363-381	LINAP	g746510	310	144	3.00E-34	48	48	
22747	ENU06541	ANI61C3955:	1386..2039	27-46	519-538	LINAP	g4107287	320	85	5.00E-36	43	39	

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database	Hit ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
22748	ENU06542	ANI61C7422:	25-44	486-508	LINAP		g731584	125	41	0.007			hypothetical 17.1 KD protein in PURS
		838..1366											3'region ; hypothetical protein
22749	ENU06543	ANI61C3946:	24-51	803-829	LINAP		g2104460	359	124	7.00E-28	34	25	(Z95397) unknown
		1..2030											[Schizosaccharomyces pombe]
22750	ENU06544	ANI61C9800:	41-68	648-669	LINAP		g4100186	110	43	0.002			(U95159) gelsolin-related protein
		2754..2065											GRPI25 [Dictyostelium discoideum]
22751	ENU06545	ANI61C3970:	34-61	722-744	LINAP		g3885836	333	156	2.00E-37	36	45	(AF091042) putative cercosporin
		853..1											transporter [Cercospora kikuchii]
22752	ENU06546	ANI61C3143:	35-54	810-829	LINAP		g3435078	362	154	8.00E-43	40	46	(U74380) cholinesterase 1
		7868..8751											[Branchiostoma floridana]
22753	ENU06547	ANI61C3210:	22-46	516-543	LINAP		g2058526	63	40	0.009			(U78523) histidine secretory acid
		894..1457											phosphatase [Leishmania donovani]
22754	ENU06548	ANI61C8088:	108-127	801-820	LINAP		g3413518	467	94	2.00E-35	38	14	(AB010810) phospholipase D
		1555..687											[Candida albicans]
22755	ENU06549	ANI61C7429:	31-49	465-485	LINAP		g2493391	303	145	2.00E-34	43	38	P450 monooxygenase STCB
		2809..3315											(cytochrome P450 62); (U34740)
													putative p450 monooxygenase
22756	ENU06550	ANI61C397:1	22-48	739-758	LINAP		g462350	324	33	2.3			[Emericella nidulans]
		674..1											sperm histone P2 precursor (protamine
													P2); protamine P2 - rhesus macaque ;
22757	ENU06551	ANI61C3228:	50-69	492-512	LINAP		g3044087	217	94	1.00E-18			(X71338) Protamine P2 [Macaca
		645..1352											mullata]
													(AF055904) acetylornithine
													deacetylase; ArgE [Myxococcus
													xanthus]
22758	ENU06552	ANI61C9804:	41-60	417-438	LINAP		g462414	320	135	2.00E-31	52	23	amino-acid permease INDA1 ; INDA1
		3576..4030											protein - fungus (Trichoderrina
													harzianum); (Z22594) INDA1
22759	ENU06553	ANI61C7396:	22-44	806-827	LINAP		g1076090	349	139	2.00E-32	33	54	[Trichoderma harzianum]
		4450..3405											probable oxygenase - Streptomyces
													fradiae ; (X87093) putative oxygenase
													[Streptomyces fradiae]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database	Hit ncbi gi	Score	Score Prob	% id	% cvrg	Description	
22760	ENU06554	ANI61C3230:	69..87	625..649	LINAP	g1730591	132	76	2.00E-13			hypothetical 41.1 KD protein ON CDC91-PAU4 intergenic region ; hypothetical protein YLR46c - yeast (Saccharomyces cerevisiae) ; (U22383)	
22761	ENU06555	ANI61C9803:	22..49	806..829	LINAP	g586486	328	71	2.00E-26	32	38	Ylr460cp [Saccharomyces cerevisiae] hypothetical 77.3 KD protein in FIG1-GIP1 intergenic region ; probable membrane protein YBR043c - yeast (Saccharomyces cerevisiae) ; (Z35912) ORF YBR043c [Saccharomyces cerevisiae]	
22762	ENU06556	ANI61C3999:	122..141	264..289	LINAP	g3581887	70	48	0.00002			"(AL031540) internalin- related, Leucine rich repeat containing protein [Schizosaccharomyces pombe]" (AB010466) multidrug resistance-associated protein (MRP)-like protein-1 (MLP-1) [Rattus norvegicus] ; (U73038) multidrug resistance-associated protein 6 [Rattus norvegicus]	
22763	ENU06557	ANI61C3208:	22..47	794..813	LINAP	g3242458	382	111	2.00E-36	38	15	(AL035637) glycoprotein endopeptidase-like protein. [Schizosaccharomyces pombe] (AL031179) importin beta subunit [Schizosaccharomyces pombe] cutinase transcription factor 1 beta ; (U51672) cutinase transcription factor 1 [Fusarium solani f. sp. pisi] N amino acid transport system protein (methyltryptophan resistance protein) ; neutral amino acid permease - Neurospora crassa ; (L34605) neutral amino acid permease [Neurospora crassa]	
22764	ENU06558	ANI61C9820:	588..235		LINAP	g4481949	149	63	7.00E-11	44	33		
22765	ENU06559	ANI61C7446:	1..1120	27..54	650..669	LINAP	g3395584	843	229	2.00E-59	42	25	
22766	ENU06560	ANI61C318:5	44..1929	23..50	792..819	LINAP	g1706177	210	110	1.00E-23	26	28	
22767	ENU06561	ANI61C9777:	22..46	810..829	LINAP	g2507070	253	51	0.000009				

Seq num	Seq id	Contig source	5 pos	3 pos	Primer Basis	Primer	Selection	aat	Blast	Blast	%	
					Database	Hit	ncbi gi	Score	Score	Prob	% id	cvg
22768	ENU06562	ANI61C7436:	125-152	437-464	LINAP	g2499507	211	46	0.000000	32	28	"6-phosphofructo-2-kinase / fructose-2,6-bisphosphatase liver isozyme (6PF-2-K/FRU-2,6-P2ASE) ; 6-phosphofructo-2-kinase (EC 2.7.1.105) / fructose-2, 6-bisphosphate 2'-phosphatase (EC 3.1.3.46) - chicken ; (S54076) 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase [chickens, liver, Peptide, 469 aa] [Gallus gallus]"
22769	ENU06563	ANI61C318:3	50-77	454-479	LINAP	g2764632	651	233	8.00E-61	73	73	(AJ001520) 19.3kD iron-sulfur subunit of mitochondrial complex I [Neurospora crassa]
22770	ENU06564	ANI61C9796:	22-48	453-472	LINAP	g2149953	141	56	9.00E-18	39	10	(U97066) sulfotyrosylurea receptor 2B [Mus musculus]
22771	ENU06565	ANI61C3216:	28-47	515-534	LINAP	g2894086	118	65	5.00E-10	38	36	(Y11395) seventransmembrane-domain protein [Homo sapiens]
22772	ENU06566	ANI61C4015:	64-83	494-513	LINAP	g2414599	74	52	0.000004	32	38	(Z99295) dihydrofolate reductase [Schizosaccharomyces pombe]
22773	ENU06567	ANI61C7419:	22-44	783-810	LINAP	g133323	68	63	0.000000	003		DNA-directed RNA polymerase II largest subunit (RPB1) ; DNA-directed RNA polymerase (EC 2.7.7.6) II large chain - Chinese hamster (fragment) ; (M19538) RNA polymerase II largest subunit [Cricetulus griseus]
22774	ENU06568	ANI61C7451:	1913-2465		LINAP	g2347100	423	136	3.00E-33	40	50	(U76846) ubiquitin-specific protease [Arabidopsis thaliana] ; (AC007168) putative ubiquitin-specific protease [Arabidopsis thaliana]
22775	ENU06569	ANI61C3238:	81-100	715-737	LINAP	g1077530	263	96	4.00E-24	32	48	hypothetical protein YDR132c - yeast (Saccharomyces cerevisiae) ; (Z48179) unknown [Saccharomyces cerevisiae] NA(+)/H(+) antiporter 2 ; (AB010106) Zsod22p [Zygosaccharomyces rouxii]
22776	ENU06570	ANI61C3257:	53-72	715-734	LINAP	g3914096	214	116	2.00E-25	38	24	

Seq num	Seq id	Contig source	Primer 3 pos	Primer Basis	Selection Database Hit	ncbi gi	aat Score	Blast Score	% id	% cvrg	Description	
22777	ENU06571	ANI61C7427:	41-60	769-788	LINAP	g549627	997	127	1.00E-28	39	37	hypothetical 83.6 KD protein in CCP1-MET1 intergenic region ; hypothetical protein YBL011w homolog YKR067w - yeast ( <i>Saccharomyces cerevisiae</i> ) ; (Z28292) ORF YKR067w
22778	ENU06572	ANI61C4052:	26-46	802-829	LINAP	g1351681	479	141	5.00E-33	36	31	[ <i>Saccharomyces cerevisiae</i> ] heat shock protein 70 homolog precursor ; (Z68136) unknown [Schizosaccharomyces pombe] ("AJ002397) beta-1,3 exoglucanase [Trichoderma harzianum]" trichodiene oxygenase (cytochrome P450 58) ; trichodiene oxygenase 4 - fungus ( <i>Fusarium sporotrichioides</i> ) ; (U22462) trichodiene oxygenase [ <i>Fusarium sporotrichioides</i> ] (AF008915) EVI-5 homolog [Homo sapiens]
22779	ENU06573	ANI61C8108:	102-127	532-558	LINAP	g2924313	226	124	5.00E-28	35	18	(AF053084) putative cinnamyl alcohol dehydrogenase [Malus domestica] hypothetical amino-acid permease in STE3-GIN10 intergenic region ; probable transport protein YKL174c - yeast ( <i>Saccharomyces cerevisiae</i> ) ; (Z26678) unknown [ <i>Saccharomyces cerevisiae</i> ] ; (Z28174) ORF YKL174c [ <i>Saccharomyces cerevisiae</i> ] ; ORF [ <i>Saccharomyces cerevisiae</i> ] (AL023288) hypothetical protein [Schizosaccharomyces pombe] (AL022305) putative transcription factor [Schizosaccharomyces pombe] salicylate 1-monoxygenase (EC 1.14.13.1) - Pseudomonas putida ; (X83926) salicylate 1-monoxygenase [Pseudomonas putida] (AF110766) transcription factor AFLR [Aspergillus parasiticus]
22780	ENU06574	ANI61C4051:	37-63	453-475	LINAP	g3915154	70	47	0.00007			
22781	ENU06575	ANI61C3252:	32-51	765-792	LINAP	g3093476	306	157	7.00E-38	33	31	
22782	ENU06576	ANI61C7454:	22-48	617-642	LINAP	g2981475	108	74	1.00E-15	31	60	
22783	ENU06577	ANI61C7447:	22-46	809-829	LINAP	g549738	610	158	4.00E-38	33	45	
22784	ENU06578	ANI61C4067:	24-43	803-829	LINAP	g3116134	379	141	6.00E-33	36	10	
22785	ENU06579	ANI61C3274:	35-55	801-820	LINAP	g3006175	524	196	2.00E-49	39	53	
22786	ENU06580	ANI61C4055:	66-85	454-473	LINAP	g1073049	70	69	1.00E-11	28	36	
22787	ENU06581	ANI61C3287:	22-48	459-478	LINAP	g4581773	111	62	0.000000	32	24	
			865..1187			002						

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Score	Blast Prob	% id	% cvrg	Description
22788	ENU06582	ANI61C815:1	22-49	776-802	LINAP	g2497523	820	260	1.00E-68	50	16	kinesin-like protein KIF1A (axonal transporter of synaptic vesicles); (X00840) axonal transporter of synaptic vesicles [Homo sapiens] (AB017641) polyketide synthase [Micromonospora griseorubida] (AL035161) putative secreted peptidase [Streptomyces coelicolor]	
22789	ENU06583	ANI61C4055:	25-48	724-747	LINAP	g84586928	757	263	9.00E-70	43	6	probable phosphatidylinositol-4-phosphate 5-kinase FAB1 (1-phosphatidylinositol-4-phosphate kinase) (PIP5K) (PTDINS4)(P-5-kinase) (diphosphoinositide kinase); (U01017) Fab1p [Saccharomyces cerevisiae]	
22790	ENU06584	ANI61C8073:	32-58	552-572	LINAP	g4154074	76	56	0.000000	36	27	[Schiosaccharomyces pombe] (U97191) similar to nucleoporins [Caenorhabditis elegans]	
22791	ENU06585	ANI61C3281:	40-59	811-829	LINAP	g462047	759	225	4.00E-58	36	12	"(U93872) ORF 73, contains large complex repeat CR 73 [Kaposi's sarcoma-associated herpesvirus] " (M63836) beta-glucuronidase [Mus musculus]	
22792	ENU06586	ANI61C7469:	102-127	415-441	LINAP	g3873550	95	41	0.004			(AL035334) serine-rich protein [Schiosaccharomyces pombe]	
22793	ENU06587	ANI61C4090:	69-87	500-519	LINAP	g1943773	94	47	0.00008	34	22	"(U93872) ORF 73, contains large complex repeat CR 73 [Kaposi's sarcoma-associated herpesvirus] " (M63836) beta-glucuronidase [Mus musculus]	
22794	ENU06588	ANI61C8141:	67-86	740-759	LINAP	g2246532	148	60	0.000000	20	24	"(U93872) ORF 73, contains large complex repeat CR 73 [Kaposi's sarcoma-associated herpesvirus] " (M63836) beta-glucuronidase [Mus musculus]	
22795	ENU06589	ANI61C329:1			LINAP	g193723	458	59	2.00E-21	33	41	"(U93872) ORF 73, contains large complex repeat CR 73 [Kaposi's sarcoma-associated herpesvirus] " (M63836) beta-glucuronidase [Mus musculus]	
22796	ENU06590	ANI61C7490:	27-54	729-749	LINAP	g2873363	841	237	8.00E-62	47	39	(U89492) arylsulfatase [Neurospora crassa]	
22797	ENU06591	ANI61C817:1	127...1	459-478	LINAP	g2654086	167	57	0.000000			(AF033013) Notch homolog [Bombyx mori]	
22798	ENU06592	ANI61C409:4	052..594	22-45	LINAP	g4455041	77	33	0.8			(AF116463) unknown [Streptomyces lincolnenensis]	
22799	ENU06593	ANI61C8142:	619..4038	117-135	LINAP	g2688966	449	130	8.00E-30	68	24	(AF027979) carnitine acetyl transferase [Magnaporthe grisea]	
22800	ENU06594	ANI61C7484:	1160..1665	22-41	LINAP	g4107317	222	104	4.00E-22	38	27	(AL035075) putative transcription factor frib component	
22801	ENU06595	ANI61C814:1	.347	5427..5005	LINAP	g226788	86	64	3.00E-10	41	5	[Schizosaccharomyces pombe] erythrocyte ankyrin [Homo sapiens]	
22802	ENU06596	ANI61C411:6	9..58		LINAP	g4335756	99	65	3.00E-10	30	66	[Arabidopsis thaliana]	

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database	Hit ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
22803	ENU06597	ANI61C814:5	23-50	796-823	LINAP	g2342601	805	100	3.00E-34	33	5	(X89442) peptide synthetase [Metarhizium anisopliae]	
22804	ENU06598	ANI61C413: 92-111	456-479	LINAP	g557084	78	56	0.000000	32	10	(L35601) ankyrin [Drosophila melanogaster]; ankyrin [Drosophila melanogaster]		
22805	ENU06599	ANI61C7512: 48-74 1..828	770-789	LINAP	g3859678	398	185	3.00E-46	36	30	(AL033503) conserved hypothetical protein [Candida albicans]		
22806	ENU06600	ANI61C3310: 22-43	541-560	LINAP	g2791489	156	70	1.00E-14	38	36	(AL021246) hypothetical protein Rv2449c [Mycobacterium tuberculosis]		
22807	ENU06601	ANI61C3306: 22-48 1895..310	806-829	LINAP	g1546072	714	129	2.00E-50	45	10	(U68040) polyketide synthase [Cochliobolus heterostrophus]		
22808	ENU06602	ANI61C413: 2028..1713	LINAP	g730197	54	43	0.0005	31	18	protein N-terminal amidase (NT-amidase); amino-terminal amidase NTA1 - yeast (Saccharomyces cerevisiae); (L3564) N-terminal amidase [Saccharomyces cerevisiae]; (Z49562) ORF YJR062c [Saccharomyces cerevisiae]; (L47993) ORF YJR062c [Saccharomyces cerevisiae]			
22809	ENU06603	ANI61C8187: 29-48 409..1	460-479	LINAP	g2497685	51	55	0.000000	2	platelet-activating factor acetylhydrolase precursor (PAF acetylhydrolase) (LDL-associated phospholipase A2) (LDL-PLA(2)) (2-acetyl-1-alkylglycerophosphocholine esterase) (1-alkyl-2-acetylglycerophosphocholine esterase) (U34246) plasma PAF acetylhydrolase [Canis familiaris]; platelet-activating factor acetylhydrolase [Canis familiaris]			
22810	ENU06604	ANI61C413:1 49-68 205..1889	612-631	LINAP	g3153851	236	94	1.00E-27	41	38	(AF064524) carboxylesterase [Anisopteromalus calandra]		
22811	ENU06605	ANI61C8185: 107-126 1..715	672-693	LINAP	g1352321	561	137	9.00E-32	45	57	ubiquitin-like protein DSK2; (L40587) ubiquitin-like protein [Saccharomyces cerevisiae]		

Seq num	Seq id	Contig source	5 pos	Primer 3 pos	Primer Basis	Selection Database Hit	ncbi gi	aat	Blast Score	Blast Prob	% id	% cvrg	Description
22812	ENU06606	ANI61C8180:	25-51	805-827	LINAP	g4522026	74	40	0.018				"(AC004886) C-terminus matches KIAA0559, N-terminus similar to Basson protein; match to PID:g3043642; similar to PID:g3413810 [Homo sapiens]"
22813	ENU06607	ANI61C7516:	24-51	427-447	LINAP	g4505121	160	78	1.00E-15	39	22		unknown ; (AF072250) methyl-CpG binding protein MBD4 [Homo sapiens] ; (AF114784) methyl-CpG binding endonuclease [Homo sapiens]
22814	ENU06608	ANI61C4132:	37-56	671-690	LINAP	g1084945	282	99	1.00E-28	35	19		probable membrane protein YPR022c - yeast [Saccharomyces cerevisiae]; (Z49274) unknown [Saccharomyces cerevisiae] ; (Z71255) unknown [Saccharomyces cerevisiae]
22815	ENU06609	ANI61C7536:	43-62	380-399	LINAP	g729786	170	89	2.00E-17	31	28		putative polyketide hydroxylase
22816	ENU06610	ANI61C8186:	22-47	589-614	LINAP	g3766365	454	212	3.00E-54	44	20		(AL031907) putative cystine-rich transcriptional regulator
			719..1										[Schizosaccharomyces pombe] (AL035592) hypothetical protein
22817	ENU06611	ANI61C7535:	44-62	566-591	LINAP	g4538674	132	70	2.00E-13	34	81		[Schizosaccharomyces pombe] hypothetical 78.3 KD protein in R1P1-URA3 intergenic region ; hypothetical protein YEL023c - yeast
22818	ENU06612	ANI61C4134:	51-70	790-815	LINAP	g731409	264	124	6.00E-28	39	36		(Saccharomyces cerevisiae) ; (U18530) Yel023cp [Saccharomyces cerevisiae] sexual differentiation process protein ISP7 ; isp7 protein - fission yeast (Schizosaccharomyces pombe); (D14064) ORF [Schizosaccharomyces pombe]
22819	ENU06613	ANI61C8218:	34-53	447-466	LINAP	g729862	120	64	3.00E-10	32	27		homolog of yeast Rae1 (Bharathi) mRNA-associated protein of 41 kDa (Kraemer); mRNA-associated protein MRNP41 (RAE1 protein homolog); (U84720) mRNA export protein [Homo sapiens]
22820	ENU06614	ANI61C4168:	38-58	429-449	LINAP	g4506399	222	32	3.4				
			2042..1557										

Seq num	Seq id	Contig source	5 pos	Primer 3 pos	Primer Basis	Selection Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
22821	ENU06615	ANI61C7519:	23-44	802-829	LINAP	g2132156	336	150	2.00E-35	36	45		(Saccharomyces cerevisiae); (U36624) Lpb1p [Saccharomyces cerevisiae] (AJ005273) Kin17 [Homo sapiens]
22822	ENU06616	ANI61C4155:	22-47	804-829	LINAP	g3850704	443	94	1.00E-40	44	59		(U50071) C. elegans ankyrin-related unc-44 (GB:U21734) [Caenorhabditis elegans]; (U39847) AO66 ankyrin [Caenorhabditis elegans] (AL031349) zinc-finger protein [Schizosaccharomyces pombe] (AB014768) chitinase [Aeromonas sp. 10S-24]
22823	ENU06617	ANI61C7554:	102-128	458-477	LINAP	g1208874	66	57	0.000000	33	8	0.08	(U50071) C. elegans ankyrin-related unc-44 (GB:U21734) [Caenorhabditis elegans]; (U39847) AO66 ankyrin [Caenorhabditis elegans] (AL031349) zinc-finger protein [Schizosaccharomyces pombe] (AB014768) chitinase [Aeromonas sp. 10S-24]
22824	ENU06618	ANI61C8221:	33-53	426-445	LINAP	g3451460	72	48	0.000002	26	25		(X79489) C-728 protein [Saccharomyces cerevisiae]; (Z35858) ORF YBL097w [Saccharomyces cerevisiae] (AJ011964) d-[lysargyl-peptide-synthetase [Claviceps purpurea] (U41278) contains similarity to G beta repeats (PROSITE:PS00670) of the beta-transducin family [Caenorhabditis elegans] (AB015708) photosynthetic reaction center M subunit [Erythrobacter sp.] (AL049498) hypothetical rho1 gdp-gtp exchange protein [Schizosaccharomyces pombe] " (AL031525) RNA binding protein, pumilio-family [Schizosaccharomyces pombe]" probable chitin biosynthesis protein C6G9..12 (CHS5 homolog) ; (Z81317) yeast chs5 homolog [Schizosaccharomyces pombe]
22825	ENU06619	ANI61C8238:	22-48	809-829	LINAP	g4115619	254	32	5.3				
22826	ENU06620	ANI61C412.5	24-48	803-828	LINAP	g586455	784	73	3.00E-12	37	15		
22827	ENU06621	ANI61C4161:	29-48	799-823	LINAP	g4499840	1058	109	3.00E-23	35	8		
22828	ENU06622	ANI61C8239:	22-44	745-765	LINAP	g1086900	178	86	2.00E-21	37	72		
22829	ENU06623	ANI61C4153:	24-51	441-460	LINAP	g3551484	107	38	0.046				
22830	ENU06624	ANI61C4153:	56-75	765-784	LINAP	g4539278	117	82	5.00E-15	24	20		
22831	ENU06625	ANI61C825.1	22-47	726-745	LINAP	g3560162	674	276	1.00E-73	54	34		
22832	ENU06626	ANI61C8266:	59-78	795-814	LINAP	g2842702	544	228	4.00E-59	44	45		
			10..898										

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database	Hit ncbi gi	Score	Score Prob	% id	% cvrg	Description
22833	ENU06627	ANI61C4186:	119..138	452..473	LINAP	g1175456	119	78	3.00E-14	34	29	hypothetical 60.5 KD protein C13G6.08 in chromosome I;
448..1												[Schizosaccharomyces pombe]; (Z54308) putative cdc protein [Schizosaccharomyces pombe] (AI02397) beta-1,3 exoglucanase [Trichoderma harzianum]" hypothetical 145.6 KD protein in SSM1B-CEG1 intergenic region; probable membrane protein YGL133w -yeast (Saccharomyces cerevisiae); (Z72655) ORF YGL133w
22834	ENU06628	ANI61C4107:	25..46	796..817	LINAP	g2924313	956	107	1.00E-29	49	18	hypothetical protein SPAC13G6.08 -fission yeast (Schizosaccharomyces pombe); (Z54308) putative cdc protein [Schizosaccharomyces pombe] (AI02397) beta-1,3 exoglucanase [Trichoderma harzianum]" hypothetical 145.6 KD protein in SSM1B-CEG1 intergenic region; probable membrane protein YGL133w -yeast (Saccharomyces cerevisiae); (Z72655) ORF YGL133w
22835	ENU06629	ANI61C8222:	22..46	805..829	LINAP	g1723918	178	62	1.00E-10	30	20	hypothetical 145.6 KD protein in SSM1B-CEG1 intergenic region; probable membrane protein YGL133w -yeast (Saccharomyces cerevisiae); (Z72655) ORF YGL133w
3752..4677												[Saccharomyces cerevisiae] (L42758) proteinase [Streptomyces lividans]; (AL035636) proteinase [Streptomyces coelicolor] (Z83857) ppsC [Mycobacterium tuberculosis]
22836	ENU06630	ANI61C8252:	23..44	661..680	LINAP	g940303	309	111	5.00E-24	29	51	melanin biosynthetic polyketide synthase PKS1 - Colletotrichum lagenarium ; (D83643) polyketide synthase [Colletotrichum lagenarium] (AB018274) KIAA0731 protein [Homo sapiens] (U97407) strong similarity to the ATP-binding transport protein family (ABC transporters) [Caenorhabditis elegans] (AC004561) putative glutathione S-transferase [Arabidopsis thaliana] suppressor of RNA polymerase B SRB4 ; RNA polymerase II suppressor protein SRB4 - yeast (Saccharomyces cerevisiae); (L12026) SRB4 [Saccharomyces cerevisiae]; (U18778) Srb4p: transcription factor [Saccharomyces cerevisiae] (Z99162) hypothetical protein [Schizosaccharomyces pombe]
22843	ENU06637	ANI61C8298:	941..481		LINAP	g2408014	288	68	3.00E-11	40	22	

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	Score	Score	Blast Prob	% id	% cvrg	Description
22844	ENU06638	ANI61C4252:	26-53	416-443	LINAP	g3688380	379	147	5.00E-35	51	26	(AJ006267) CipX-like protein [Homo sapiens]	
22845	ENU06639	ANI61C8280:	26-45	603-622	LINAP	g3953466	201	73	3.00E-27	34	28	(AC002228) F20N2.11 [Arabidopsis thaliana]	
22846	ENU06640	ANI61C4233:	47-66	803-829	LINAP	g3004489	351	100	1.00E-34	43	75	(AJ223304) geranylgeranyl transferase type I [Schizosaccharomyces pombe]	
22847	ENU06641	ANI61C4220:	22-42	806-829	LINAP	g1351690	216	104	8.00E-22	24	47	hypothetical 63.5 KD protein C3H1.06C in chromosome 1; (Z68144) putative major facilitator superfamily transporter [Schizosaccharomyces pombe]	
22848	ENU06642	ANI61C8282:	67-86	772-795	LINAP	g3451312	1627	126	3.00E-42	45	17	(AL031324) membrane atpase [Schizosaccharomyces pombe] (Z83123) Similarity to S pombe ATP-dependent DNA helicase (SW:Q09811); cDNA EST EMBL:D27628 comes from this gene; cDNA EST CEMSC83FB comes from this gene; cDNA EST EMBL:D35012 comes from this gene; cDNA EST yk398al.3 comes from...	
22849	ENU06643	ANI61C8303:	41-60	414-438	LINAP	g3879389	147	78	3.00E-14	50	9	(AL031324) membrane atpase [Schizosaccharomyces pombe] (Z83123) Similarity to S pombe ATP-dependent DNA helicase (SW:Q09811); cDNA EST EMBL:D27628 comes from this gene; cDNA EST CEMSC83FB comes from this gene; cDNA EST EMBL:D35012 comes from this gene; cDNA EST yk398al.3 comes from...	
22850	ENU06644	ANI61C4272:	36-55	796-813	LINAP	g4007734	256	44	0.001			(AL034447) putative transmembrane protein [Streptomyces coelicolor] "proline-rich phosphoprotein" (gene PRH1, Db allele) - human "	
22851	ENU06645	ANI61C8296:	1..1707		LINAP	g88462	162	37	0.00001	31	70	gene from NF2/meningioma region of 22q12 ; gene anonymous protein - human ; (L18972) anonymous protein - human ; (L18972) anonymous [Homo sapiens]	
22852	ENU06646	ANI61C4276:	46-65	414-433	LINAP	g4505829	108	76	2.00E-13	32	21	Cubitus interruptus dominant protein ; DNA-binding protein ci (D) - fruit fly (Drosophila melanogaster) ; (X54360) cID product [Drosophila melanogaster] "SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2 ; SNF2alpha protein - human ; (D26155) hSNF2a [Homo sapiens]"	
22853	ENU06647	ANI61C8291:	23-42	457-479	LINAP	g116415	147	79	2.00E-14	37	8	"SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2 ; SNF2alpha protein - human ; (D26155) hSNF2a [Homo sapiens]"	
22854	ENU06648	ANI61C4283:	37-56	454-473	LINAP	g4507069	143	42	0.000000	05		"SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2 ; SNF2alpha protein - human ; (D26155) hSNF2a [Homo sapiens]"	

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database	Hit	ncbi gi	aat Score	Score	Prob	% id	% cvrg	Description
22855	ENU06649	ANI61C8302:	24-43	810-829	LINAP	g2342601	375	95	5.00E-19	27	5	(X89442) peptide synthetase [Metarhizium anisopliae]		
22856	ENU06650	ANI61C8316:	23-44	627-646	LINAP	g1730692	54	49	0.00003			putative transcriptional regulatory protein in BIO3-HXT17 intergenic region ; probable membrane protein YNR063w - yeast (Saccharomyces cerevisiae) ; (Z711678) ORF YNR063w [Saccharomyces cerevisiae]		
22857	ENU06651	ANI61C4300:	42-69	460-479	LINAP	g4008551	647	144	4.00E-40	52	28	(AL034490) pseudouridylylate synthase [Schizosaccharomyces pombe]		
22858	ENU06652	ANI61C8320:	24-51	422-449	LINAP	g729298	231	107	6.00E-23			RHO-type GTPase activating protein RGA1/DBM1 ; DBM1 protein - yeast (Saccharomyces cerevisiae) ; (U07421) Dbm1p [Saccharomyces cerevisiae] ; (X90518) ORF O3290 [Saccharomyces cerevisiae] ; (X94335) YOR3290w [Saccharomyces cerevisiae] ; (Z75035) ORF YOR127w [Saccharomyces cerevisiae] ; GTPase-activating protein [Saccharomyces cerevisiae]		
22859	ENU06653	ANI61C8338:	22-43	404-428	LINAP	g1706094	122	76	9.00E-15	34	31	cytochrome P450 4F5 (CYPIVFS) ; cytochrome P450 4F5 protein - rat ; (U39207) cytochrome P450 4F5 [Rattus norvegicus] mucin 5AC (clone JER58) - human (fragment) ; (Z34278) mucin [Homo sapiens]		
22860	ENU06654	ANI61C8332:	22-48	271-290	LINAP	g1082604	106	42	0.002			tRNA nucleotidyltransferase precursor (tRNA adenylyltransferase) (tRNA CCA-pyrophosphorylase) (CCA-adding enzyme) ; tRNA nucleotidyltransferase - yeast (Saccharomyces cerevisiae) ; (M59870) transfer RNA nucleotidyltransferase [Saccharomyces cerevisiae] ; (U18922) Ccalp: tRNA nucleotidyltransferase(tRNA CCA-pyrophosphorylase) [Saccharomyces cerevisiae]		
22861	ENU06655	ANI61C8344:	48-70	787-814	LINAP	g135969	619	274	6.00E-73					
			1..905											

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat	Blast Score	Blast Prob	% id	% cvrg	Description
22862	ENU06656	ANI61C8337:	22-46	807-826	LINAP	g3810845	686	243	1.00E-63	46	53	(AL032684) possible ubiquitin carboxyl-terminal hydrolase	
22863	ENU06657	ANI61C8362:	31-53	480-499	LINAP	g3746895	258	98	8.00E-20	36	30	[Schizosaccharomyces pombe] (AF088906) clock-controlled gene-9 protein [Neurospora crassa]	
22864	ENU06658	ANI61C8308:	22-48	452-479	LINAP	g3729853	62	45	0.0003	29	50	protein-tyrosine-phosphatase precursor ; dual specificity phosphatase (EC 3.1.3.-) IphP - Nostoc commune ; (L11392) protein tyrosine/serine phosphatase [Nostoc commune]	
22865	ENU06659	ANI61C8356:	50-69	785-804	LINAP	g728850	78	54	0.000001			"glucoamylase S1/S2 precursor (glucan 1,4-alpha-glucosidase) (1,4-alpha-D-glucan glucohydrolase) ; glucan 1,4-alpha-glucosidase (EC 3.2.1.3) - yeast (Saccharomyces cerevisiae) ; (Z38061) mal5, stal, lcn: 1367, CAI: 0.3, AMYH_YEAST P08640 glucoamylase S1 (EC 3.2.1.3) [Saccharomyces cerevisiae] ; (U30626) glucoamylase [Saccharomyces cerevisiae var. diastaticus]"	
22866	ENU06660	ANI61C1000	22-48	803-822	LINAP	g2132941	157	57	3.00E-18	29	57	probable membrane protein YOR301w - yeast (Saccharomyces cerevisiae) ; (Z75209) ORF YOR301w [Saccharomyces cerevisiae]	
22867	ENU06661	ANI61C1002	22-49	802-829	LINAP	g2497214	508	114	5.00E-45	44	27	hypothetical 107.7 KD protein in TSP3-IPP2 intergenic region ; probable membrane protein YMR266w - yeast (Saccharomyces cerevisiae) ; (Z49260) unknown [Saccharomyces cerevisiae]	
22868	ENU06662	ANI61C1000	24-43	792-811	LINAP	g2498597	699	206	1.00E-52	42	27	mRNA transport regulator MTR10 ; MTR10 protein - yeast (Saccharomyces cerevisiae) ; (U55020) Mtr10p [Saccharomyces cerevisiae] ; (Z75068) ORF YOR160w [Saccharomyces cerevisiae]	

Seq num	Seq id	Contig source	5 pos	Primer 3 pos	Primer Basis	Selection Database Hit	aat ncbi gi	blast Score	blast Prob	% id	% cvrg	Description	
22869	ENU06663	ANI61C1004	7.3106..992	22-41	805-829	LINAP	g731872	777	99	3.00E-20	34	"putative 108.8 KD transcriptional regulatory protein in FKH1-STH1 intergenic region ; probable membrane protein YIL130w - yeast (Saccharomyces cerevisiae) ; (Z38059) orf, len: 964, CAT: 0.15, possible regulatory protein [Saccharomyces cerevisiae]"	
22870	ENU06664	ANI61C1006	24-45	713-737	LINAP		g2924771	181	64	0.000000	001	(AC002334) putative dimethylaniline monoxygenase [Arabidopsis thaliana] hypothetical 43.9 KD protein C13G7.10 in chromosome I ; hypothetical protein - fission yeast (Schizosaccharomyces pombe) ; (Z69729) hypothetical protein [Schizosaccharomyces pombe] (AC006248) putative copia polyprotein [Arabidopsis thaliana]	
22871	ENU06665	ANI61C1005	5:379..755	39-58	449-476	LINAP	g1723454	219	55	0.000000	33	4	hypothetical 63.9 KD protein C13G7.10 in chromosome I ; hypothetical protein - fission yeast (Schizosaccharomyces pombe) ; (Z69729) hypothetical protein [Schizosaccharomyces pombe] (AC006248) putative copia polyprotein [Arabidopsis thaliana]
22872	ENU06666	ANI61C1008	4:878..441	208-229	388-411	LINAP	g4335736	44	64	5.00E-10		hypothetical 63.9 KD protein C1F12.09 in chromosome I ; hypothetical protein - fission yeast (Schizosaccharomyces pombe) ; (Z69944) unknown [Schizosaccharomyces pombe] (D90903) esterase [Synechocystis sp.]	
22873	ENU06667	ANI61C1009	9:1217..228	22-48	777-800	LINAP	g1723513	250	64	0.000000	31	49	hypothetical 63.9 KD protein C1F12.09 in chromosome I ; hypothetical protein - fission yeast (Schizosaccharomyces pombe) ; (Z69944) unknown [Schizosaccharomyces pombe] (D90903) esterase [Synechocystis sp.]
22874	ENU06668	ANI61C1010	6:336..699	22-44	456-479	LINAP	g1652216	93	68	3.00E-11		hypothetical 63.9 KD protein C1F12.09 in chromosome I ; hypothetical protein - fission yeast (Schizosaccharomyces pombe) ; (Z69944) unknown [Schizosaccharomyces pombe] (D90903) esterase [Synechocystis sp.]	
22875	ENU06669	ANI61C1008	5:5678..6236	28-55	502-521	LINAP	g4335736	166	85	1.00E-18	32	14	(AC006248) putative copia polyprotein [Arabidopsis thaliana]
22876	ENU06670	ANI61C1012	6:445..1	102-121	449-476	LINAP	g630383	178	85	3.00E-16	40	25	proline transport protein - Entericella nidulans
22877	ENU06671	ANI61C1010	1:357..32	112-139	450-477	LINAP	g1352914	132	63	0.000000	37	40	"putative 40S ribosomal protein YJR113C ; probable ribosomal protein S7, mitochondrial - yeast (Saccharomyces cerevisiae) ; (Z49613) ORF YJR113c [Saccharomyces cerevisiae]"
22878	ENU06672	ANI61C1015	1:1039..1346	22-42	279-299	LINAP	g3617954	105	65	4.00E-10			(AF079900) tetracycline efflux protein [Streptomyces rimosus]
22879	ENU06673	ANI61C1016	5:1056..686	54-77	328-350	LINAP	g3746666	91	57	0.000000	42	30	(AF076348) trihydroxytoluene oxygenase [Burkholderia cepacia]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database	Hit ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
22880	ENU06674	ANI61C1011	26-53	457-477	LINAP	g4107286	50	59	0.000000	03	(AL035076) putative zinc-finger protein [Schizosaccharomyces pombe] (Z92771) hypothetical protein Rv3272		
22881	ENU06675	ANI61C1017	66-85	456-478	LINAP	g1877327	162	96	1.00E-19		[Mycobacterium tuberculosis] (X67953)		
22882	ENU06676	ANI61C1018	22-41	452-472	LINAP	g47149	90	62	0.000000	003	carboxyphosphoenolpyruvate mutase [Streptomyces hygroscopicus]		
22883	ENU06677	ANI61C1020	42-61	311-332	LINAP	g1942321	69	59	0.000000	29	"Bacterial Chitobiase Complexed With Chitobiase (Dinag) ; Bacterial Chitobiase, Glycosyl Hydrolase Family 20"		
22884	ENU06678	ANI61C1019	122-149	635-658	LINAP	g2498702	138	55	9.00E-14	35	sterigmatocystin 7-O-methyltransferase precursor ; (L25835) O-methyltransferase [Aspergillus flavus] ; (L25834) O-methyltransferase [Aspergillus parasiticus] ; (L22091) O-methyltransferase [Aspergillus parasiticus]		
22885	ENU06679	ANI61C1022	36-61	802-829	LINAP	g1709181	283	78	6.00E-14	28	"high affinity methionine permease ; methionine transport protein, high affinity - yeast (Saccharomyces cerevisiae) ; (U40316) high affinity methionine permease [Saccharomyces cerevisiae] ; (Z72840) ORF YGR055w [Saccharomyces cerevisiae]"		
22886	ENU06680	ANI61C1023	64-83	461-480	LINAP	g2501427	152	66	9.00E-19	45	tyrosinase (monophenol monooxygenase) ; (U66807) tyrosinase [Podospora anserina] ; (U66808) tyrosinase [Podospora anserina] (AL033388) leucine-rich repeat protein - weak similarity to adenylate cyclase [Schizosaccharomyces pombe]		
22887	ENU06681	ANI61C1062	41-60	576-594	LINAP	g3850105	179	65	3.00E-15	38			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit ncbi gi	Score	Score Prob	% id	% cvrg	Description		
22888	ENU06682	ANI61C1024	22-49	367-386	LINAP	g1172542	267	88	3.00E-27	60	dolichyl-phosphate-mannose-protein mannosyltransferase 4 ; dolichyl-phosphate-mannose-protein mannosyltransferase (EC 2.4.1.109)		
22889	ENU06683	ANI61C1065	41-62	619-639	LINAP	g4584202	123	42	0.000000	29	45	(AJ000394) chromate transport protein [Bacillus cereus]	
22890	ENU06684	ANI61C1058	22-47	805-829	LINAP	g3150136	460	90	1.00E-18	33	38	(AL023594) protein complex assembly protein [Schizosaccharomyces pombe] regulatory protein algR3 - Pseudomonas aeruginosa	
22891	ENU06685	ANI61C1058	9:3081..1748 9:9595..10143	22-44	503-528	LINAP	g94816	98	42	0.002		(U62933) multidrug resistance protein 1 [Aspergillus fumigatus] ; (U62934) multidrug resistance protein 1 [Aspergillus fumigatus]	
22892	ENU06686	ANI61C1024	23-46	657-681	LINAP	g2673951	324	140	8.00E-33	36	17	(U62933) multidrug resistance protein 1 [Aspergillus fumigatus] ; (U62934) multidrug resistance protein 1 [Aspergillus fumigatus]	
22893	ENU06687	ANI61C1058	100-119	713-732	LINAP	g3130045	203	89	3.00E-17	31	17	(AL023518) hypothetical protein [Schizosaccharomyces pombe]	
2			9:10697..1163										
22894	ENU06688	ANI61C4949:	22-48	756-780	LINAP	g3080393	1399	118	1.00E-34	39	50	(AL022603) NADH dehydrogenase like protein [Arabidopsis thaliana] (Z99168) putative heat shock transcription factor	
22895	ENU06689	ANI61C4971:	640..2097 681..319	22-46	421-442	LINAP	g3327019	80	63	0.000000	001	[Schizosaccharomyces pombe] (AL023776) prephenate dehydrogenase [Schizosaccharomyces pombe]	
22896	ENU06690	ANI61C4972:	739..1406	614-633	LINAP	g3184059	536	96	4.00E-48	65	39	glutathione-dependent formaldehyde dehydrogenase (FDH) (FALDH); (L33464) alcohol dehydrogenase 3 [Methyllobacter marinus]	
22897	ENU06691	ANI61C4990:	809..255	119-144	486-505	LINAP	g1345955	106	46	3.00E-12	31	40	(Y13967) alpha-amino adipate reductase large subunit [Penicillium chrysogenum]
22898	ENU06692	ANI61C1067	51-70	767-786	LINAP	g3282044	216	99	3.00E-20	35	17		
			2:1359..546										

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	Score	Score Prob	% id	% cvrg	Description
22399	ENU06693	ANI61C4929:	52-71	585-603	LINAP	g125727	291	76	5.00E-29			killer toxin alpha and beta subunits precursor (RF2 protein) (endochitinase ; RF2 protein - yeast ( <i>Kluyveromyces marxianus</i> var. <i>lactis</i> ) plasmid k1 ; (X07127) RF2 gene product (AA 1 - 1146) [Kluyveromyces lactis] ; (X00762) ORF2 (put. killer toxin large subunit) [Kluyveromyces lactis] ; (X01095) URFP2 (put. 97 kd glycoprotein 31 kd subunit precursor of the killer toxin ; aa 1-1146) [Kluyveromyces lactis]
22900	ENU06694	ANI61C4929:	25-44	469-493	LINAP	g584748	53	52	0.000004			autolysin (N-acetylglucosaminyl-L-alanine amidase) ; autolysin – Enterococcus faecalis ; (M58002) bacterial cell wall hydrolase [Streptococcus faecalis] alpha-glucosidase precursor (maltase) ; alpha-glucosidase (EC 3.2.1.20) - yeast ( <i>Candida tsukubensis</i> ) ; (X56024) alpha-glucosidase [Pseudozyma tsukubaensis]
22901	ENU06695	ANI61C1068	79-98	360-380	LINAP	g113517	95	72	3.00E-12			probable membrane protein YLR277c - yeast ( <i>Saccharomyces cerevisiae</i> ) ; (T11245) Ysh1p; subunit of polyadenylation factor I (PFI) [Saccharomyces cerevisiae]
22903	ENU06697	ANI61C1069	36-59	442-461	LINAP	g2507475	87	57	0.000000 27	9	06	paired amphipathic helix protein ; regulatory protein SIN3 - yeast ( <i>Saccharomyces cerevisiae</i> ) ; (Z74746) ORF YOL004w [Saccharomyces cerevisiae]
22904	ENU06698	ANI61C1068	22-48	758-784	LINAP	g2618766	327	153	7.00E-38 39	46		(U94362) glycogenin-2 alpha [Homo sapiens] (U44088) TDAG51 [Mus musculus]
22905	ENU06699	ANI61C5009:	61-80	515-534	LINAP	g1469400	50	34	0.6			lactose permease ; lactose permease - yeast ( <i>Kluyveromyces marxianus</i> var. <i>lactis</i> ) ; (X06997) lactose permease (AA 1-587) [Kluyveromyces lactis]
22906	ENU06700	ANI61C1025	22-45	802-829	LINAP	g125935	418	118	6.00E-26 29	44		
		1:1382..3059										

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	Score	Score	Blast Prob	% id	% cvrg	Description
22907	ENU06701	ANi61C1027	4:1..2053	22-48	804-824	LINAP	g3559970	656	66	8.00E-24	37	28	[Streptomyces coelicolor] (AL031514) putative beta-mannosidase
22908	ENU06702	ANi61C85337:	52-71	765-789	LINAP	g121087	162	56	3.00E-18				GCY protein ; GCY1 protein - yeast (Saccharomyces cerevisiae) ; (X13228) GCY protein (AA 1-312), [Saccharomyces cerevisiae] ; (X90518) ORF O31567 [Saccharomyces cerevisiae] ; (X94335) YOR3269w [Saccharomyces cerevisiae] ; (X96740) GCY protein [Saccharomyces cerevisiae] ; (Z75028) ORF YOR120w [Saccharomyces cerevisiae]
22909	ENU06703	ANi61C5049:	102-121	539-558	LINAP	g3367750	322	81	2.00E-28	46	34	(AL031155) putative amidase [Streptomyces coelicolor]	
22910	ENU06704	ANi61C8646:	22-48	807-829	LINAP	g1351677	241	88	9.00E-17	35	72	hypothetical 36.9 KD protein C21E11.07 in chromosome I; hypothetical protein SPAC21E11.07 - fission yeast (Schizosaccharomyces pombe) ; (Z67999) hypothetical protein [Schizosaccharomyces pombe] (AJ000482) Hormone-sensitive lipase [Sus scrofa] ; (AJ000483) hormone-sensitive lipase [Sus scrofa] (Z95396) putative ubiquitin transferase [Schizosaccharomyces pombe] (AC002376) Contains similarity to human dimethylamine monooxygenase (gb M64082). [Arabidopsis thaliana] (Z97209) aldolase reductase [Schizosaccharomyces pombe]	
22911	ENU06705	ANi61C5053:	48-68	448-467	LINAP	g2764520	117	61	0.000000	42	16	[Schizosaccharomyces pombe] (AJ000482) Hormone-sensitive lipase [Sus scrofa] ; (AJ000483) hormone-sensitive lipase [Sus scrofa] (Z95396) putative ubiquitin transferase [Schizosaccharomyces pombe] (AC002376) Contains similarity to human dimethylamine monooxygenase (gb M64082). [Arabidopsis thaliana] (Z97209) aldolase reductase [Schizosaccharomyces pombe]	
22912	ENU06706	ANi61C1070	25-44	726-753	LINAP	g2104438	429	138	2.00E-43	50	22	kinesin-like protein 1 - African clawed frog ; (X82012) kinesin-like protein 1 [Xenopus laevis]	
22913	ENU06707	ANi61C1027	8:1752..1	44-71	472-499	LINAP	g2494132	74	70	9.00E-12			(M80368) pathway-specific regulatory protein [Neurospora crassa] (U28739) similar to alcohol dehydrogenase/rabbit dehydrogenase [Caenorhabditis elegans]
22914	ENU06708	ANi61C8658:	41-68	802-829	LINAP	g2239203	431	89	2.00E-36	39	92		
22915	ENU06709	ANi61C5032:	1172..303	22-49	809-828	LINAP	g2134102	564	198	6.00E-50	48	19	
22916	ENU06710	ANi61C1024	7:1405..1982	48-67	537-555	LINAP	g168849	114	77	6.00E-15	33	13	
22917	ENU06711	ANi61C1024	7:4812..6215	22-43	803-825	LINAP	g2731377	988	175	3.00E-43	32	29	

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database	Hit ncbi gi	Score	Score	Blast Prob	% id	% cvrg	Description
22918	ENU06712	ANI61C507:2	89-116	453-479	LINAP	g3080535	391	177	4.00E-44	57	7	(AL022600) RNA helicase	
22919	ENU06713	ANI61C1024	22-42	453-479	LINAP	g2495215	184	94	8.00E-19	39	67	[Schizosaccharomyces pombe] hypothetical 20.9 KD protein in ROX1-SPE3 intergenic region ; hypothetical protein YPR067w - yeast	
22920	ENU06714	ANI61C1073	42-61	644-671	LINAP	g1351612	256	90	3.00E-29	39	64	[Saccharomyces cerevisiae] ; (Z49219) unknown [Saccharomyces cerevisiae] ; (Z71255) unknown [Saccharomyces cerevisiae]	
		3:1577..2268											
22921	ENU06715	ANI61C507:3	32-52	481-502	LINAP	g2135950	122	39	0.017			(Schizosaccharomyces pombe) PQ-rich protein - human ; (Z50194) PQ-rich protein [Homo sapiens]	
22922	ENU06716	ANI61C1028	23-46	678-700	LINAP	g1175484	276	110	2.00E-28	41	15	ATP-dependent DNA helicase HUS2 ; hypothetical protein SPAC2G11.12-fission yeast (Schizosaccharomyces pombe) ; (Z54354) atp-dependent dna helicase hus2 [Schizosaccharomyces pombe] ; (Y09426) DNA-helicase [Schizosaccharomyces pombe]	
22923	ENU06717	ANI61C5107:	22-46	455-479	LINAP	g1077552	286	135	2.00E-31	40	49	hypothetical protein YDR051c - yeast (Saccharomyces cerevisiae) ; (Z49209) unknown [Saccharomyces cerevisiae] ; (Z74347) ORF YDR051c [Saccharomyces cerevisiae]	
		503..913											
22924	ENU06718	ANI61C505:1	34-53	810-828	LINAP	g2114323	106	41	0.011	21	32	(D88734) membrane glycoprotein [Equine herpesvirus 1]	
22925	ENU06719	ANI61C1028	47-66	365-388	LINAP	g115918	128	63	1.00E-17			cell division control protein 2 cognate ; protein kinase (EC 2.7.1.37) cdc2 homolog C - fruit fly (Drosophila sp.) ; (X57486) p34-cdk2 homologue [Drosophila melanogaster]	
		1:2699..3282											

Seq num	Seq id	Contig source	5 pos	Primer 3 pos	Primer Basis	Selection Database Hit	aat ncbi gi	Score 860	Blast 292	Prob 2.00E-78	% id 49	% cvg 22	Description
22926	ENU06720	ANI61C1074	22-45	773-790	LINAP	g1351636	860	292	2.00E-78	49	22	hypothetical 143.3 KD TRP-ASP repeats containing protein C12G12.13C in chromosome I; hypothetical protein SPAC12G12.13c - fission yeast ( <i>Schizosaccharomyces pombe</i> )	
22927	ENU06721	ANI61C1028	35-58	785-812	LINAP	g112713	184	63	0.000000	003	0	0	"1-amino cyclopropane-1-carboxylate synthase CMW33 (ACC synthase) (S-adenosyl-L-methionine methylthioadenosine-lyase); 1-amino cyclopropane-1-carboxylate synthase (EC 4.4.1.14), wound-induced - winter squash ; (D01032) 1-amino cyclopropane-1-carboxylate synthase [Cucurbita maxima] ; amino cyclopropane carboxylate synthase [Cucurbita maxima] ; amino cyclopropane carboxylate synthase: ISOType=wound-induced [Cucurbita maxima]" hypothetical 77.3 KD protein in FIG1-GIP1 intergenic region ; probable membrane protein YBR043c - yeast (Saccharomyces cerevisiae); (Z35912) ORF YBR043c [Saccharomyces cerevisiae]
22928	ENU06722	ANI61C1027	0:612..1042	31-50	419-438	LINAP	g586486	90	57	0.000000	06	0	"hypothetical 77.3 KD protein in FIG1-GIP1 intergenic region ; probable membrane protein YBR043c - yeast (Saccharomyces cerevisiae); (Z35912) ORF YBR043c [Saccharomyces cerevisiae]" UDP-glucose 4-epimerase (galactowaldenase) / aldose 1-epimerase (mutarotase) ; UDP-glucose 4-epimerase (EC 5.1.3.2) - yeast (Pachysolen tannophilus) ; (X68593) UDP-galactose- 4-epimerase [Pachysolen tannophilus]
22930	ENU06724	ANI61C8668:	22-45	520-539	LINAP	g2147899	275	77	2.00E-21	40	32	0	phosphate transporter - Glomus versiforme ; (U38650) phosphate transporter [Glomus versiforme]; phosphate transporter [Glomus versiforme]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat	Blast Score	Blast Prob	% id	% cvrg	Description	
22931	ENU06725	ANI61C8674:	32-51	673-692	LINAP	g1730741	143	51	0.000000	002			MAS5 intergenic region ; probable membrane protein YNL065w - yeast (Saccharomyces cerevisiae) ; (U12141) membrane protein [Saccharomyces cerevisiae] ; (Z71341) ORF YNL065w	
22932	ENU06726	ANI61C5139:	211-230	628-647	LINAP	g500628	280	120	1.00E-26	37	37		[Saccharomyces cerevisiae] (U05211) Ttp1p [Saccharomyces cerevisiae]	
22933	ENU06727	ANI61C1070	22-44	638-657	LINAP	g3219924	276	112	2.00E-24	36	43		hypothetical 57.6 KD protein C30D10.15 in chromosome II ; (Z97992) conserved hypothetical protein [Schizosaccharomyces pombe] (AL035216) probable involvement in ergosterol biosynthesis	
22934	ENU06728	ANI61C8669:	46-65	542-561	LINAP	g4160344	171	88	6.00E-17	51	23		[Schizosaccharomyces pombe] (AF038585) pyruvate dehydrogenase kinase isoform 1; PDK1 [Zea mays] (X97119) pectate lyase [Erwinia chrysanthemi]	
22935	ENU06729	ANI61C5129:	24-50	446-471	LINAP	g3746431	244	62	0.000000	44	24		cyclosporin synthetase - Tolypocladium inflatum ; (Z28383) cyclosporine synthetase [Tolypocladium inflatum] putative 89.3 KD transcriptional regulatory protein C1F7.11C ; hypothetical protein SPAC1F7.11c - fission yeast (Schizosaccharomyces pombe) ; (Z67998) unknown [Schizosaccharomyces pombe] (AL021837) histone promoter control 2 protein [Schizosaccharomyces pombe] (X89442) peptide synthetase [Metarhizium anisopliae]	
22936	ENU06730	ANI61C1027	22-41	748-775	LINAP	g1765918	190	61	0.000000	34	57		(S58126) Unknown [Saccharomyces cerevisiae]	
22937	ENU06731	ANI61C1067	22-41	719-743	LINAP	g1083855	388	131	9.00E-30	35	1		(AL049497) hypothetical protein [Streptomyces coelicolor] "(AJ002397) beta-1,3 exoglucanase [Trichoderma harzianum]"	
22938	ENU06732	ANI61C5136:	22-44	457-476	LINAP	g1351672	63	38	0.001	21	20			
			1914..1594											
22939	ENU06733	ANI61C1030	22-44	458-479	LINAP	g2894295	162	90	6.00E-18	40	39			
22940	ENU06734	ANI61C1067	36-55	805-828	LINAP	g2342601	571	140	1.00E-32	32	5			
22941	ENU06735	ANI61C8697:	7:3220..1716	295-314	LINAP	g4261597	79	55	0.000000	30	11			
22942	ENU06736	ANI61C5133:	1460..1832	39-58	807-829	LINAP	g4539214	817	177	1.00E-43	52	64		
22943	ENU06737	ANI61C1077	22-43	454-473	LINAP	g2924313	109	64	6.00E-10	27	15			
			0:1696..2012											

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database	Hit ncbi gi	aat Score	blast Score	blast Prob	% id	cvg	Description
22944	ENU06738	ANI61C8696:	43-63	628-647	LINAP		g2499841	1691	315	3.00E-85	54	31	26S proteasome regulatory subunit MTS4 (19S regulatory CAP region of 26S protease subunit 2) ; (Y09819) 19S regulatory cap region of 26S protease subunit 2 [Schizosaccharomyces pombe]
22945	ENU06739	ANI61C506:1 ..420	121-140	307-326	LINAP		g3550985	194	63	8.00E-10	35	34	(AB010740) OsSSa [Oryza sativa]
22946	ENU06740	ANI61C8681:1356..1			LINAP		g1293655	407	107	1.00E-22	35	35	(U51327) versicolorin B synthase [Aspergillus parasiticus] ; (U51328) versicolorin B synthase [Aspergillus parasiticus]
22947	ENT06741	ANI61C1079: 26-46	452-479	LINAP			g3550283	80	55	0.000000	31	40	(AJ007590) XRP2 protein [Homo sapiens]
22948	ENU06742	ANI61C5149: 109-129	571-590	LINAP			g133322	78	49	0.00003			DNA-directed RNA polymerase II largest subunit ; DNA-directed RNA polymerase (EC 2.7.7.6) II large chain - Caenorhabditis elegans ; (M29235) RNA polymerase II [Caenorhabditis elegans]
22949	ENU06743	ANI61C1032 3:115..1300		LINAP			g1805251	275	92	6.00E-18	30	51	(U58946) transposase [Aspergillus awamori]
22950	ENU06744	ANI61C1077 7:2749..3110	41-59	262-285	LINAP		g479395	77	51	0.000005	34	6	probable serine/threonine protein kinase (EC 2.7.1.-) - yeast (Saccharomyces cerevisiae)
22951	ENU06745	ANI61C1031 7:1497..1193	29-48	459-479	LINAP		g2224683	121	68	6.00E-11	28	10	(AB002369) KIAA0371 [Homo sapiens]
22952	ENU06746	ANI61C1078 7:109..687	25-46	536-558	LINAP		g4503247	126	55	0.000000	33	29	novel nuclear protein 1 ; NNP-1 protein (D21S2056E) ; (U79775) NNP-1 [Homo sapiens]
22953	ENU06747	ANI61C1032 1:1452..1008	34-53	459-479	LINAP		g2950464	185	75	4.00E-17	55	17	(AL022071) hypothetical protein [Schizosaccharomyces pombe] (AL023592) betaine-aldehyde dehydrogenaseprecursor
22954	ENU06748	ANI61C1032 0:2635..2956	24-51	453-479	LINAP		g3136055	76	57	0.000000	24	27	[Schizosaccharomyces pombe] [Cochliobolus heterostrophus]
22955	ENU06749	ANI61C8702: 2218..1	32-51	710-730	LINAP		g1546072	925	108	7.00E-23	32	10	(U68040) polyketide synthase

Seq num	Seq id	Contig source	5 pos	Primer 3 pos	Primer Basis	Selection Database	Hit ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvg	%	Description
22956	ENU06750	ANI61C8694:	53-72	803-821	LINAP		g481230	566	104	4.00E-30	41	63	L-iditol 2-dehydrogenase (EC 1.1.1.14) precursor - rat ; (X74593) L-iditol 2-dehydrogenase [Rattus norvegicus] (AF080119) similar to [Saccharomyces cerevisiae]	
22957	ENU06751	ANI61C5154:	22-49	782-802	LINAP		g414689	329	146	1.00E-34	30	30	(X75561) GTPase activating protein Schizosaccharomyces pombe isp4 protein (GB:D14061) [Arabidopsis thaliana]	
22958	ENU06752	ANI61C1078	27-46	653-674	LINAP		g3600039	103	59	1.00E-10	25	31	Schizosaccharomyces pombe isp4 protein (GB:D14061) [Arabidopsis thaliana]	
22959	ENU06753	ANI61C8703:	27-46 1195..649	459-478	LINAP		g2132846	139	73	2.00E-12			probable membrane protein YOL119c - yeast (Saccharomyces cerevisiae); (Z74861) ORF YOL119c [Saccharomyces cerevisiae]; (X95258) unknown protein [Saccharomyces cerevisiae]	
22960	ENU06754	ANI61C1079	22-43	804-829	LINAP		g2414601	414	149	3.00E-35	39	43	(Z99295) phosphatidyl synthase [Schizosaccharomyces pombe] putative transporter C1B3.16C; (Z98598) putative transporter [Schizosaccharomyces pombe] (AL023634) hypothetical protein [Schizosaccharomyces pombe]	
22961	ENU06755	ANI61C8703:	66-93	572-591	LINAP		g3183364	178	100	1.00E-20	33	30	"hypothetical 32.9 KD protein in NFO-FRUA intergenic region ; (U00007) yeiN [Escherichia coli] ; (AE000306) orf, hypothetical protein [Escherichia coli] ; yeiN gene [Escherichia coli]"	
22962	ENU06756	ANI61C1033	8:176..494	116-143	450-473	LINAP	g3150252	62	50	0.00001	38	6		
22963	ENU06757	ANI61C1145	9:2028..411	34-54	754-780	LINAP	g465602	389	70	2.00E-11				
22964	ENU06758	ANI61C5147:	22-42 2509..3155	598-625	LINAP		g464482	235	100	1.00E-20	42	11	exocyst complex component SEC3 (PSL1 protein) ; PSL1 protein -yeast (Saccharomyces cerevisiae) ; (L22204) Psllp [Saccharomyces cerevisiae] ; (U18778) Sec3p [Saccharomyces cerevisiae]	
22965	ENU06759	ANI61C1081	7:1303..337	22-47	804-823	LINAP	g3334796	373	154	1.00E-45	41	55	(AL031107) putative secreted glucosidase [Streptomyces coelicolor]	

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description	
22966	ENU06760	ANI61C1147	22-44	452-479	LINAP	g127992	117	31	6			"beta-(1->2)glucan export ATP-binding protein NDVA ; beta-1,2-glucan export protein ndvA- Rhizobium meliloti ; (M20726) ndvA peptide (put.) ; putative [Rhizobium meliloti]"	
22967	ENU06761	ANI61C8695:	22-44	460-479	LINAP	g1799532	77	59	0.000000	33	38	(AB000564) salicylate hydroxylase [Sphingomonas sp.]	
22968	ENU06762	ANI61C5176:	40-59	572-591	LINAP	g2193933	66	46	0.0002			[Z9680] hypothetical protein Rv0312 [Mycobacterium tuberculosis]	
22969	ENU06763	ANI61C1079	27-46	767-786	LINAP	g1020413	464	143	2.00E-33	34	50	(D63703) isobutene-forming enzyme and benzoate 4-hydroxylase [Rhodotorula minuta]	
22970	ENU06764	ANI61C1032	22-49	807-829	LINAP	g3023956	787	256	2.00E-67	51	20	vegetable incompatibility protein HET-E-1 ; (L28125) beta transducin-like protein [Podospora anserina] (AL031154) hypothetical protein [Schizosaccharomyces pombe]	
22971	ENU06765	ANI61C8710:			LINAP	g3367797	472	208	2.00E-53	55	22	(AC005917) putative zinc finger protein [Arabidopsis thaliana] (AL035480) putative polyketide synthase [Mycobacterium leprae] (AF018639) unknown [Dictyostelium discoideum]	
22972	ENU06766	ANI61C5177:	108-127	454-477	LINAP	g4191793	71	40	0.000000			(U80050) short region of weak similarity to rat dihydroxypolyprenylbenzoate methyltransferase (GI:457372)	
22973	ENU06767	ANI61C1079	22-43	732-751	LINAP	g4455664	347	166	2.00E-40	37	13	[Schizosaccharomyces pombe]	
22974	ENU06768	ANI61C1032	40-59	490-508	LINAP	g2582351	370	164	4.00E-40	43	40	[YJR110w] yeast ORF YJR110w [Saccharomyces cerevisiae]	
22975	ENU06769	ANI61C5177:	22-49	456-479	LINAP	g1703534	68	67	7.00E-11	43	29		
			1806..1464										
22976	ENU06770	ANI61C1082	36-55	648-669	LINAP	g3023956	801	243	6.00E-69	51	20	[Caenorhabditis elegans] vegetal incompatible protein HET-E-1 ; (L28125) beta transducin-like protein [Podospora anserina]	
22977	ENU06771	ANI61C1034	3:1453..323	25-44	802-829	LINAP	g1352911	983	112	2.00E-35	41	38	NNFI intergenic region ; hypothetical protein YJR110w - yeast (Saccharomyces cerevisiae) ; (Z49610) ORF YJR110w [Saccharomyces cerevisiae]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database	Hit ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
22978	ENU06772	ANI61C1147	22-47	809-829	LINAP	g1708195	190	66	5.00E-11				HFM1 protein ; (U22156) Hfm1p [Saccharomyces cerevisiae]
22979	ENU06773	ANI61C1081	22-47	805-829	LINAP	g538067	461	141	6.00E-33	34	18		(M77661) putative pol polyprotein [Magnaporthe grisea]
22980	ENU06774	ANI61C1035	22-46	805-824	LINAP	g1723769	247	55	0.000000	5			putative transporter YGR260W ; probable membrane protein YGR260W - yeast (Saccharomyces cerevisiae) ; (Z73044) ORF YGR260w [Saccharomyces cerevisiae] ; (Y07777) YGR260w ORF [Saccharomyces cerevisiae]
22981	ENU06775	ANI61C1081	22-41	495-518	LINAP	g127060	184	77	4.00E-24	40	92		zinc finger protein MFG-1 (zinc finger protein 58) ; finger protein mfg1 - mouse (fragment) ; (M28513) zinc finger protein mfg1 mRNA (put.) ; putative [Mus musculus] elongation factor 3B (EF-3B) ; probable membrane protein YNL014w - yeast (Saccharomyces cerevisiae) ; (Z71290) ORF YNL014w [Saccharomyces cerevisiae]
22982	ENU06776	ANI61C1034	22-46	779-806	LINAP	g1706591	412	175	3.00E-43	48	23		[fatty acid synthase, subunit alpha [contains: EC 1.1.1.100; EC 2.3.1.41]; fatty-acid synthase (EC 2.3.1.85) alpha chain - yeast (Candida albicans); (L29063) fatty acid synthase alpha subunit [Candida albicans]" ; (A011849) fengycin synthetase [Bacillus subtilis]]
22983	ENU06777	ANI61C1030	43-62	807-826	LINAP	g1169645	227	32	5.3				(AF000149) ATP-binding cassette transporter [Mus musculus] (AL033389) putative antioxidant protein [Schizosaccharomyces pombe] ; sepB protein - Emericella nidulans ; sepB protein - Emericella nidulans ; (X86399) sepB [Emericella nidulans]
			8:2197..1015										
22984	ENU06778	ANI61C5932:	22-41	771-791	LINAP	g3724089	212	58	4.00E-16	35	8		
22985	ENU06779	ANI61C5994:	22-46	798-825	LINAP	g2547314	466	192	3.00E-48	40	12		(AF000149) ATP-binding cassette transporter [Mus musculus] (AL033389) putative antioxidant protein [Schizosaccharomyces pombe] ; sepB protein - Emericella nidulans ; sepB protein - Emericella nidulans ; (X86399) sepB [Emericella nidulans]
22986	ENU06780	ANI61C5187:	22-44	454-477	LINAP	g3850080	120	58	3.00E-14				
22987	ENU06781	ANI61C1148	25-46	737-755	LINAP	g1078634	2239	323	e-127	97	35		
			5:319..1797										

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	Score	Score	Prob	% id	% cvrg	Description
22988	ENU06782	ANI61C6060:	58-83	482-501	LINAP	g549628	413	171	4.00E-43	57	90		MET1 intergenic region ; hypothetical protein YKR068c - yeast
			1366..2025										(Saccharomyces cerevisiae) ; (Z28293) ORF YKR068c [Saccharomyces cerevisiae]
22989	ENU06783	ANI61C1080	53-72	807-829	LINAP	g125727	533	90	8.00E-35				
		7:3996..5261											killer toxin alpha and beta subunits precursor (RF2 protein) (endochitinase ; RF2 protein - yeast (Kluyveromyces marxianus var. lactis) plasmid k1 ; (X07127) RF2 gene product (AA 1-1146) [Kluyveromyces lactis] ; (X00762) ORF2 (put. killer toxin large subunit) [Kluyveromyces lactis] ; (X01095) URFP2 (put. 97 kd glycoprotein 31 kd subunit precursor of the killer toxin ; aa 1-1146) [Kluyveromyces lactis]
22990	ENU06784	ANI61C6076:	27-46	802-829	LINAP	g3560253	470	139	7.00E-37	50	39		(AL031532) sap2 family putative cell cycle dependent phosphatase associated protein [Schizosaccharomyces pombe] (AJ224865) IgE-binding protein [Aspergillus fumigatus]
22991	ENU06785	ANI61C1148	22-47	423-448	LINAP	g2980819	135	88	5.00E-17				[Aspergillus fumigatus] alpha-glucosidase precursor (maltase) ; (D45356) alpha-glucosidase [Aspergillus niger]
22992	ENU06786	ANI61C8728:	29-51	805-827	LINAP	g3023267	950	209	8.00E-58	45	26		(Y12527) HMWP1 protein [Yersinia enterocolitica]
22993	ENU06787	ANI61C6090:	63-80	308-327	LINAP	g2765195	79	58	0.000000				(AF030886) telomere-associated recQ-like helicase [Ustilago maydis]
22994	ENU06788	ANI61C1163:	72-92	469-488	LINAP	g2642224	61	57	0.000000	26	16		HST1 protein (homologous TO SIR2 protein 1) ; HST1 protein - yeast (Saccharomyces cerevisiae) ; (L47120) homolog of SIR2; transcribed ORF flanked by NUF2 (X72225) and RTG1 (M97690) [Saccharomyces cerevisiae] ; (U39041) Hst1p [Saccharomyces cerevisiae] ; (Z74810) ORF YOL068c [Saccharomyces cerevisiae]
22995	ENU06789	ANI61C1084	49-67	766-785	LINAP	g1708325	638	137	9.00E-32	45	46		
		6:668..1854											

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	Score	Score	Blast Prob	% id	% cvrg	Description	
22996	ENU06790	ANI61C8729:			LINAP	g1731071	66	72	2.00E-12	30	35		hypothetical 47.0 KD protein in GLNQ-ANSR intergenic region ; (D84432) YqjH [Bacillus subtilis] ; (Z99116) similar to DNA-damage repair protein [Bacillus subtilis]	
22997	ENU06791	ANI61C5223: 2348..825	23-44	805-827	LINAP	g2394451	212	59	0.000000 04	31	18		(AF024496) contains similarity to Plasmodium falciparum glycophorin-binding protein homolog 2 (GB:X69769) [Caenorhabditis elegans] (AB02377) KIAA0379 [Homo sapiens]	
22998	ENU06792	ANI61C1086	97-117	432-451	LINAP	g2224699	117	80	1.00E-14	31	18		[Oncotocerca volvulus] (M74066) Major body wall myosin (AP000003) 348aa long hypothetical dehydrogenase [Pyrococcus horikoshii]	
22999	ENU06793	ANI61C1036	5:1658..1991	30-49	364-385	LINAP	g159893	80	52	0.000004				regulatory protein CYS3 ; regulatory protein cys-3 - Neurospora crassa ; (M26008) cys-3 [Neurospora crassa] (AL034563) putative yeast CF Ib (RNA3' Cleavage factor Ib) homolog; ribonucleoprotein
23000	ENU06794	ANI61C5213: 1108..1539			LINAP	g3257063	123	45	1.00E-10				[Schizosaccharomyces pombe] cell cycle protein kinase CDC5/MSD2; protein kinase CDC5 (EC 2.7.1.-) - yeast (Saccharomyces cerevisiae); (M84220) PKX2 protein kinase [Saccharomyces cerevisiae]; (Z48613) Cdc5p [Saccharomyces cerevisiae] (AJ011965) oxidoreductase [Claviceps purpurea]	
23001	ENU06795	ANI61C1085	6:2845..2191	22-48	593-620	LINAP	g118126	226	71	9.00E-12	33	91		[Schizosaccharomyces pombe] (AE001017) conserved hypothetical protein [Archaeoglobus fulgidus]
23002	ENU06796	ANI61C1034	9:3166..4194	44-64	797-816	LINAP	g4049514	642	153	2.00E-45	49	53		UV-endonuclease - Neurospora crassa
23003	ENU06797	ANI61C1178: 1625..2522	22-49	772-799	LINAP	g416768	438	203	1.00E-51	41	36			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit ncbi gi	Score	Score Prob	% id	% cvrg	Description
23009	ENU06803	ANI61C1037	22-49	805-824	LINAP	g2655202	1286	206	3.00E-70	56	[AF026402] U5 snRNP 100 kD protein [Homo sapiens]
23010	ENU06804	ANI61C9209:	22-44	522-541	LINAP	g3914934	129	99	2.00E-20		probable RNA 3'-terminal phosphate cyclase (RNA-3'-phosphate cyclase) (RNA cyclase) : (AP000006) 369aa long hypothetical phosphate cyclase [Pyrococcus horikoshii]
23011	ENU06805	ANI61C9263:	22-43	441-460	LINAP	g2414601	235	106	8.00E-23	43	[Z99295] phosphatidyl synthase [Schizosaccharomyces pombe]
23012	ENU06806	ANI61C5998:	135-158	484-503	LINAP	g3123165	372	167	7.00E-41	42	[X98253] zinc finger protein 183 ; (ZNF183 [Homo sapiens] ; [AC002477] zinc-finger protein [Homo sapiens] (AB004535) ATP-dependent RNA helicase MSS116 precursor
23013	ENU06807	ANI61C9250:	37-56	798-825	LINAP	g2257514	480	182	2.00E-45	39	[Schizosaccharomyces pombe]
23014	ENU06808	ANI61C8731:	59-78	807-829	LINAP	g1169823	219	109	2.00E-23	28	regulatory protein GAL4 ; regulatory protein GAL4 - yeast (Saccharomyces cerevisiae) ; (K01486) GAL4 protein [Saccharomyces cerevisiae] ; (Z67751) GAL4 [Saccharomyces cerevisiae] ; (Z73604) ORF YPL248c [Saccharomyces cerevisiae]
23015	ENU06809	ANI61C5930:	175-195	499-518	LINAP	g125935	56	45	0.0004	24	lactose permease ; lactose permease - yeast (Kluyveromyces marxianus var. lactis) ; (X06997) lactose permease (AA 1-587) [Kluyveromyces lactis] "succinyl-CoA ligase (GDP-forming), beta-chain precursor (succinyl-CoA synthetase, beta chain) (SCS-beta) ; beta-succinyl CoA synthetase - rumen fungus (Neocallimastix frontalis) ; (X84222) beta-succinyl CoA synthetase [Neocallimastix frontalis] " synthetase [Neocallimastix frontalis] " (U58946) transposase [Aspergillus awamori]
23016	ENU06810	ANI61C120:1	30-57	797-824	LINAP	g1711577	697	222	2.00E-68	53	[AL031764] putative FAD synthetase [Schizosaccharomyces pombe] (AL033534) serine-rich protein [Schizosaccharomyces pombe]
23017	ENU06811	ANI61C5930:	24-43	803-822	LINAP	g1805251	1122	289	1.00E-77	50	
23018	ENU06812	ANI61C5245:	3180..1803	452..1	LINAP	g3668151	111	59	0.000000	32	[Schizosaccharomyces pombe]
23019	ENU06813	ANI61C9251:	23-47	513-536	LINAP	g3873550	105	50	0.00002	28	[Schizosaccharomyces pombe]
			295..851								

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	Score	Score	% id	% cvrg	Description
23020	ENU06814	ANI61C8754:	23-48	783-810	LINAP	g138350	121	57	0.000000	1		X precursor - equine herpesvirus 1 (strain Ab4p) ; (M86664) membrane glycoprotein [Equine herpesvirus 1] (AJ223012) rifamycin polyketide synthase, type 1 [Amycolatopsis mediterranei] ; (AF040570) polyketide synthase [Amycolatopsis mediterranei]
23021	ENU06815	ANI61C6099:	22-46	575-602	LINAP	g2764761	51	34	0.0006	"		
23022	ENU06816	ANI61C1086	22-46	780-806	LINAP	g1353088	176	89	4.00E-17	32	69	hypothetical 36.4 KD protein in MOCC-MOCA intergenic region (ORF334) ; hypothetical protein 334 - Rhizobium meliloti ; (X78503) ORF334 [Sinorhizobium meliloti] putative amidase CY50_19C ; (Z77137) amiB2 [Mycobacterium tuberculosis] (Z70310) predicted using Genefinder; Similarity to Mouse ankyrin (PIR Acc. No. S37771); cDNA EST EMBL:T01923 comes from this gene; cDNA EST EMBL:D32335 comes from this gene; cDNA EST EMBL:D32723 comes from this gene; cDNA EST E... ; (Z70686) predicted using Genefinder; Similarity to Mouse ankyrin (PIR Acc. No. S37771); cDNA EST EMBL:T01923 comes from this gene; cDNA EST EMBL:D32335 comes from this gene; cDNA EST EMBL:D32723 comes from this gene; cDNA EST E...
23023	ENU06817	ANI61C1159:	27-46	616-640	LINAP	g1703266	249	109	2.00E-23	41	43	putative amidase CY50_19C ; (Z77137) amiB2 [Mycobacterium tuberculosis] (Z70310) predicted using Genefinder; Similarity to Mouse ankyrin (PIR Acc. No. S37771); cDNA EST EMBL:T01923 comes from this gene; cDNA EST EMBL:D32335 comes from this gene; cDNA EST EMBL:D32723 comes from this gene; cDNA EST E... ; (Z70686) predicted using Genefinder; Similarity to Mouse ankyrin (PIR Acc. No. S37771); cDNA EST EMBL:T01923 comes from this gene; cDNA EST EMBL:D32335 comes from this gene; cDNA EST EMBL:D32723 comes from this gene; cDNA EST E...
23024	ENU06818	ANI61C6067:	2562..1697		LINAP	g3879121	265	128	4.00E-29			
23025	ENU06819	ANI61C5243:	109-132	364-391	LINAP	g1711534	261	112	1.00E-24	47	37	succinate semialdehyde dehydrogenase (NAD(+)-dependent succinic semialdehyde dehydrogenase) ; succinate-semialdehyde dehydrogenase (EC 1.2.1.24) - human (fragment) ; (L34820) succinate semialdehyde dehydrogenase [Homo sapiens]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database	Hit ncbi gi	Score	Score	% id	% cvrg	Description	
23026	ENU06820	ANI61C1160:	22-45	663-690	LINAP	g119164	271	134	5.00E-31	40	48	elongation factor 1-gamma (EF-1-gamma) ; translation elongation factor eEF-1 gamma chain - brine shrimp ; (M28020) elongation factor 1-gamma [Artemia sp.]	
23027	ENU06821	ANI61C9253:	4863..4221		LINAP	g2494878	828	319	1.00E-89	90	55	guanine nucleotide-binding protein alpha subunit ; (U49917) FadA [Emeticella nidulans]	
23028	ENU06822	ANI61C8748:	22-45	654-679	LINAP	g1172741	337	111	1.00E-37	40	36	peptide transporter PTR2 ; (U09781) peptide transporter [Candida albicans] (AL035247) putative spindle pole body-associating protein	
23029	ENU06823	ANI61C9281:	48-67	769-789	LINAP	g4164426	403	159	2.00E-38	42	29	[Schizosaccharomyces pombe] transaldolase ; transaldolase (EC 2.2.1.2) - yeast (Saccharomyces cerevisiae) ; (U19102) Tal1p; Transaldolase [Saccharomyces cerevisiae]	
23030	ENU06824	ANI61C8743:	23-50	570-589	LINAP	g1729825	101	47	6.00E-10	31	57	[Schizosaccharomyces pombe] transaldolase ; transaldolase (EC 2.2.1.2) - yeast (Saccharomyces cerevisiae) ; (U19102) Tal1p; Transaldolase [Saccharomyces cerevisiae]	
23031	ENU06825	ANI61C5255:	1577..1250	22-46	451-478	LINAP	g1176486	114	80	1.00E-14	34	25	hypothetical 63.9 KD protein in IME2-MEF2 intergenic region ; protein YKR029c homolog YIL105w - yeast (Saccharomyces cerevisiae) ; (X85021) YKR029c homologue [Saccharomyces cerevisiae] ; (Z49380) ORF YIL105w [Saccharomyces cerevisiae] putative cytochrome P450 T10B9.5 in chromosome II ; (Z48717) similar to cytochrome P450 [Caenorhabditis elegans]
23032	ENU06826	ANI61C1084	7:693..1	22-45	572-592	LINAP	g2493399	74	77	1.00E-13			putative mitochondrial carrier YHR002W ; hypothetical protein YHR002W - yeast (Saccharomyces cerevisiae) ; (U10555) Yhr002wp [Saccharomyces cerevisiae]
23033	ENU06827	ANI61C9282:	533..1	22-43	449-468	LINAP	g731628	436	167	2.00E-44	59	44	

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	Score	Score Prob	% id	% cvrg	Description
23034	ENU06828	ANI61C8744:	39-58	803-822	LINAP	g1175977	738	185	3.00E-58	47	48	hypothetical 61.8 KD peptidase in MPR1-GCN20 intergenic region ; probable membrane protein YFR006w - yeast ( <i>Saccharomyces cerevisiae</i> ) ; (D50617) YFR006W [ <i>Saccharomyces cerevisiae</i> ]
23035	ENU06829	ANI61C6078:	23-43	446-473	LINAP	g284667	100	36	0.13			neurofilament triplet H1 protein - rabbit (fragment) ; (M94315) neurofilament-H [Oryctolagus cuniculus]
23036	ENU06830	ANI61C5244:	26-46	562-584	LINAP	g586937	171	34	0.66			zinc-finger protein 2 (zinc-finger homeodomain protein 2) ; homeotic protein zfh-2 - fruit fly ( <i>Drosophila melanogaster</i> ) ; (M63450) zinc-finger homeodomain protein 2 [ <i>Drosophila melanogaster</i> ]
23037	ENU06831	ANI61C1088	22-47	656-675	LINAP	g2492758	123	38	2.00E-10	34	66	probable short-chain type dehydrogenase/reductase VLDC
23038	ENU06832	ANI61C8753:	52-71	807-829	LINAP	g114967	244	71	2.00E-17	35	30	beta-glucosidase (gentiobiose cellobiase) (beta-D-glucoside glucohydrolase) : beta-glucosidase (EC 3.2.1.21) - Agrobacterium tumefaciens ; (M59852) beta-D-glucosidase [Agrobacterium tumefaciens] (AB025420) Family 19 chitinase (pRYA1 ORF) [ <i>Aeromonas</i> sp. 10S-24]
23039	ENU06833	ANI61C527:1	25-44	306-325	LINAP	g4587324	142	39	0.011			(D90908) hypothetical protein [Synechocystis sp.]
23040	ENU06834	ANI61C1187:	54-73	459-478	LINAP	g1652749	201	117	4.00E-26	45	65	(AL035076) putative carboxylesterase-lipase family member
23041	ENU06835	ANI61C1089	38-59	781-800	LINAP	g4107289	654	94	2.00E-18	32	47	[Schizosaccharomyces pombe] (D88802) ydhJ [ <i>Bacillus subtilis</i> ] ; (Z99107) similar to hypothetical proteins [ <i>Bacillus subtilis</i> ]
23042	ENU06836	ANI61C1090	22-47	464-483	LINAP	g1945094	145	48	0.00004	31	51	high-affinity glucose transporter ; (U22525) high affinity glucose transporter [ <i>Kluyveromyces lactis</i> ]
23043	ENU06837	ANI61C6147:	45-64	801-820	LINAP	g1346290	423	137	1.00E-31	33	45	
		1..1043										

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database	Hit ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
23044	ENU06838	ANI61C9285:	58-77	568-590	LINAP	g1082283	125	34	0.78				protein kinase (EC 2.7.1.37) cdc2-related PITSLRE alpha 2-1 - human
23045	ENU06839	ANI61C8762:	25-52	530-557	LINAP	g992626	64	49	0.00003	29	35	(X91243) XtpFibeta1 [Xenopus laevis]	
23046	ENU06840	ANI61C6148:	536..1492		LINAP	g3002558	72	57	0.000000	26	9	(AF026032) ATRX protein [Mus musculus]	
23047	ENU06841	ANI61C1210:	47-73	740-759	LINAP	g1730773	211	103	2.00E-21				hypothetical 73.8 KD protein in SPC98-TOM70 intergenic region ; probable membrane protein YNL125c-yeast [Saccharomyces cerevisiae]; (Z46843) orf23 [Saccharomyces cerevisiae] ; (Z69382) Identical to putative protein ESBP6 [Saccharomyces cerevisiae] ; (Z71401) ORF YNL125c [Saccharomyces cerevisiae]
23048	ENU06842	ANI61C9292:	23-50	480-506	LINAP	g1749536	235	103	8.00E-22	45	44	(D89164) unnamed protein product [Schizosaccharomyces pombe]	
23049	ENU06843	ANI61C8740:	64-83	459-478	LINAP	g123927	84	54	1.00E-12			"epoxide hydrolase (microsomal epoxide hydrolase) (epoxide hydratase) ; epoxide hydrolase (EC 3.3.2.3), microsomal - rabbit ; (M21496) microsomal epoxide hydrolase (EC 3.3.2.3) [Oryctolagus cuniculus]" (AC022294) Similar to transcription factor gb[Z46606]1658307 and others [Arabidopsis thaliana] "YI8350" U2 snRNP auxiliary factor, large subunit [Nicotiana plumbaginifolia]"	
23050	ENU06844	ANI61C6153:	1472..1033		LINAP	g2443387	166	61	0.000000	29	11		
23051	ENU06845	ANI61C5274:	53-74	528-549	LINAP	g3850821	247	33	1.8	45	26		
23052	ENU06846	ANI61C1214:	22-44	364-391	LINAP	g3283028	182	53	8.00E-17	40	30	(AF022435) odd-paired-like [Danio rerio]	
23053	ENU06847	ANI61C9286:	22-45	775-795	LINAP	g538067	718	270	7.00E-72	47	20	(M77661) putative pol polyprotein [Magnaporthe grisea]	
23054	ENU06848	ANI61C8761:	037..324		LINAP	g1805251	475	190	8.00E-48	42	42	(U58946) transposase [Aspergillus awamori]	

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	Score	Score Prob	% id	% cvrg	Description
23055	ENU06849	ANI61C526:1	25-45	662-689	LINAP	g3219917	167	89	3.00E-17	31	85	hypothetical 27.4 KD protein (Z97992) conserved hypothetical protein [Schizosaccharomyces pombe] Lipase (E.C.3.1.1.3) (Triacylglycerol Hydrolase); Lipase (E.C.3.1.1.3) (Triacylglycerol Hydrolase) (AB02377) KJAA0379 [Homo sapiens]
23056	ENU06850	ANI61C1092	0:1147..1	LINAP	g493955	223	71	1.00E-11	35	38	Lipase (E.C.3.1.1.3) (Triacylglycerol Hydrolase); Lipase (E.C.3.1.1.3) (Triacylglycerol Hydrolase)	
23057	ENU06851	ANI61C9299:	105-124	597-616	LINAP	g2224699	133	49	2.00E-13	32	23	(AB02377) KJAA0379 [Homo sapiens]
23058	ENU06852	ANI61C122:3	22-49	278-304	LINAP	g731739	188	92	1.00E-18	50	19	hypothetical 55.5 KD GTP-binding protein in CDC23-DBP8 intergenic region ; probable purine nucleotide-binding protein YHR168w - yeast (Saccharomyces cerevisiae); (U00027) Yhr168wp [Saccharomyces cerevisiae] (AL031154) hypothetical protein
23059	ENU06853	ANI61C8758:	22-47	807-827	LINAP	g3367789	530	109	2.00E-23	48	50	[Schizosaccharomyces pombe] (U13646) homeotic region most like HMPB_DROME; homeotic proboscipedia protein [Caenorhabditis elegans]
23060	ENU06854	ANI61C6155:	22-41	629-647	LINAP	g532113	77	41	0.01			
23061	ENU06855	ANI61C5259:	33-54	809-828	LINAP	g2133035	226	82	8.00E-30	36	51	probable membrane protein YPR157w - yeast (Saccharomyces cerevisiae); (U28371) P9584-4 gene product [Saccharomyces cerevisiae] (X89442) peptide synthetase [Metarhizium anisopliae] TOXD protein ; (X92391) unique to isolates that make the cyclic peptide HC-toxin [Cochliobolus carbonum] (AL021428) hypothetical protein Rv0063 [Mycobacterium tuberculosis] hypothetical 36.4 KD protein in MOCC-MOCA intergenic region (ORF334); hypothetical protein 334 - Rhizobium meliloti ; (X78503) ORF334 [Sinorhizobium meliloti]
23062	ENU06856	ANI61C9288:	27-53	801-828	LINAP	g2342601	408	101	9.00E-21	29	5	
23063	ENU06857	ANI61C8774:	22-48	272-291	LINAP	g1729996	69	54	0.000000	29	51	
23064	ENU06858	ANI61C6159:	54-73	477-494	LINAP	g2808720	152	55	0.000000	32	27	
23065	ENU06859	ANI61C5247:	30-50	454-476	LINAP	g1353088	151	75	5	3.00E-13	34	
			1364..936									

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database	Hit ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
23066	ENU008860	ANI61C1092	22-42	529-552	LINAP		g30233677	67	50	0.00001			probable translation initiation factor EIF-2B gamma subunit (EIF-2B GDP-GTP exchange factor) ; (Z98602)
			9:1120..1693										translation initiation factor eif-2b gamma subunit [Schizosaccharomyces pombe]

(AL022600) RNA helicase  
 [Schizosaccharomyces pombe]  
 D-3-phosphoglycerate dehydrogenase (PGDH) ; phosphoglycerate dehydrogenase  
 Methanococcus jannaschii ; (U67544)  
 phosphoglycerate dehydrogenase  
 (serA) [Methanococcus jannaschii]

Seq num	Seq id	Contig source	5 pos	3 pos	Basis	Primer	Primer	Selection
23069	ENU06863	ANT61C1091	22-47	419-439	LINAP	Database Hit	ncbi gi	aat
			5:3250.2860	g2780921	29	Score	Score	Blast
					41	Prob	0.004	Blast
					% id	cvrg	%	Description
								"Chain A, Cyclooxygenase-2)
								(Prostaglandin Synthase-2) Complexed
								With A Non-Selective Inhibitor,
								Flurbiprofen ; Chain B,
								Cyclooxygenase-2 (Prostaglandin
								Synthase-2) Complexed With A Non-
								Selective Inhibitor, Flurbiprofen ;
								Chain C, Cyclooxygenase-2)
								(Prostaglandin Synthase-2) Complexed
								With A Non-Selective Inhibitor,
								Flurbiprofen ; Chain D,
								Cyclooxygenase-2 (Prostaglandin
								Synthase-2) Complexed With A Non-
								Selective Inhibitor, Flurbiprofen ;
								Chain A, Cyclooxygenase-2
								(Prostaglandin Synthase-2) Complexed
								With A Non-Selective Inhibitor,
								Indomethacin ; Chain B,
								Cyclooxygenase-2 (Prostaglandin
								Synthase-2) Complexed With A Non-
								Selective Inhibitor, Indomethacin ;
								Chain C, Cyclooxygenase-2
								(Prostaglandin Synthase-2) Complexed
								With A Non-Selective Inhibitor,
								Indomethacin ; Chain D,
								Cyclooxygenase-2 (Prostaglandin
								Synthase-2) Complexed With A Non-
								Selective Inhibitor, Indomethacin ;
								Chain A, Uninhibited Mouse
								Cyclooxygenase-2 (Prostaglandin
								Synthase-2) ; Chain B, Uninhibited
								Mouse Cyclooxygenase-2
								(Prostaglandin Synthase-2) ; Chain C,
								Uninhibited Mouse Cyclooxygenase-2
								(Prostaglandin Synthase-2) ; Chain D,
								Uninhibited Mouse Cyclooxygenase-2
								(Prostaglandin Synthase-2) ; Chain A,
								Cyclooxygenase-2 (Prostaglandin
								Synthase-2) Complexed With A
								Selective Inhibitor, Sc-558 In I222
								Space Group ; Chain B,
								Cyclooxygenase-2 (Prostaglandin
								Synthase-2) Complexed With A
								Selective Inhibitor, Sc-558 In I222

Sed num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database	Hit	nebi gi	aat Score	Score Prob	% id	% cvrg	Description
23070	ENU06864	ANI61C9267:	22-47	416-435	LINAP		g1706177	147	48	0.00004	38	15	(U51672) cutinase transcription factor 1 beta ; cutinase
23071	ENU06865	ANI61C8784:	28-53	762-781	LINAP		g2781417	162	109	3.00E-23	25	15	(AF081920) polyketide synthase type I; PtC [Pseudomonas fluorescens]
23072	ENU06866	ANI61C6188:	93-113	678-700	LINAP	,	g4102999	440	168	3.00E-41	46	64	(AF019630) pathogenicity protein [Magnaporthe grisea]
23073	ENU06867	ANI61C5275:	40-59	756-783	LINAP	1687..3309	g1176583	924	162	3.00E-61	49	28	hypothetical 102.5 KD protein in KRE1-HXT14 intergenic region ; probable membrane protein YNL321w - yeast (Saccharomyces cerevisiae); (Z46259) NO339 [Saccharomyces cerevisiae] ; (Z71597) ORF YNL321w [Saccharomyces cerevisiae]
23074	ENU06868	ANI61C1191:	45-68	784-808	LINAP	1157..10509	g2832742	576	199	3.00E-50	42	59	(Z99163) similar to nitrogen permease regulator. [Schizosaccharomyces pombe]
23075	ENU06869	ANI61C8791:	22-48	331-352	LINAP	1038..702	g4455009	91	60	0.00000	01	1	(AF11179) G-septin alpha [Rattus norvegicus]
23076	ENU06870	ANI61C6183:	45-72	742-767	LINAP	1..1296	g3288709	997	139	2.00E-62	50	18	(AB010442) PMR1 [Penicillium digitatum]
23077	ENU06871	ANI61C1191:	22-48	730-749	LINAP	11790..13388	g586394	369	100	9.00E-23			hypothetical 98.1 KD TRP-ASP repeats containing protein in PAF1-MRPL27 intergenic region ; hypothetical protein YBR281c - yeast (Saccharomyces cerevisiae) ; (X76053) YBR2018-ORF [Saccharomyces cerevisiae] ; (Z36150) ORF YBR281c [Saccharomyces cerevisiae] ; ORF YBR2018-ORF [Saccharomyces cerevisiae]
23078	ENU06872	ANI61C8759:	52-71	779-798	LINAP	5302..4296	g1173638	301	144	7.00E-34	30	75	(U35779) 1-aminoacyclopropane-1-carboxylate synthase [Triticum aestivum]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit ncbi gi	Score	Score	% id	cvg	%	Description	
23079	ENU06873	ANi6IC5284:	82-101	712-732	LINAP	g1168817	847	136	1.00E-48	52	20	cell division control protein 7 ; protein kinase cdc7 - fission yeast	
			1696..245			(Schizosaccharomyces pombe); (X78799) cdc7 [Schizosaccharomyces pombe]; (AL035537) cell division control protein 7							
23080	ENU06874	ANi6IC1093:	61-87	587-614	LINAP	g1397341	85	44	7.00E-10	35	23	[Schizosaccharomyces pombe] (U61955) Similar to kinesin-like protein; coded for by C. elegans cDNA ykl184h5.3; coded for by C. elegans cDNA ykl184h5.5; coded for by C. elegans cDNA ykl13d7.3; coded for by C. elegans cDNA ykl13d7.5; coded for by C. elegans cDNA yk31e1.5; co...; (AF057567) kinesin-like protein ZEN-4a [Caenorhabditis elegans]	
23081	ENU06875	ANi6IC1212:	22-48	503-528	LINAP	g131653	62	45	0.000008			proline utilization trans-activator ; transcription activator PUT3 - yeast (Saccharomyces cerevisiae); (X55384) orf5; homologous to S.cerevisiae PUT3 gene [Saccharomyces cerevisiae]; (Z28015) ORF YKL015w	
23082	ENU06876	ANi6IC5251:	49-68	433-452	LINAP	g132172	108	63	0.000000 26	28		[Saccharomyces cerevisiae] PIM1 protein ; pim1 hypothetical protein - fission yeast	
23083	ENU06877	ANi6IC1095	6:243..861	22-47	565-584	LINAP	g2773363	85	52	0.000002 26	11		(Schizosaccharomyces pombe) (AF041382) microtubule binding protein D-CLIP-190 [Drosophila melanogaster] (AL049608) putative protein
23084	ENU06878	ANi6IC6137:	937..280	22-45	599-618	LINAP	g4584545	125	84	7.00E-16 35	55		[Arabidopsis thaliana] cell-cycle nuclear autoantigen SG2NA (SG2 nuclear antigen) ; nuclear autoantigen - human ; (U17989) GS2NA [Homo sapiens]
23085	ENU06879	ANi6IC2185:	438..805	71-90	455-476	LINAP	g3122872	177	65	3.00E-11 31	20		

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database	Hit ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
23086	ENU06880	ANI61C1239:	98-118	456-474	LINAP		g547902	89	35	0.37			putative mucin core protein precursor 24 (multi-glycosylated core protein 24) (MGC-24) (MUC-24) (CD164 antigen); core protein MGC-24 - human; (D14043) MGC-24 precursor [Homo sapiens]
23087	ENU06881	ANI61C2134:	24-51	506-529	LINAP		g559044	160	68	4.00E-11	26	27	(L29296) alpha-adducin [Homo sapiens]
23088	ENU06882	ANI61C8786:	22-48	609-629	LINAP		g559964	145	52	4.00E-15	40	68	(J05282) insect-type dehydrogenase [Pseudomonas cepacia]
23089	ENU06883	ANI61C6181:	22-49	803-828	LINAP		g2842510	423	96	2.00E-19	26	30	(AL021748) hypothetical protein [Schizosaccharomyces pombe]
23090	ENU06884	ANI61C5251:	24-45	741-765	LINAP		g1076802	106	64	0.000000	34	11	(Z34465) extensin-like protein - maize; extensin-like protein - maize; (Zea mays); extensin-like domain [Zea mays]
23091	ENU06885	ANI61C1216:	22-48	806-829	LINAP		g538067	2006	169	2.00E-41	38	19	(M77661) putative pol polyprotein [Magnaporthe grisea]
23092	ENU06886	ANI61C8786:	22-49	675-693	LINAP		g1709181	249	42	0.000000	36	40	"high affinity methionine permease"; methionine transport protein, high affinity - yeast (Saccharomyces cerevisiae); (U40316) high affinity methionine permease [Saccharomyces cerevisiae]; (Z72840) ORF YGR055w [Saccharomyces cerevisiae]"
23093	ENU06887	ANI61C1216:	28-47	804-829	LINAP		g2132868	160	34	1.4			probable membrane protein YOR053w - yeast (Saccharomyces cerevisiae); (Z74961) ORF YOR053w
23094	ENU06888	ANI61C1096	22-47	586-605	LINAP		g3319315	340	150	1.00E-35	38	26	[Saccharomyces cerevisiae]; (Z70678) YOR29-04 [Saccharomyces cerevisiae] (AF074951) cellobiose dehydrogenase [Thielavia heterothallica]
23095	ENU06889	ANI61C2160:	9:515..1175	102-126	447-474	LINAP	g117154	113	66	1.00E-10	34	23	cytochrome P450 3A2 (CYP3A2) (P450-PCN2); cytochrome P450 3A2-rat ; (M13646) cytochrome P450 [Rattus norvegicus]
23096	ENU06890	ANI61C9256:	23-42	805-829	LINAP		g1083855	340	96	2.00E-19	25	1	cyclosporin synthetase - Tolypocladium inflatum; (Z28383) cyclosporine synthetase [Tolypocladium inflatum]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	Score	Score Prob	% id	% cvrg	Description
23097	ENU06891	ANI61C877:	22-48	804-829	LINAP	g1491795	672	248	4.00E-65	47	28	"(U39812) beta-1,4-mannanase [Caldicellulosiruptor saccharolyticus]"
23098	ENU06892	ANI61C6218:	37-57	809-828	LINAP	g4522004	160	94	9.00E-19	31	38	"(AC007069) putative histidine kinase, sensory transduction [Arabidopsis thaliana]"
23099	ENU06893	ANI61C5291:	22-44	615-638	LINAP	g3850084	85	83	1.00E-15	37	62	(AL033389) alcohol dehydrogenase [Schizosaccharomyces pombe] [AF039713] Similar to phosphoglycerate mutase; coded for by C. elegans cDNA yk357d11.5; coded for by C. elegans cDNA yk387c10.5; coded for by C. elegans cDNA yk384f12.5; coded for by C. elegans cDNA cm10f9; coded for by C. elegans cDNA cm18g...
23100	ENU06894	ANI61C9272:	83-102	603-625	LINAP	g2773203	545	224	8.00E-61	51	43	(AB012696) DNA polymerase V [Schizosaccharomyces pombe]; (AL022305) DNA polymerase V [Schizosaccharomyces pombe] lipase-like enzyme - Alcaligenes eutrophus ; (L36817) lipase-like enzyme [Alcaligenes eutrophus] ; ORF 8 [Rastonia eutropha] "(U42580) 4 ankyrin repeats; similar to Drosophila melanogaster ankyrin, encoded by GenBank Accession Number L35601 [Paramaecium bursaria Chlorella virus 1]" (AC005167) unknown protein [Arabidopsis thaliana]
23101	ENU06895	ANI61C8802:	22-46	793-812	LINAP	g3395351	350	79	3.00E-14	29	25	(U62933) multidrug resistance protein 1 [Aspergillus fumigatus] ; (U62934) multidrug resistance protein 1 [Aspergillus fumigatus] White collar 1 protein (WC1); (X94300) wc-1 [Neurospora crassa] (AL049495) hypothetical protein [Schizosaccharomyces pombe]
23102	ENU06896	ANI61C5300:	22-41	453-473	LINAP	g2120949	87	77	9.00E-14	37	28	
23103	ENU06897	ANI61C1095	72-95	376-400	LINAP	g1181493	97	61	0.000000	33	21	
23104	ENU06898	ANI61C219:1	22-48	595-615	LINAP	g3757521	302	121	4.00E-27	40	17	
23105	ENU06899	ANI61C9301:	23-46	414-432	LINAP	g2673951	172	50	4.00E-14	31	11	
23106	ENU06900	ANI61C8766:	34-53	802-821	LINAP	g2494692	999	118	6.00E-26	36	22	
23107	ENU06901	ANI61C219:3	22-47	781-800	LINAP	g4539260	123	53	0.000003			

Seq num	Seq id	Contig source	Primer 3 pos	Primer Basis	Selection	Database Hit	ncbi gi	aat	Blast Score	Blast Prob	% id	% cvrg	Description
23108	ENU06902	ANI61C8806:	29-50	444..463	LINAP	g1723291	489	150	6.00E-36	47	69		C13D6.03C in chromosome I; (Z69725) unknown
23109	ENU06903	ANI61C625:6	39-58	626..643	LINAP	g464347	135	82	3.00E-15	29	17		[Schizosaccharomyces pombe] peroxisome biosynthesis protein PASS (peroxin-6); (Z22556) PASS [Pichia pastoris]
23110	ENU06904	ANI61C5296:	53-80	724..746	LINAP	g2094857	599	108	5.00E-23	42	32		[Schizosaccharomyces pombe] (AL033514) similar to ABC transporters ; ABC transporter
23111	ENU06905	ANI61C1098:	22-44	627..649	LINAP	g3980042	135	85	6.00E-16				transmembrane region. [Caenorhabditis elegans] (AC05275) predicted protein of unknown function [Arabidopsis thaliana]
23112	ENU06906	ANI61C8822:	31-50	778..804	LINAP	g4262148	772	190	1.00E-47	40	35		[Schizosaccharomyces pombe] putative sterigmatocystin biosynthesis monooxygenase STCW ; (U34740) putative FAD-containing monooxygenase [Emericella nidulans]
23113	ENU06907	ANI61C6255:	143-170	592..612	LINAP	g2388993	392	98	1.00E-35	49	10		hypothetical 126.9 KD protein C22G7.04 in chromosome I; hypothetical protein SPAC22G7.04 - fission yeast (Schizosaccharomyces pombe) ; (Z54328) putative poly(a)- specific ribonuclease subunit [Schizosaccharomyces pombe] fibrillarin (nucleolar protein 1) ; nucleolar protein NOP1 - yeast (Saccharomyces cerevisiae) ; (I05230) fibrillarin [Saccharomyces cerevisiae] ; (Z48432) nucleolar protein NOP1 (J05230) [Saccharomyces cerevisiae] ; (Z74062) ORF YDL014w [Saccharomyces cerevisiae] ; (D85895) diacylglycerol lipase [Aspergillus oryzae]
23117	ENU06911	ANI61C5311:	1889..2799	977..99	LINAP	g1772352	181	106	1.00E-22	34	52		

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat	Blast Score	Blast Prob	% id	% evrg	Description
23118	ENU06912	ANI61C1099	107-132	254-273	LNAP	g3122326	90	59	0.000000	43	17	LEC14B	protein [Lithospermum erythrorhizon]
23119	ENU06913	ANI61C8817:	5:1443..1117	41-60	454-473	LNAP	85			29			
23120	ENU06914	ANI61C1099:	1268..1617	34-53	731-755	LNAP	g1175399	288	89	4.00E-17			
			2673..422										
23121	ENU06915	ANI61C930:1	033..2253	29-51	796-815	LNAP	g84154078	472	98	9.00E-30	37	29	hypothetical 180.2 KD protein C31A2.05C in chromosome I;
23122	ENU06916	ANI61C6811:	812..364	122-142	427-446	LNAP	g1171755	279	82	3.00E-23	54	36	hypothetical protein SPAC31A2.05c - fission yeast (Schizosaccharomyces pombe); (Z50113) unknown [Schizosaccharomyces pombe] ; (AB016866) Mis4 [Schizosaccharomyces pombe] (AL035161) putative efflux protein [Streptomyces coelicolor]
23123	ENU06917	ANI61C2244:	684..1034	22-41	460-479	LNAP	g549706	183	68	4.00E-11	38	35	"neutral protease II precursor (deuterolysin) (NPII) ; neutral proteinase II - Aspergillus oryzae; (S53810) neutral protease II, NPII [Aspergillus oryzae, Peptide, 352 aa] [Aspergillus oryzae] ; neutral protease II [Aspergillus oryzae]" KTI12 protein ; KTI12 protein - yeast (Saccharomyces cerevisiae); (Z228110) ORF YKL110c [Saccharomyces cerevisiae]; (X77511) KTI12 [Saccharomyces cerevisiae]
23124	ENU06918	ANI61C6808:	1232..232	22-45	613-633	LNAP	g3559998	312	116	2.00E-27	37	62	[Saccharomyces cerevisiae] (AL031515) hypothetical protein SC5C7.08 [Streptomyces coelicolor] (AF016585) polyketide synthase module 3 [Streptomyces caelestis] hypothetical 84.5 KD protein C24H6.09 in chromosome I ; hypothetical protein SPAC24H6.09 - fission yeast (Schizosaccharomyces pombe); (Z54142) putative guanine nucleotide exchange factor [Schizosaccharomyces pombe]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	Score	Score	Prob	% id	% cvrg	Description
23127	ENU06921	ANTI6IC6265:	50-69	693-712	LINAP	g2275336	263	44	0.001				(AF001978) differentially expressed in relation to the extent of cell elongation [Candida albicans]
23128	ENU06922	ANTI6IC931:1	102-125	552-573	LINAP	g4490644	155	66	2.00E-10	36	18		"(Z98762) SPAC4A8.06c, unknown, len:578aa, some similarity e.g. to BAH_STRHY, Q01109, acetyl-hydrolase, (299aa), fasta score, opt:259, E:0.8; 2e-17, (35.6% identity in 118 aa overl ap) [Schizosaccharomyces pombe]" (U34807) extracellular lipase [Candida albicans]
23129	ENU06923	ANTI6IC8833:	22-42	810-829	LINAP	g4096660	376	104	1.00E-27				
		1833...609				g2257504	171	90	1.00E-17	37	39		(AB004535) similar to S.pombe unknown protein : DDBJ ACC# D89156 [Schizosaccharomyces pombe] (UT2998) EpmM [Borrelia burgdorferi]
23130	ENU06924	ANTI6IC6788:	22-49	451-478	LINAP	g2627268	71	36	0.35	28	57		
		3962..4460				g3367791	149	65	4.00E-10	31	26		(AL031154) hypothetical protein [Schizosaccharomyces pombe] (Y10491) putative cytochrome P450 [Glycine max]
23131	ENU06925	ANTI6IC6269:	35-54	810-829	LINAP	g3334663	59	38	0.00003	31	21		(AF0059442) putative polyprotein of LTR transposon [Arabidopsis thaliana] (AF016449) Similar to cytochrome P450 [Caenorhabditis elegans]
23132	ENU06926	ANTI6IC1209:	23-47	428-455	LINAP	g3924609	91	34	0.38				
		7140..6797				g2315475	59	52	0.000002				regulatory protein MSR1 - yeast (Saccharomyces cerevisiae); (Z68329) unknown [Saccharomyces cerevisiae]; (Z70202) unknown [Saccharomyces cerevisiae]
23133	ENU06927	ANTI6IC9291:	48-67	608-627	LINAP	g2133082	128	79	3.00E-14	38	29		
		1..1100											
23134	ENU06928	ANTI6IC6814:	67-86	299-320	LINAP								
		1..341											
23135	ENU06929	ANTI6IC6274:	22-44	420-439	LINAP								
		607..1048											
23136	ENU06930	ANTI6IC1259:	967..385		LINAP								
23137	ENU06931	ANTI6IC1098	22-49	559-580	LINAP	g2271503	156	45	0.0006	26	51		
		1:5200..5803											
23138	ENU06932	ANTI6IC9265:	122-144	657-680	LINAP	g3650376	283	122	3.00E-27	37	24		(AL031740) dna ligase protein [Schizosaccharomyces pombe]
		11512..10812				g1825739	123	39	0.016	24	59		(U88309) T23B3.5 gene product [Caenorhabditis elegans]
23139	ENU06933	ANTI6IC8847:	22-47	452-479	LINAP								
		740..1109											

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit ncbi gi	aat Score	Blast Prob	Blast % id	% cvrg	Description		
23140	ENU06934	ANI61C5355:	105-124	648-666	LINAP	g2257531	155	68	4.00E-19	34	15	[Schizosaccharomyces pombe]; (AL022072) web1 homolog; protein transport protein; WD-repeat protein [Schizosaccharomyces pombe]	
23141	ENU06935	ANI61C1208:	25-43	452-472	LINAP	g3123302	150	81	6.00E-15	31	24	hypothetical 75.1 KD protein C22E12.19 in chromosome I	
23142	ENU06936	ANI61C6833:	22-48	433-452	LINAP	g1351664	310	78	9.00E-24	43	28	hypothetical 59.0 KD protein C30D11.14 in chromosome I; hypothetical protein SPAC30D11.14 - fission yeast (Schizosaccharomyces pombe); (Z67961) hypothetical protein [Schizosaccharomyces pombe]	
23143	ENU06937	ANI61C6224:	22-48	802-829	LINAP	g1168457	782	130	1.00E-29	29	15	Ankyrin ; ankyrin - mouse ; (M84756)	
23144	ENU06938	ANI61C2250:	4438..6280	315..754	LINAP	g1172906	165	60	7.00E-11	31	24	cell division cycle related-protein RES2/PCT1 ; cell cycle regulator res2 - fission yeast (Schizosaccharomyces pombe) ; RES2 protein - fission yeast (Schizosaccharomyces pombe) ; (D17761) cell cycle regulator Res2 [Schizosaccharomyces pombe] ; (Z54285) Res2 [Schizosaccharomyces pombe]	
23145	ENU06939	ANI61C932:8	44-63	682-701	LINAP	g731024	711	259	2.00E-68	62	59	"branched-chain amino acid aminotransferase, mitochondrial precursor (BCAT) (TWT1 protein); TWT1 protein - yeast (Saccharomyces cerevisiae) ; (U00029) Bat1P: Branched-Chain Amino Acid Transaminase [Saccharomyces cerevisiae] ; (X78961) TWT1 [Saccharomyces cerevisiae]" (Z95620) putative ribose-phosphate pyrophosphokinase	
23146	ENU06940	ANI61C628:3	106-128	444-471	LINAP	g2117302	710	173	7.00E-43	49	48	[Saccharomyces pombe] (D89176) unnamed protein product [Schizosaccharomyces pombe]	
23147	ENU06941	ANI61C5335:	905..2028	22-46	799-818	LINAP	g1749560	134	41	0.00003			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	Score	Score	Prob	% id	cvg	%	Description
23148	ENU06942	ANI61C1273:	69-88	260-282	LINAP	g547991	62	57	0.00000	25	35	NA(+)/H(+) antiporter ; Na+/H+-exchanging protein - fission yeast		
			1086..712											(Schizosaccharomyces pombe); (Z11736) putative sodium/proton antiporter [Schizosaccharomyces pombe]
23149	ENU06943	ANI61C1100:	22-48	481-500	LINAP	g2497628	114	65	4.00E-10	38	62	microsomal SIGNAL peptidase 21.3 KD subunit; probable membrane protein YLR066w - yeast		
			2655..3211											(Saccharomyces cerevisiae); (X94607) L2186 [Saccharomyces cerevisiae]; (Z73238) ORF YLR066w [Saccharomyces cerevisiae]; (U92975) signal peptidase subunit [Saccharomyces cerevisiae]
23150	ENU06944	ANI61C2231:	22-40	502-521	LINAP	g2462679	56	58	0.000000	25	22	(Z99568) putative regulatory protein; zinc finger [Schizosaccharomyces pombe]		
			637..1			g1711351	585	83	2.00E-15					SCY1 protein ; SCY1 protein - yeast (Saccharomyces cerevisiae); (X97305) suppressor of GTPase mutant [Saccharomyces cerevisiae]; (Z72605) ORF YGL083w [Saccharomyces cerevisiae]
23151	ENU06945	ANI61C932:1	33-52	762-783	LINAP	g1711351	585	83	2.00E-15					hypothetical 147.4 KD protein C12C2.02C in chromosome II; (Z54140) conserved hypothetical protein [Schizosaccharomyces pombe]; (AJ223984) Ste20 protein
			682..3727			g1175418	1174	229	2.00E-59	43	21			[Schizosaccharomyces pombe] 50S ribosomal protein L1 ; (M94319) ribosomal protein L1 [Citrus greening disease-associated bacterium-like organism]; ribosomal protein L1 [Citrus greening disease-associated bacterium] (Y11520) vanillin dehydrogenase [Pseudomonas sp.]
23153	ENU06947	ANI61C6256:	28-47	590-609	LINAP	g548757	202	106	2.00E-22	33	83			
			4907..4259											
23154	ENU06948	ANI61C1100	22-45	773-800	LINAP	g1946288	442	200	9.00E-51	46	55			
			7:1209..2066											

Seq num	Seq id	Contig source	5 pos	Primer 3 pos	Primer Basis	Selection Database Hit	aat ncbi gi	Blast Score	Blast Prob	% id	% cvrg	Description
23155	ENU06949	ANI61C2241:	33-51	808..827	LINAP	g131777	746	247	2.00E-77	53	25	DNA repair protein RAD13 ; excision repair protein - fission yeast
23156	ENU06950	ANI61C9340:	30-57	446-473	LINAP	g117090	259	80	9.00E-25			(Schizosaccharomyces pombe) ; (X66795) excision repair protein [Schizosaccharomyces pombe]
		1050..1515										cytochrome C oxidase polypeptide IV precursor ; cytochrome-c oxidase (EC 1.9.3.1) chain IV precursor - yeast (Saccharomyces cerevisiae) ; (X01418) cytochrome c oxidase subunit IV precursor [Saccharomyces cerevisiae] ; (X91489) cytochrome C oxidase chain IV precursor [Saccharomyces cerevisiae] ; (Z72709) ORF YGL187c [Saccharomyces cerevisiae]
23157	ENU06951	ANI61C8861:	22-45	548-575	LINAP	g417762	227	114	5.00E-25	30	18	exocyst complex component SEC8 ; SEC8 protein - yeast (Saccharomyces cerevisiae) ; (X64693) SEC8 [Saccharomyces cerevisiae] ; (Z49219) Sec8p [Saccharomyces cerevisiae] ; (Z71255) Sec8p [Saccharomyces cerevisiae]
		2192..2787				g4107287	474	83	6.00E-24			(AL035076) putative allantoin permease [Schizosaccharomyces pombe] (AF030027) 71 [Equine herpesvirus 4]
23158	ENU06952	ANI61C1098	56-75	780-799	LINAP	g2606019	84	38	0.061			nitrogen assimilation transcription factor NIRA ; nitrate assimilation regulatory protein nirA - Emericella nidulans ; (M68900) NIR A protein [Emericella nidulans]
23159	ENU06953	ANI61C2241:	40-59	429-448	LINAP	g128340	262	120	1.00E-26	30	29	6-hydroxy-D-nicotine oxidase [Athrobacter oxidans]
23160	ENU06954	ANI61C1098	44-63	771-790	LINAP	g448109	160	82	6.00E-15	33	34	probable membrane protein YLR020c-yeast (Saccharomyces cerevisiae) ; (Z73192) ORF YLR020c [Saccharomyces cerevisiae]
23161	ENU06955	ANI61C8867:	22-41	675-694	LINAP	g2132661	378	180	1.00E-44	42	45	
23162	ENU06956	ANI61C1230:	32-51	636-655	LINAP	7214..8025						

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	Score	Score	Prob	% id	% cvrg	Description	
23163	ENU06957	ANI61C6860:	31-50	720-746	LINAP	g464912	1190	256	1.00E-68	47	19		helicase SGS1 (helicase TPS1); DNA helicase TPS1 - yeast (Saccharomyces cerevisiae); (L07870) bps. 390..881 = homology to E.coli recQ; bps. 414..430 = ATP binding site [Saccharomyces cerevisiae]; (Z47815) Tps1p [Saccharomyces cerevisiae]; (U22341) Sgs1p [Saccharomyces cerevisiae] (AF042799) suppressor of white apricot homolog 2 [Mus musculus] (AL031013) putative secreted protein [Streptomyces coelicolor]	
23164	ENU06958	ANI61C9827:	41-60	810-829	LINAP	g3941324	65	38	0.092					
23165	ENU06959	ANI61C9347:	33-54	633-659	LINAP	g3288616	100	53	0.000001					
23166	ENU06960	ANI61C6815:	22-48	448-475	LINAP	g1176967	105	42	0.000000	30	43		hypothetical 37.6 KD protein in GNTR-HTPG intergenic region; (AB005554) see SWISS_PROT ACC#: P42106 [Bacillus subtilis]; (Z99124) yxaG [Bacillus subtilis] (Z99113) polyketide synthase [Bacillus subtilis]	
23167	ENU06961	ANI61C9346:	1850..1301		LINAP	g2634103	157	80	1.00E-14	29	4			
23168	ENU06962	ANI61C2233:	22-46	767-790	LINAP	g1706177	322	109	3.00E-23	32	27		cutinase transcription factor 1 beta; (U51672) cutinase transcription factor 1 [Fusarium solani f. sp. pisi]	
23169	ENU06963	ANI61C8870:	22-42	455-479	LINAP	g3183529	60	64	6.00E-10				interleukin enhancer-binding factor 1 (cellular transcription-factor ILF-1); (U58196) interleukin enhancer binding factor 1 [Homo sapiens]	
23170	ENU06964	ANI61C6839:	22-43	378-398	LINAP	g3287948	152	82	2.00E-15	34	32		hypothetical 44.8 KD protein C57A10.01 in chromosome I	
23171	ENU06965	ANI61C6278:	41-60	781-800	LINAP	g228213	2404	265	4.00E-70	56	16		GAM1 gene [Saccharomyces cerevisiae]	
23172	ENU06966	ANI61C2238:	1..1351	29-54	767-786	LINAP	g1077569	996	255	2.00E-67	47	39		probable membrane protein YDR109c - yeast (Saccharomyces cerevisiae); (Z48758) unknown [Saccharomyces cerevisiae]
23173	ENU06967	ANI61C9335:	24-47	437-456	LINAP	g1001338	62	63	0.000000	001			(D64006) Ap-4-A phosphorylase II [Synechocystis sp.]	
			2550..2129											

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit ncbi gi	aat Score	Blast Prob	% id	cvg	%
23174	ENU06968	ANI61C6798:	23-42	802-829	LINAP	g1708909	356	62	1.00E-19	27	56
23175	ENU06969	ANI61C1229:	50-69	460-479	LINAP	g2146829	173	91	5.00E-18	43	54
		9252..8767									
23176	ENU06970	ANI61C9328:	28-47	776-794	LINAP	g2342601	1390	166	1.00E-40	35	5
		3897..405									
23177	ENU06971	ANI61C6798:	22-44	453-479	LINAP	g4160354	125	69	1.00E-11	47	28
		9347..9688									
23178	ENU06972	ANI61C2212:			LINAP	g3549891	170	75	7.00E-17	33	34
		5316..5983									
23179	ENU06973	ANI61C9349:	24-51	787-809	LINAP	g2144467	1068	159	1.00E-54	44	42
		1842..294									
23180	ENU06974	ANI61C6835:	158-179	476-499	LINAP	g3395590	193	90	1.00E-17	37	56
		7388..6866									
23181	ENU06975	ANI61C6308:	48-67	527-549	LINAP	g3702642	398	98	7.00E-42	56	41
		570..1									
23182	ENU06976	ANI61C1322:	22-42	777-797	LINAP	g125731	162	75	1.00E-16	30	32
		407..1279									
23183	ENU06977	ANI61C2259:	36-55	442-467	LINAP	g3123282	98	56	0.000000	20	7
		1529..1856									
23184	ENU06978	ANI61C9795:	22-49	804-829	LINAP	g4589488	54	75	9.00E-13	24	11
		9306..10624									
		[Homo sapiens]									

Seq num	Seq id	Contig source	Primer 3 pos	Primer Basis	Selection Database Hit	aat ncbi gi	blast Score	blast Prob	% id	% cvrg	Description
23185	ENU06979	ANI61C8832:	22-46	795-822	LINAP	g3122656	1264	161	2.00E-61	57	50 (glutamine phosphoribosylpyrophosphate amidotransferase) (ATASE); (U32992)
23186	ENU06980	ANI61C5401:	22-48	380-398	LINAP	g1438949	60	53	0.000001		glutamine phosphoribosylpyrophosphate amidotransferase [Saccharomyces kuyveri] (U61841) cutinase G-box binding protein [Fusarium solani f. sp. pisi] "AJ223012" rifamycin polyketide synthase, type 1 [Amycolatopsis mediterranei]; (AF040570) polyketide synthase [Amycolatopsis mediterranei]"
23187	ENU06981	ANI61C227:1	22-48	806-825	LINAP	g2764761	171	104	6.00E-22	30	5 synthase, type 1 [Amycolatopsis mediterranei]; (AF040570) polyketide synthase [Amycolatopsis mediterranei]"
23188	ENU06982	ANI61C8882:	22-43	736-761	LINAP	g2497111	304	123	2.00E-27	30	35 hypothetical 84.6 KD protein in GLO1-YPT7 intergenic region ; probable membrane protein YML002w - yeast
23189	ENU06983	ANI61C5382:	22-45	476-495	LINAP	g2494239	241	100	3.00E-24	37	52 (Saccharomyces cerevisiae) probable peroxisomal enoyl-CoA hydratase ; peroxisomal enoyl hydratase-like protein - rat ; (U08976) peroxisomal enoyl hydratase-like protein [Rattus norvegicus] (AL049559) putative short-chain dehydrogenase [Schizosaccharomyces pombe]
23190	ENU06984	ANI61C2257:	22-43	434-453	LINAP	g4581525	170	75	4.00E-13	34	27 cell division control protein 7 ; protein kinase cdc7 - fission yeast (Schizosaccharomyces pombe); (X78799) cdc7 [Schizosaccharomyces pombe]; (AL035537) cell division control protein 7
23191	ENU06985	ANI61C8894:	22-44	794-817	LINAP	g1168817	418	143	6.00E-35	37	24 [Schizosaccharomyces pombe]"SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 5 ; (AB010882) hSNF2H [Homo sapiens]"
23192	ENU06986	ANI61C6882:	36-60	587-610	LINAP	g4507075	250	122	2.00E-27	40	17 "SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 5 ; (AB010882) hSNF2H [Homo sapiens]"

Sed num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database	Hit ncbi gi	Score	Score Prob	% id	% cvrg	Description	
23193	ENU06987	ANI61C5397:	22-46	414-434	LINAP		g2499778	176	41	0.007		cell binding factor 2 precursor (antigen PEB4A) ; cell binding factor 2 - Campylobacter jejuni ; (X84703) cell binding factor 2 [Campylobacter jejuni]	
23194	ENU06988	ANI61C1337:	24-43	565-585	LINAP		g3122986	160	110	1.00E-23	33	42	beta-TRCP (beta-transducin repeat-containing protein) (BTRCP) ; beta-transducin repeat-containing protein - African clawed frog ; (M98268) beta-TRCP [Xenopus laevis] ; (AE000314) of, hypothetical protein [Escherichia coli]
23195	ENU06989	ANI61C5418:	24-45	443-466	LINAP		g1788578	90	63	0.000000	001		
23196	ENU06990	ANI61C1329:	34-53	810-829	LINAP		g2499839	331	94	2.00E-18			thyroid receptor interacting protein 12 (TRIP12) (KIAA0045) ; (D28476) KIAA0045 [Homo sapiens]
23197	ENU06991	ANI61C2215:	31-50	777-796	LINAP		g3183326	351	151	5.00E-36	31	31	hypothetical 93.2 KD TRP-ASP repeats containing protein C4F8.11 in chromosome I ; (Z98530) beta-transducin [Schizosaccharomyces pombe]
23198	ENU06992	ANI61C1330:	22-45	782-801	LINAP		g2656001	294	109	2.00E-23	35	31	(Z98977) hypothetical protein [Schizosaccharomyces pombe]
23199	ENU06993	ANI61C8878:	25-45	559-586	LINAP		g2132218	263	139	2.00E-32	42	32	hypothetical protein YPL169c - yeast (Saccharomyces cerevisiae) ; (Z73525) ORF YPL169c [Saccharomyces cerevisiae] ; (X96770) P2520 protein [Saccharomyces cerevisiae]
23200	ENU06994	ANI61C539:2	64-83	542-567	LINAP		g3915438	151	89	2.00E-17	31	62	hypothetical protein C10D6.08 in chromosome 1 ; (Z98951) hypothetical protein [Schizosaccharomyces pombe] (Z97337) hypothetical protein [Arabidopsis thaliana]
23201	ENU06995	ANI61C1360:	66-93	776-795	LINAP		g2244866	215	80	6.00E-23	35	13	(U53189) Os-1p [Neurospora crassa]
23202	ENU06996	ANI61C538:8	22-45	758-781	LINAP		g1354473	2931	180	2.00E-90	67	21	hypothetical protein YPL051w - yeast (Saccharomyces cerevisiae) ; (U39205) Lpe21p [Saccharomyces cerevisiae] ; (AF017142) ADP-ribosylation factor-like protein 1 [Saccharomyces cerevisiae]